SUPPORTING INFORMATION

SUPPORTING TEXT

***Phylogenetic binning of microbiome scaffolds* -** Microbiome scaffolds were binned with PhyloPythia, a phylogenetic classifier which uses a multi-class Support Vector machine (SVM) for the composition-based characterization of sequence fragments at different taxonomic ranks (1). Generic models for the taxonomic ranks of domain, phylum and class were combined with models for 15 genera and 14 family-level clades in the sample. The generic models represent all clades covered by three or more species at the corresponding ranks among all sequenced microbial isolates. At the rank of family, a sample-specific model for TS28 and TS29 was created for Enterobacteriaceae, Bacteroidaceae, Streptococcaceae, Methanobacteriaceae, Bifidobacteriaceae, Clostridiaceae, Coriobacteriaceae, Erysipelotrichaceae, Rikenellaceae, Porphyromonadaceae, Lachnospiraceae, Eubacteriaceae, Ruminococcaceae, and 'Other.' A sample-specific model for abundant genera in TS28 and TS29 was created for Providencia, Bacteroides, Ruminococcus, Streptococcus, Lactococcus, Clostridium, Bifidobacterium, Eubacterium, Methanobrevibacter, Colinsella, Dorea, Faecalibacterium, Alistipes, Parabacteroides, and 'Other.'

The family- and genus-level models were trained with sample-specific contigs identified based on their homology to sequenced human gut isolates and with data from 1,775 finished or draft genome sequences [NCBI database as of May 2009 combined with sequences from gut microbial genomes (118 gut microbial genomes included in total; **Table S7**)]. Contigs for training were selected through BLASTN comparisons of all contigs to the database of 118 gut genomes. High confidence matches were selected using stringent parameters: e-value<10^{-5}, bitscore>50, percent identity>90, percent sequence aligned>90, and total contig length>2Kbp. Additionally, we required that all significant matches were from the same reference genome.

For each model, five sample-specific multi-class SVMs were created using fragments with lengths of 3, 5, 10, 15 and 50Kbp, respectively. All input sequences were extended by their reverse complement prior to computing the compositional feature vectors. The parameters w and l were both set to 5 for the sample-specific models. The final classifier, consisting of the sample-specific and generic clade models, was used to assign all fragments >1Kbp from the fecal microbiomes. In the case of conflicting assignments, preference was given to those from the sample-specific models.

Fecal microbiome sequence bins were validated using a set of 30 marker genes, previously shown to have generally consistent phylogeny to the 16S rRNA gene (2). All genes from the microbiome bins were assigned to STRING orthologous groups (version 7.1; BLASTP e-value cutoff =10^{-10}). Each set of marker genes from the 122 gut microbial genomes and the microbiome bins were translated into amino acid sequences and then aligned using clustalw prior to building a neighbor-joining tree (3). Individual sequences were assigned to taxa based on the consensus taxonomy of all sequences found at the first node. Additionally, the frequency of consistent taxonomy between database marker genes and nearest neighbor sequences was tallied, and used as a control for the frequency of mis-assignment due to alignment errors, improper clustering, and/or disagreement with the marker genes and NCBI taxonomy. Overall, the results were consistent with accurate binning at each taxonomic level evaluated (**Fig. S3**). Additionally, gene clusters from the microbiome bins showed a level of taxonomic consistency similar to the gut microbial genomes, providing additional support for the binning method (**Fig. S2B**).

***Analysis of gene, bin, and transcript abundance* -** All pre-processed DNA and cDNA sequencing reads were mapped against our database of 122 gut microbial genomes and microbiome bins using SSAHA2 (4) (**Table S7**). On average, 72.67±1.61% of the DNA sequences and 73.75±11.45% of the cDNA sequences were mapped. Of the assigned sequences, 99% of the DNA sequences mapped to coding sequences (CDS), as opposed to only 5% of the cDNA sequences due to the high representation of non-coding rRNA transcripts (**Fig. S10A,B**). An analysis of 18 shallower fecal microbiome datasets (5) revealed that addition of the microbiome bins to the database improved the percentage of assignments for all samples, but had the largest impact on TS28 and TS29 (**Fig. S11E**).

The unassigned DNA sequences formed a bimodal length distribution (**Fig. S10C**), indicating that roughly 17% were unassigned due to their short length, while the other 83% may be either sequencing errors or novel unassembled sequences. To explore this further, we isolated the unassigned reads from all datasets (1,343,346 in total) and assembled them with Newbler based on flowgram information (average large contig size=904bp) (**Table S13**). The resulting assembly consisted of 106,978 contigs, comprised of 41.93% of the unassigned reads, leaving 508,756 unmapped singletons. BLASTN comparison of the contigs and singleton reads against the NCBI Entrez nucleotide database (November 3, 2009 release) resulted in assignment of an additional 7,554 contigs (7.1%) and 64,158 sequencing reads (12.6%; BLASTN E-value$\leq 10^{-5}$, Bitscore≥ 50, %identity≥ 50, and $\geq 50\%$ of the query sequence aligned); these were split between matches to uncultured bacterial sequences (22% of matches) and to microbial genomes (78%, e.g. gut microbial genomes which were missed in the more stringent SSAHA search). The remaining unmapped contigs represent putative novel genomic fragments or viruses found at relatively low abundance in the surveyed gut microbiomes.

Comparisons of the frequency of sequence assignments to the microbiome bins and the 122 gut microbial genomes revealed that most DNA sequences mapped best to the bins, while cDNA sequences were more evenly split between bins and gut genomes (**Fig. S11A,B**). As expected, DNA and cDNA sequences from TS28 were more likely to match TS28 bins while sequences from TS29 were more likely to match TS29 bins. However, in each case sequences were found that mapped more closely to bins from the co-twin's gut microbiome (**Fig. S11C,D**).

Genes were defined as having high (High-Expr) or low (Low-Expr) relative expression based on the ratio of cDNA to DNA relative abundance: i.e. the number of transcripts matching a given gene divided by the total number of mapped transcripts, divided by the number of DNA sequences matching a given gene divided by the total number of mapped gene sequences. A 10-fold difference (natural log ratio=2.3) was chosen as the threshold cutoff based on all pairwise comparisons of technical replicate datasets obtained from DNA or cDNA sequencing of each sample (**Fig. S8A,** n=3-4 replicates per sample per method). The bulk of the ratios from all datasets were found within the cutoff, which was close to the top and bottom 5% of ratios. The distribution of ratios for transcripts was slightly higher between technical replicates, potentially due to noise introduced during sample preparation. The distribution of ratios was significantly different relative to the combined distribution of technical replicates in both biological comparisons discussed in the text: TS28 cDNA versus TS28 DNA and TS29 cDNA versus TS29 DNA (F-test of variance; $P<10^{-3}$; **Tables S11,S12**).

Eighteen fecal samples subjected to a shallower depth of microbiome sequencing (including the first sequencing run from the TS28 and TS29 samples prior to their deep sequencing; **Table S1**) were preprocessed and mapped to the 122 gut genomes and/or microbiome bins as described above. Detailed meta-data regarding these samples can be obtained in our prevoius manuscript (5).

16S rRNA gene sequence datasets - Seven test datasets were used to calibrate noise removal and diversity estimates. The first dataset is referred to as an 'artificial community' and was composed of 454 GS FLX pyrosequencing reads from a unequal mixture of DNA from 90 cloned V5 16S rRNA gene sequences amplified from DNA isolated from a lake community (6). The sequences of these clones were also independently determined using the chain terminating method of Sanger. Six additional 'mock community' datasets were prepared by mixing DNA extracted from pure cultures of 67 gut bacterial strains in either even (Even1, Even2, Even3) or variable concentrations (Uneven1, Uneven2, Uneven3) (**Table S3**). The 16S rRNA gene sequences of these organisms were either known from existing databases, or determined through PCR amplification and sequencing. All six mock communities were analyzed by V2 16S rRNA gene pyrosequencing, using the same protocol employed for the human fecal samples.

In addition to these datasets, we conducted very deep pyrosequencing of V2 amplicons generated from fecal communities of the TS28 and TS29 co-twins. We also re-analyzed 281 shallow fecal V2 16S rRNA gene datasets from monozygotic (MZ) and dizygotic (DZ) human twins and their mothers (four samples with <70 sequences were removed after pre-processing) (5), in addition to 814 shallow V2 16S rRNA gene datasets obtained from samples harvested from multiple human body habitats (7).

***Filtering* -** Noisy individual bases have been shown to be associated with low quality pyrosequencing reads (8). In addition, noise increases towards the end of the reads. Consequently we terminated all flowgrams at the first noisy signal (defined by an intensity of 0.5-0.7), then removed any flowgrams with length less than 360 flows and subsequently truncated the remaining flowgrams at 360 flows. We also removed any reads that failed to match the primer or barcode sequences. The 'clean' read numbers, after filtering of each dataset are shown in **Table S14**.

***Pyrosequencing noise removal* -** To remove pyrosequencing noise, a modified version of the PyroNoise flowgram clustering program was used (6). In this modification, flowgrams were not aligned with each other; instead distances were calculated without alignment. This ensured that only pyrosequencing and not PCR errors were removed. The signal intensity distributions as a function of homopolymer length used to define the distance between flowgrams in this algorithm were calculated from the three 'Even' datasets (**Fig. S12**).

***PCR noise removal* -** We used the same principles underlying the PyroNoise algorithm (6) to develop a procedure for removing PCR errors. We began by defining a distance that reflects the probability that a given read **r** could have been generated from a true sequence **s,** given PCR error. This probability is simply the sum of the necessary nucleotide transitions: i.e., the probability that a nucleotide m is observed when the true nucleotide is n, $P(m|n)$. The total probability of the read will be the product of these, and we take the negative logarithm to generate a sequence error corrected distance between zero and infinity. We also normalize by length:

$$d(\mathbf{r},\mathbf{s}) = -\log\left[P(\mathbf{r} \mid \mathbf{s})\right]/M = -\log\left[\prod_{l=1}^{M} P\left(r^{l} = m \mid s^{l} = n\right)\right]/M = \sum_{l=1}^{M} -\log\left[P\left(r^{l} = m \mid s^{l} = n\right)\right]/M$$

This requires alignment of the read to the sequence. Alignment was performed by using a specially modified version of the Needleman-Wunsch algorithm (9) with a reduced gap cost for homopolymer insertion and deletions. This accounted for the possibility of pyrosequencing noise on low frequency reads, which may not have been removed in the flowgram clustering. Gap penalties were included in the distance measure.

The nucleotide transition probabilities were calculated by comparing all reads with pyrosequencing noise removed from the three ‘Even’ datasets (**Table S15**). The error frequency as a function of position along the sequences exhibited a steady background, due to point mutations, with peaks associated with nucleotide polymorphisms; these we tentatively assign to the formation of hetero-duplexes, effectively single nucleotide chimeras.

We assume that the sample can be described as a mixture model, where each component of the mixture corresponds to a true sequence about which observed noisy reads are distributed. The relative weights of each component are the true frequencies of the sequences. The reads are assumed to be distributed as exponentially decaying functions of their sequence error corrected distance from these true sequences. The magnitude of the sequence noise is described by the characteristic length of these exponentials, σ. A maximum likelihood fit of the mixture model can be obtained using an Expectation-Maximization algorithm, initialized using the clusters formed from a hierarchical clustering of sequences at a given distance cut-off, c. In this study, we used parameter values of $\sigma = 0.04$ and $c = 0.08$ for the V2 16S rRNA datasets but reduced □ to 0.033 for the V5 artificial community which exhibited fewer sequencing errors. A standard gap was given a penalty of 10.0 and a homopolymer gap, 4.0. To quantify the relative importance of pyrosequencing and PCR noise to the formation of phylotypes (operational taxonomic units; OTUs) defined at different levels of sequence identity (%ID), we calculated phylotype number following complete linkage clustering as a function of cut-off for the ‘Artificial Community' dataset (**Fig. S13**).

***Chimera removal* -** The third source of noise in pyrosequenced amplicons is from PCR chimeras. Chimeras are generated when incomplete extension occurs in one round of PCR and then the resulting sequence fragment acts as a primer for a different sequence in the next round. Consequently chimeras are composed of two (or occasionally more) true sequences with a discrete break point where the transition from one sequence to another occurs. For our 7 test datasets, we were able to determine which sequences were likely chimeras by aligning each sequence against the known reference sequences and finding the putative parents and break point that gave the closest match to the query sequence. We also searched for chimeras comprised of three and four different reference sequences. We did this for the unique sequences remaining following pyrosequencing and PCR noise removal.

If the closest match to a chimera of two sequences was at least three nucleotides or better than that to a single reference sequence, then the query was considered as a possible two-sequence chimera or ‘bimera.’ Similarly if the match was further improved by three nucleotides when two break points were allowed, it was classified as possibly comprised of three sequences (a ‘trimera’), and again for the transition to a composite of four sequences (a ‘quadramera’). However, the sequence was only assigned these putative definitions if the absolute match was deemed sufficiently good as measured in terms of the sequence error corrected distance ($d < 0.15$). Otherwise, the sequence was denoted as ‘unclassified’; these could include contaminants, real unidentified 16S rRNA operons, gross pyrosequencing or PCR errors, or most likely a chimera that failed to fall under our rather strict definition.

Table S16 shows the number of unique sequences remaining following pyrosequencing and PCR noise removal for the 7 test datasets, and the proportion of these sequences that were classified as good, bimeric, trimeric, quadrameric and unclassified. From this, we observe large numbers of bimeras, and substantial numbers of the higher order trimeras. Quadrameras are rare. Unclassified sequences appear in comparable numbers to the good sequences.

We might expect that good sequences are more likely to appear multiple times across technical replicates than chimeric ones. We investigate this for the ‘Uneven' datasets in **Table S17,** where we give frequencies for the number of times each category of sequence appeared in one, two or three of the samples. We found that the ‘good’ sequences are more likely to be shared; roughly two thirds appear in at least two datasets; this is only true for 5% of the chimeric sequences. The four ‘Unclassified’ sequences that appear in at least two datasets had perfect matches to 16S rRNA sequences in GenBank (*Bacteroides capillosus, Acinetobacter sp., Lysobacter enzymogenes, and Bifidobacterium bifidum*). The *Acinetobacter* and *Lysobacter* should not have been present in the mock community and thus likely represent rare contaminants. The

Bacteroides and Bifidobacterium were probably 16S rRNA genes from the mock gut communities that had not been identified through genomic or full-length 16S rRNA gene sequencing.

For the real datasets we do not have a comprehensive database of known reference sequences and, therefore, it was necessary to develop a method for removing chimeras. To do this, we used the conjecture that both parents of a chimera will be present in the dataset and with a frequency likely to be at least equal to the chimera. The justification for this conjecture is that the parent must experience at least one more PCR round than the chimera that will appear initially as just a single sequence. This ignores the possibility of the chimera experiencing preferential PCR bias over its parents, but it will be true in the vast majority of cases. Thus, we queried each sequence against all those with equal or higher frequency to find the parents and break point with the closest match. We allow for trimeras and quadrameras but only if they increase the match by at least three nucleotides. We then define two indices. The first index of chimericity I_c - is defined simply as the sequence error corrected distance between the sequence and its best matching chimera. Therefore, the larger this quantity the less likely the sequence is to be a chimera. The second index of evolvability I_e reflects the probability that the observed chimeric pattern could have evolved. Aligning the query sequence **C**, the closest matching parent **A,** and the more distant parent **B**, we calculate using parsimony the sequence ancestral to all three. We find the number of base pair changes along the three branches to **A**, **B**, **C** and denote these x, y, and z respectively. We resolve changes to the two parts of alignment, either the part of the chimera matching parent **A** or parent **B**, and denote these x^A and x^B, y^A and y^B, and z^A and z^B. For a given chimera to be observed, three independent events must occur; changes to the distant parent **B** must occur on that part of the alignment matching **A**. Assuming all base changes are equally likely, the distribution of changes across the two parts will be binomial distributed with probability proportional to the size of each part. Therefore, we can calculate the probability of the changes being as biased or more so than were observed. The same arguments apply for the changes to the closer parent: they should all lie in the part matching the more distant and we can calculate that probability. Finally we also require that changes do not occur along the branch to the chimera itself. Assuming that a change is equally likely to occur on the branch leading to **B** as to **C**, then this too will be binomially distributed with probability 0.5. We then multiply the three probabilities together and take the negative log to obtain an index that will increase the less likely a chimeric pattern is to have evolved. This index is defined for two parent chimeras (our 'bimeras'); it can be extended to higher order chimeras but we did not do this, finding that it sufficed for identifying these anyway.

The problem of identifying chimeras is an example of supervised learning. For the three 'Even' datasets, we calculated the two indices of chimericity and evolvability for each sequence and then used the known classifications to either good or chimeric (bimera, trimera or quadramera), determined through comparison with the reference 16S rRNA gene sequences to train a two dimensional logistic regression. We also added to our training dataset the result of taking those reference sequences obtained from genome sequencing, and hence most likely to be non-chimeric, and calculating their indices without regard to sequence frequency: i.e., comparing all sequences to all others. We only trained the classifier for sequences with $I_c < 0.15$; if the index of chimericity I_c is very large then no good chimeric match was found. Consequently, we classified all sequences with $I_c \geq 0.15$ as good sequences. The regression was performed using the R software package. All variables were judged highly significant, with $\alpha = -1.179$, $\beta = -13.996$, and $\gamma = 0.341$, where the probability of classification to a chimera is given by:

$$P(C) = \frac{1}{1 + \exp(-[\alpha + \beta I_c + \gamma I_e])}$$

The regression itself was also highly significant with the null deviance of 1226.2 on 4608 degrees of freedom reduced to 404.1. Our classification rule was to assign a sequence as chimeric if $P(C) > 0.5$ which should minimize misclassifications. To validate this classifier, we applied it to the four other datasets not used to parameterize the logistic regression (**Table S18**). From this we saw that we achieved a remarkably high sensitivity, successfully detecting over 98% of bimeric sequences and at least 95% of the trimeras. The frequency of quadrameras was too low to properly evaluate. The false positive rate was also relatively low with ~10% of good sequences being falsely judged chimeric.

So far, to determine chimericity we have only used sequence information implicitly by restricting potential parents to having at least the same abundance as the query. However, a sequence with low frequency is more likely to be a chimera than a sequence with high frequency, something we verified by direct examination of those sequences classified through comparison with the known references. As we expect, this is also true of the results of our classifier although less perfectly because of misclassifications. We illustrate this for the 'Uneven1' data in **Fig. S14** where frequency-abundance distributions for those sequences judged to be either good or chimeric types are shown. The chimeric sequences clearly have a different distribution to the good and this is something we can use to improve our classifier. We began by assuming that the indices I_c and I_e are distributed independently of abundance, an approach similar in principle to that used in a 'naïve Bayes classifier' (10). The probability that a sequence *i* is chimeric given its abundance *n* is then:

$$P(C,n) = \frac{P(C)P(n \mid C)}{P(C)P(n \mid C) + (1 - P(C))P(n \mid G)}$$

where $P(C)$ is our probability of chimericity independent of *n* taken from the logistic regression, and $P(n|C)$ and $P(n|G)$ are the probabilities of observing a sequence in the sample *n* times if it is 'chimeric' or 'good', respectively. To calculate these quantities we extended an existing method for fitting abundance distributions that accounts for sampling noise (11). We fitted an abundance distribution to those sequences classified as good using maximum likelihood obtaining parameters θ_g, and a separate distribution to those classified chimeric with parameters θ_c. We can then calculate for each distribution the probability that an arbitrary sequence would appear *n* times in the sample. These are approximately compound-Poisson distributions and we denote them $P_n(\theta)$. Since we are only interested in observed sequences, we normalized this by the probability that we will observe the sequence, $P_n(\theta)= P_n(\theta)/(1-P_0(\theta))$.To obtain self-consistent estimates for the P(C, n), and parameters, θ_c, θ_g, we then repeated this process, classifying sequences as chimeric if $P(C,n) > 0.5$ and recalculating the distributions. We iterated this until we got convergence to improved probabilities $P(C,n)$ that account for sequence abundance. We used a log-normal distribution for fitting the abundance distributions but the algorithm is not sensitive to this choice. In **Fig. S14** we show the final fitted distributions and distributions of good and chimeric sequences after incorporating the abundance information. The application of this algorithm to the four validation datasets is shown in **Table S19**. In all four cases incorporating abundance information improved classification resulting in very high accuracies. Therefore, we incorporated sequence abundances into the chimera detection protocol used in this study.

Diversity estimates in the 'Uneven' mock communities - Following noise removal and chimera detection using abundance information, fairly flat rarefaction curves were obtained for the three Uneven mock communities (**Fig. S15)**, suggesting we had been successful in removing most of the noise. The total 97%ID phylotype richness of the V2 16S rRNA control sequences was 62. The observed 97%ID phylotype richness in 'Uneven1' exceeded this figure slightly probably due to contaminants, unidentified 16S rRNA operons in the mock community, and/or some chimeras that were not identified. In `Uneven2' and `Uneven3', the diversity was slightly less. Under-estimation of richness could occur through a combination of false positive chimera classification and PCR amplification bias. Estimates of total diversity in these validation data-sets using both non-parametric, Chao, and parametric diversity estimators (fitting log-normal and Sichel distributions (11) are shown in **Table S20**. These values tended to somewhat but not dramatically over-estimate the true diversity with the range of possible values for the parametric estimators including some quite reasonable estimates. This gave us confidence in applying our noise removal and diversity estimation procedures to real datasets.

Accuracy of phylotype construction in the test datasets - To test the accuracy of our noise and chimera removal algorithms, we constructed phylotypes from both the de-noised reads and from the known reference sequences for the 'Artificial Community.' We used a complete linkage hierarchical clustering with sequence distances derived from pairwise alignments to form the phylotypes. At increasing sequence differences, we then counted the number of phylotypes that were comprised of both pyrosequencing reads and the known reference sequences. These can be considered ‘true phylotypes’ that have been detected. The number of phylotypes that only contain reference sequences correspond to phylotypes that have been missed, and phylotypes composed only of pyrosequencing reads comprise noise (**Fig. S16**). At 97%ID no phylotypes were missed and just two false phylotypes were present, consisting of unidentified chimeras each comprising a single read.

For the ‘Artificial Community’ composed of cloned 16S rRNA gene amplicons, we can compare the observed phylotypes relative abundances after de-noising with their relative concentration in the mixture. In this case, because all clones had sequences that were perfect matches to the V5 primers we used, there was a strong correlation ($R^2 = 0.96$) between observed abundance and concentrations (**Fig. S17**). This was not true for the ‘mock community’ datasets that contained DNA extracted from real organisms. In this case substantial variation in abundance was observed even for the ‘Even’ datasets where the organisms were mixed in equal abundances (**Fig. S4**). The deviation in relative abundance from expected is large for many of the phylotypes in the mock community, potentially due to a combination of primer bias (multiple mismatches in many of the Bifidobacterium, see **Fig. S4A**), differences in DNA quality, differences in 16S rRNA copy number (which showed a poor correlation to abundance, although the copy number data is largely incomplete due to the quality of each draft genome, data not shown), and possibly differences in genomic copy number (12). These results emphasize the need for new methods to enable accurate quantification of bacteria from complex communities at the level of cell count, as opposed to 16S rRNA copy number or gene content.

We can calculate the accuracy of phylotype construction for the mock communities following de-noising and chimera removal just as we did for the 'Artificial Community.' We show these accuracies for the 'Uneven1' dataset in **Fig. S18**. In this case we have to account for the possibility that some reference sequences may not be present in the pyrosequencing reads because of primer bias. We did this by only including those reference sequences in our comparison that had a non-zero number of raw filtered reads matching to within 2% nucleotide sequence difference. While the number of true phylotypes missed is still low at higher cut-offs (at 97%ID just one is missed), there are more false phylotypes than were found for the 'Artificial Community' (22 in total at the 97% cutoff). These phylotypes must be derived from chimeric and unclassified de-noised sequences that were judged to be good in **Table S19**. Most of these are singletons but a few are more frequent and have good matches in GenBank; as discussed above these are either contaminants or true 16S rRNA genes from the reference organisms that were not included in our collection of reference sequences.

***Diversity estimates and phylotype overlaps in experimental datasets* -** In **Table S21,** we show chimera numbers at 50% classification cut-off (see above) incorporating sequence abundance information for the deeply sampled twins' fecal V2 16S rRNA datasets (TS28-Deep; TS29-Deep). The rarefaction curves for 97%ID phylotypes built with non-chimeric sequences are shown in **Fig. 1A**. To verify that the high chimera identification rates were not simply an effect of the large sample sizes we applied the noise removal algorithms to two shallow sequenced V2 sequence datasets from the same fecal samples (5). These are also shown in **Table S21** and the 97%ID phylotype rarefaction curves in **Fig. S19**. The curves from the shallow datasets initially reproduce those from the deeply sequenced datasets but slightly over estimate diversity at larger sample sizes. This suggests that some noise in the low abundance phylotypes is not being removed from the shallow datasets, a conclusion that is supported by the 97%ID phylotype overlaps presented in **Table S22**. The 95%ID phylotype overlaps are given in **Table S23**.

Normalized overlap - We would expect all of the phylotypes found in the shallow datasets to appear in the corresponding large dataset; the fact that only about 90% are found indicates that ~10% of phylotypes in the shallow datasets either should have been removed and were not, or have been falsely removed from the larger datasets. Additionally, the figures for the deep sequenced samples in **Tables S22,S23** do not give a true estimate of the proportion of phylotypes present in one twin that are also found in the other. This is because they do not take account of the fact that a given phylotype may be present, but at an abundance too low to be seen even in these very large datasets. **Fig. S20** shows the distribution of shared 97%ID phylotype frequencies in TS29 relative to TS28; while shared phylotype abundances vary significantly in the fecal communities of the co-twins, this is rarely by more than two orders of magnitude; in fact this is true of 95% of shared phylotypes. Consequently, as noted in the main text, we can define a normalized overlap between the samples by only considering phylotypes that have a relative frequency sufficiently large that if they appear with a frequency 100 times less in the other sample we would still expect to see at least five copies of them (the latter being a number large enough that random sampling effects can be ignored). This is true of 68 97%ID phylotypes in TS28 fecal sample and 46 of these appear in TS29. The normalized overlap is thus 46/68 or 68%. Similarly of the 65 97%ID phylotypes in TS29 that satisfy this criterion, 51 appear in TS28 giving an overlap of 79%. For 95%ID phylotypes, the normalized overlaps are 46/60 (76.7%) and 49/57 (86%) for TS28 phylotypes in TS29 and *vice versa,* respectively. Accounting for differences in relative frequency and sampling, reveals that while the phylotype overlaps between these genetically identical co-twins are quite substantial, a significant proportion of phylotypes do not co-occur.

Larger cohort - To determine if this observation holds across a larger cohort of sampled fecal bacterial communities, we de-noised all 281 fecal V2 16S rRNA gene sequence datasets (277 samples were retained after pre-processing) and 814 samples from 27 body habitats (see the *16S rRNA gene sequence datasets* section above). Following chimera removal, we built 97%ID phylotypes using complete linkage and associated each phylotype with its most abundant sequence. We then aligned each of these sequences in turn against the 97%ID phylotypes in the two 'Deep Twins' datasets and calculated the proportion that had a closest match with less than 3% nucleotide difference. Because almost all these samples were at least two orders of magnitude less than the 'Deep Twins' datasets (the largest had 10,989 reads, but the median size was 1,670), we did not need to normalize overlap as above. In **Fig. 1C**, we show these samples with the TS29 overlap plotted on the y-axis and the TS28 overlap on the x-axis. There is a large range of overlaps (20-60%) and the overlaps are correlated, probably because TS28 and TS29 themselves are more similar than most other fecal community samples. We repeated this for the 814 'Whole Body' samples; the overlaps were significantly reduced in the samples from the rest of the body (see **Fig. 1C** and the main text).

To investigate the phylotype diversity in the gut microbiomes of the population as a whole, we took the 250 'Shallow Twins' (TSAll-Shallow) de-noised samples with at least a 1,000 reads. We then subsampled these to 1,000 reads to produce a dataset of 250,000 reads evenly distributed among 250 samples from 146 individuals. We then applied an extra de-noising step to the complete dataset; this step consisted of forming clusters after an average linkage clustering using our sequence error corrected distances at a cut-off of 0.10. This cut-off will correspond to ~1% nucleotide sequence difference. The purpose of this step was to remove noise from those sequences that might be common in one sample but rare and hence potentially noisy in another. We then used these sequences to build phylotypes following a complete linkage clustering. In **Figs. 1B,S21**, we show the rarefaction curves for 97%ID phylotypes and 95%ID phylotypes respectively in these 250 samples and for comparison the deeply sequenced TS28 and TS29 datasets.

Contribution of chimeras to diversity - As we mention above, chimera removal in these 'Shallow Twins' datasets will not be perfect. We can estimate for TS28 and TS29 how many 97%ID phylotypes are attributable to chimeras by searching their most abundant sequences against the corresponding 'Deep Twins' dataset. If we do this prior to removing chimeras from the 'Deep Twins' data then any phylotype from the shallow dataset that does not have a match must be chimeric; since the chimera co-occurrence frequency in **Table S17** is about 5%, this will reveal the majority of remaining chimeras. For both TS28 and TS29, four chimeric phylotypes are found in the shallow datasets. This is a small contribution to the per sample diversity but over 250 datasets, since each chimeric phylotype is likely to be novel, it could contribute up to a 1,000 false phylotypes. To account for this and to obtain a lower bound on the total population diversity we applied an alternative chimera removal procedure, eliminating all de-noised sequences that did not appear in more than one of the ‘Shallow Twins’ datasets. This will remove some genuine variation and may even miss some chimeras but it gives us something to compare with the results above. We then subsampled the same 250 datasets to 1,000 reads again and built phylotypes. The resulting 97%ID and 95%ID phylotype rarefaction curves are also shown in **Figs. 1B,S21**. The diversities observed in these co-occurring sequences are considerably reduced but they are still larger than in the individual ‘Deep Twins’ samples. This is a consequence of the less than complete phylotype overlaps between individuals. There is a much higher total diversity from the population than within a single individual at the same level of sampling for human fecal microbiota.

The degree to which the individual phylotypes are spread across the 250 ‘Shallow Twins’ samples varies greatly (**Fig. 1C**). In **Fig. 1D** we plot the relative abundance of each phylotype in the whole dataset against the proportion of samples in which it was observed (phylotypes were constructed after removing all putative chimeric sequences that only appeared once, see above). If the phylotypes were evenly spread across all samples, we would not expect them to appear in every sample due to random chance. This will also be a function of abundance: a relative abundance of 0.1% would result in a mean of 1 sequence per sample: since we have 250 samples and a total sample size of 250,000, the expected occupancy would be 63%. To investigate this, we used a sampling approach: at each observed abundance level we generated a null dataset assuming that each read in an phylotype was equally likely to come from any sample and calculated the proportion of samples the phylotype appeared in. We repeated this for 1,000 replicates and generated medians and 95% confidence intervals (**Fig. 1D**). The observed occupancies fall below these null values at all relative abundances indicating that phylotypes are more aggregated than we would expect by chance. Occupancies generally increased with relative abundance but at a given relative abundance there is a great deal of variation in occupancy, indicating that some phylotypes are intrinsically more cosmopolitan than others.

To investigate the effect of sampling throughout the human body on observed phylotype numbers, we generated phylotypes for 250 samples randomly chosen from the 515 'Whole Body' samples that had more than a 1,000 reads. These datasets were then de-noised, chimeras were removed, and the datasets were subsampled to 1,000 reads just as for the 'Shallow Twins' fecal datasets. The resulting rarefaction curves are also shown in **Figs. 1B,S21**. This pre-processed 'Whole Body' dataset gives the highest observed diversities at all levels of sampling: i.e., diversity is maximized by sampling from different individuals and from different body habitats.

We then calculated the observed phylotype numbers for all the datasets (**Table 1**). The true number of phylotypes will be larger than this because of sampling limitations. Therefore, we also calculated Chao's estimate of the true diversity for each of the samples (13). This is a non-parametric estimator that requires no assumption regarding the form of the underlying abundance distribution. However, it strictly only gives a lower bound on diversity, and is highly sensitive to small sample sizes. This explains why Chao's estimator increases dramatically from the shallowly sequenced samples (TS28-Shallow, TS29-Shallow) to the equivalent deeply sequenced samples ('Deep Twins', TS28-Deep, TS29-Deep) (**Table 1**).

Parametric diversity estimators are more robust to sample size and potentially give a better indication of the unseen diversity, but they are sensitive to the assumed form of the abundance distribution (14). The very large 'Deep Twins' datasets provided us with an opportunity to determine what form the abundance distribution takes in individual human fecal microbial communities. We used a Bayesian method to fit four different abundance distributions to the 'Deep Twins' samples, and to the two corresponding 'Shallow Twins' datasets (11). The log-normal and Inverse-Gaussian distributions (both two-parameter) were used, as well as their three-parameter generalizations (log-Student's t and Sichel distributions). These distributions have been shown to be effective at fitting microbial taxa abundances (11). One hundred thousand Monte Carlo samples were generated from the posterior distribution by a Metropolis algorithm. The first 25,000 samples were then discarded as a burn-in period and all results quoted calculated over the last 75,000. We used the Deviance Information Criterion (DIC) to determine goodness of fit. This accounts automatically for parameter number and the smaller the DIC the better the fit. In **Tables S24,S25**, we give DIC values for the four fits to the 97%ID and 95%ID phylotype abundance distributions for individual fecal samples. For the two shallow datasets all four distributions fit equally well reflecting the low level of sampling. For both 'Deep Twins' datasets the Sichel distribution fit best, although it was only significantly better than the log-normal for TS28. This was true for both 97%ID and 95%ID phylotypes. Consequently we can tentatively conclude, that the Sichel distribution best describes individual human gut samples.

In **Tables S26, S27**, we give the total number of 97% and 95% phylotypes predicted from fitting these distributions. The DIC values discussed above imply that the results from the Sichel are most dependable. There are two things to note from the tables. *First*, at least for TS28, the shallow dataset predictions overlap those of the 'Deep Twins', and they are not dramatically different for TS29, illustrating the robustness of the parametric fits to sample size. *Second*, although the observed diversity is substantially lower in TS29, the total diversity may be similar. Observed diversity is sensitive to the presence of a few highly abundant phylotypes. In TS29 the most abundant 97%ID phylotype comprises 39% of the diversity as opposed to 18% in TS28. Therefore, this phylotype may be skewing the observed diversities even though the total community diversity is similar.

***Additional microbiomes and meta-transcriptomes* -** Five additional samples from two sets of MZ co-twins and one unrelated individual were included (Samples labeled 'TSDA1-5' in **Fig. S9**). All of these individuals were lean, born in Missouri, were 23-27 years old, did not have a history of gastrointestinal disease, and had not consumed antibiotics in the 12 months prior to sampling. Sequences were obtained using the 454 GS FLX instrument (DNA) and the Illumina GAIIx instrument (cDNA). On average, 25,093±3,357 DNA and 316,500±34,675 cDNA sequencing reads per sample (mean±s.e.m) matched protein-coding genes from the 122 gut microbial genomes and microbiome bins.

SUPPORTING TABLES

Table S1: DNA sequencing statistics.

	Pyrosequencer run designation	454 GS Platform	Number of nucleotides	Number of sequences	Average sequence length (nt)
16S rRNA	**TS28 shallow**	FLX	1,564,183	6,694	234
16S rRNA	**TS28 run1**	FLX	118,156,493	505,607	234
16S rRNA	**TS28 run2**	FLX	114,723,622	490,496	234
16S rRNA	**TS28 run3**	FLX	114,073,518	497,968	229
16S rRNA	**TS28 total**	FLX	348,517,816	1,500,765	232
Single-end	**TS28 run1**	Titanium	138,364,927	399,717	346
Single-end	**TS28 run2**	Titanium	313,831,777	1,301,031	241
Single-end	**TS28 run3**	Titanium	587,766,394	1,430,201	411
Single-end	**TS28 run4**	Titanium	528,420,892	1,279,604	413
Paired-end	**TS28 run5**	Titanium	311,918,140	960,050	325
Paired-end	**TS28 run6**	Titanium	292,301,943	920,894	317
	TS28 total	Titanium	2,172,604,073	6,291,497	345
16S rRNA	**TS29 shallow**	FLX	556,046	2,411	231
16S rRNA	**TS29 run1**	FLX	60,095,930	275,066	218
16S rRNA	**TS29 run2**	FLX	114,039,159	478,796	238
16S rRNA	**TS29 run3**	FLX	103,067,369	430,287	240
16S rRNA	**TS29 total**	FLX	277,758,504	1,186,560	234
Single-end	**TS29 run1**	Titanium	239,971,702	672,196	357
Single-end	**TS29 run2**	Titanium	387,493,057	1,096,053	354
Single-end	**TS29 run3**	Titanium	531,122,832	1,438,709	369
Paired-end	**TS29 run4**	Titanium	222,933,173	634,861	351
	TS29 total	Titanium	1,381,520,764	3,841,819	360

Table S2: cDNA sequencing statistics (values represent the number or percentage of sequencing reads assigned to each category).

Sample	TS28 run1	TS28 run2	TS28 run3	TS29 run1	TS29 run2	TS29 run3	TOTAL
Non-adapter sequences	4,817,384	7,265,680	3,348,023	1,215,083	3,569,577	2,253,015	22,468,762
16S sequences	1,460,662	2,208,065	169,460	271,628	907,464	140,324	5,157,603
23S sequences	2,489,579	3,762,454	2,534,858	700,801	1,880,230	1,763,104	13,131,026
5S sequences	17,150	25,140	932	17,295	108,870	757	170,144
CDS	181,986	275,795	154,189	85,871	180,933	73,604	952,378
Intergenic sequences[a]	8,179	11,978	3,928	1,418	2,368	700	28,571
tRNA sequences	509	850	135	1,117	1,013	90	3,714
Mapped sequences	4,158,065	6,284,282	2,863,502	1,078,130	3,080,878	1,978,579	19,443,436
Unmapped sequences	659,319	981,398	484,521	136,953	488,699	274,436	3,025,326
% of sequences mapped	86.31	86.49	85.53	88.73	86.31	87.82	-
% of mapped from CDS	4.38	4.39	5.38	7.96	5.87	3.72	-
% of sequences unmapped	13.69	13.51	14.47	11.27	13.69	12.18	-

[a] Intergenic sequences include matches to genes with no predicted coding sequence and matches to miscellaneous noncoding RNAs.

Table S3: Percentage of purified genomic DNA added to control 'mock community' pools for 16S rRNA gene sequencing.

Isolate	Taxonomy	Even1	Even2	Even3	Uneven1	Uneven2	Uneven3
1	Actinobacteria; Bifidobacterium adolescentis	1.47	1.47	1.47	5.13E-02	1.03E-01	1.03E-04
2	Actinobacteria; Bifidobacterium angulatum	1.47	1.47	1.47	1.03E+01	5.13E-04	1.03E-01
3	Actinobacteria; Bifidobacterium bifidum	1.47	1.47	1.47	5.13E-01	1.03E-01	5.13E+00
4	Actinobacteria; Bifidobacterium breve	1.47	1.47	1.47	5.13E-03	5.13E-02	1.03E-02
5	Actinobacteria; Bifidobacterium gallicum	1.47	1.47	1.47	1.03E+01	5.13E-04	1.03E-04
6	Actinobacteria; Bifidobacterium catenulatum	1.47	1.47	1.47	1.03E-03	2.57E+00	1.03E+01
7	Actinobacteria; Bifidobacterium dentium	1.47	1.47	1.47	2.57E-01	5.13E-03	1.03E-01
8	Actinobacteria; Bifidobacterium pseudocatenulatum	1.47	1.47	1.47	1.03E-01	5.13E-02	1.03E-01
9	Actinobacteria; Collinsella intestinalis	1.47	1.47	1.47	1.03E-01	1.03E-01	1.03E-04
10	Actinobacteria; Collinsella stercoris	1.47	1.47	1.47	1.03E-04	1.03E+01	1.03E-03
11	Bacteroidetes; Alistipes putredinis	1.47	1.47	1.47	2.57E-01	5.13E-04	5.13E-03
12	Bacteroidetes; Bacteroides pectinophilus	1.47	1.47	1.47	5.13E-03	1.03E-03	5.13E-03
13	Bacteroidetes; Bacteroides coprocola	1.47	1.47	1.47	2.57E+00	2.57E-01	5.13E-01
14	Bacteroidetes; Bacteroides coprophilus	1.47	1.47	1.47	5.13E-02	1.03E+01	5.13E-04
15	Bacteroidetes; Bacteroides dorei	1.47	1.47	1.47	5.13E-04	2.57E-01	1.03E-02
16	Bacteroidetes; Bacteroides eggerthii	1.47	1.47	1.47	1.03E+00	1.03E-02	1.03E-01
17	Bacteroidetes; Bacteroides finegoldii	1.47	1.47	1.47	1.03E-02	1.03E+00	1.03E-03
18	Bacteroidetes; Bacteroides intestinalis	1.47	1.47	1.47	5.13E-04	1.03E+01	5.13E-04
19	Bacteroidetes; Bacteroides plebeius	1.47	1.47	1.47	5.13E-01	5.13E-04	1.03E-04
20	Bacteroidetes; Bacteroides caccae	1.47	1.47	1.47	5.13E-03	1.03E-04	1.03E+01
21	Bacteroidetes; Bacteroides cellulosilyticus	1.47	1.47	1.47	1.03E-04	1.03E-01	5.13E+00
22	Bacteroidetes; Bacteroides ovatus	1.47	1.47	1.47	2.57E-01	5.13E-03	5.13E-02
23	Bacteroidetes; Bacteroides stercoris	1.47	1.47	1.47	5.13E-03	1.03E-04	5.13E-03
24	Bacteroidetes; Parabacteroides johnsonii	1.47	1.47	1.47	5.13E-04	2.57E-01	1.03E-02
25	Bacteroidetes; Prevotella copri	1.47	1.47	1.47	5.13E+00	2.57E+00	5.13E-02

26	Firmicutes; Anaerococcus hydrogenalis	1.47	1.47	1.47	1.03E-01	2.57E-01	1.03E+00
27	Firmicutes; Anaerofustis stercorihominis	1.47	1.47	1.47	1.03E-01	1.03E-03	5.13E+00
28	Firmicutes; Anaerotruncus colihominis	1.47	1.47	1.47	1.03E-03	5.13E-04	1.03E-03
29	Firmicutes; Butyrivibrio crossotus	1.47	1.47	1.47	1.03E+00	1.03E-04	1.03E-02
30	Firmicutes; Catenibacterium mitsuokai	2.94	2.94	2.94	7.70E-01	3.59E+00	5.24E+00
31	Firmicutes; Clostridium sporogenes	1.47	1.47	1.47	2.57E+00	5.13E+00	5.13E-01
32	Firmicutes; Clostridium asparagiforme	1.47	1.47	1.47	1.03E-04	2.57E-01	5.13E-03
33	Firmicutes; Clostridium bartlettii	1.47	1.47	1.47	1.03E+00	1.03E-03	5.13E-01
34	Firmicutes; Clostridium celatum	1.47	1.47	1.47	5.13E-04	5.13E-01	2.57E+00
35	Firmicutes; Clostridium hathewayi	1.47	1.47	1.47	5.13E-02	1.03E+00	5.13E-02
36	Firmicutes; Clostridium hiranonis	1.47	1.47	1.47	1.03E-03	2.57E+00	5.13E-01
37	Firmicutes; Clostridium hylemonae	1.47	1.47	1.47	1.03E-01	5.13E-02	1.03E-01
38	Firmicutes; Clostridium methylpentosum	1.47	1.47	1.47	2.57E-01	1.03E-02	5.13E-04
39	Firmicutes; Clostridium nexile	1.47	1.47	1.47	1.03E-04	5.13E-01	1.03E-03
40	Firmicutes; Clostridium orbiscindens	1.47	1.47	1.47	5.13E+00	1.03E-01	2.57E-01
41	Firmicutes; Clostridium ramosum	1.47	1.47	1.47	2.57E+00	1.03E+00	1.03E-04
42	Firmicutes; Clostridium saccharolyticum-related	1.47	1.47	1.47	5.13E+00	1.03E-03	2.57E+00
43	Firmicutes; Coprococcus comes	1.47	1.47	1.47	1.03E-01	1.03E+00	5.13E-02
44	Firmicutes; Dorea formicigenerans	1.47	1.47	1.47	1.03E-01	5.13E+00	5.13E-01
45	Firmicutes; Eubacterium biforme	1.47	1.47	1.47	5.13E-02	1.03E-01	2.57E-01
46	Firmicutes; Eubacterium ramulus	1.47	1.47	1.47	1.03E+01	1.03E+01	1.03E+01
47	Firmicutes; Holdemania filiformis	1.47	1.47	1.47	5.13E+00	5.13E-01	5.13E+00
48	Firmicutes; Mitsuokella multacida	1.47	1.47	1.47	5.13E+00	1.03E+01	1.03E+00
49	Firmicutes; Roseburia faecis	1.47	1.47	1.47	5.13E-01	1.03E-02	1.03E-02
50	Firmicutes; Roseburia intestinalis	1.47	1.47	1.47	1.03E+01	1.03E-04	5.13E-04
51	Firmicutes; Roseburia inulinivorans	1.47	1.47	1.47	1.03E+00	5.13E+00	1.03E-01
52	Firmicutes; Ruminococcus hansenii	1.47	1.47	1.47	5.13E-03	5.13E-03	5.13E-02
53	Firmicutes; Ruminococcus torques	1.47	1.47	1.47	1.03E-03	5.13E+00	5.13E-04

54	Firmicutes; Ruminococcus gnavus-related	1.47	1.47	1.47	2.57E+00	1.03E-04	1.03E-01
55	Firmicutes; Ruminococcus lactaris	1.47	1.47	1.47	1.03E-02	1.03E-01	1.03E-03
56	Firmicutes; Streptococcus infantarius	1.47	1.47	1.47	5.13E-01	5.13E-01	1.03E+00
57	Firmicutes; Subdoligranulum variabile	1.47	1.47	1.47	1.03E-03	1.03E-01	5.13E-03
58	Proteobacteria; Providencia rustigianii	1.47	1.47	1.47	5.13E-04	5.13E-03	2.57E-01
59	Proteobacteria; Cedecea davisae	1.47	1.47	1.47	1.03E-01	1.03E-02	1.03E+00
60	Proteobacteria; Citrobacter sp.	1.47	1.47	1.47	1.03E+01	5.13E-03	2.57E+00
61	Proteobacteria; Desulfitobacterium hafniense	1.47	1.47	1.47	1.03E-04	5.13E-01	1.03E+01
62	Proteobacteria; Edwardsiella tarda	1.47	1.47	1.47	1.03E-02	5.13E-02	1.03E+00
63	Proteobacteria; Enterobacter cancerogenus	1.47	1.47	1.47	1.03E-02	5.13E-02	2.57E+00
64	Proteobacteria; Proteus penneri	1.47	1.47	1.47	2.57E+00	1.03E-03	2.57E-01
65	Proteobacteria; Providencia alcalifaciens	1.47	1.47	1.47	1.03E+00	2.57E+00	1.03E+01
66	Proteobacteria; Providencia rettgeri	1.47	1.47	1.47	1.03E-02	1.03E-02	2.57E-01
67	Proteobacteria; Providencia stuartii	1.47	1.47	1.47	5.13E-02	5.13E+00	2.57E+00

Table S4: Observed and total diversity estimates of 97%ID phylotypes for the ‘Deep twins’ TS28 and TS29 datasets.

Dataset	Size	Phylotypes	Chao	Log-normal	Sichel
TS28-Deep	848,512	473	626.5	919;**1373**;2926	724;**878**;1686**
TS29-Deep	553,416	344	557.8	874;**1787**;7015	577;**768**;1812*
TS28-Shallow	3,288	135	375.3	537;**2119**;8803	242;**386**;830*
TS29-Shallow	1,178	81	127.3	364;**1920**;9664*	134;**209**;457

Legend - The results from fitting the log-normal and Sichel distributions are **medians** with 95% confidence intervals from the posterior distribition (11).** indicates a significantly better fit while * indicates a non-significantly better fit to the log-normal or Sichel distribution.

Table S5: Assembly of the gut microbiome.

	TS28	TS29
Reads assembled	5,881,372	3,560,194
Reads partially assembled	377,943	307,154
Singleton reads	345,834	256,003
Repeat reads	377,903	186,308
Outlier reads	59,549	30,398
%Reads assembled	83.51	82.03
Total number reads	7,042,601	4,340,057
Number large contigs[a]	92,104	61,460
Bases in large contigs	152,096,866	96,081,634
Average large contig size	1,651	1,563
N50 large contig size	2,448	2,055
Largest contig size	514,016	571,641
Total number of contigs	205,019	144,376
Total bases in contigs	189,049,946	123,910,240
Number of scaffolds	11,780	6,392
Number of bases	99,989,509	61,353,614
Average scaffold size	8,488	9,598
N50 scaffold size	15,510	20,555
Largest scaffold size	1,243,730	1,626,224

[a] Large contigs defined as >500bp.

Table S6: PhyloPythia binning results (family- and genus-level).

Bin	Number of scaffolds TS28	Number of scaffolds TS29	Size of scaffolds (bp) TS28	Size of scaffolds (bp) TS29	Number of genes in bin TS28	Number of genes in bin TS29
Ruminococcus	2,791	1,802	18,138,443	17,185,247	16,487	21,294
Bacteroides	1,862	962	10,531,625	12,157,161	8,506	12,292
Clostridium	1,315	778	12,556,908	4,279,082	10,897	4,987
Eubacterium	1,299	433	10,492,400	2,092,398	9,006	2,259
Faecalibacterium	1,129	889	22,388,736	9,586,340	22,867	10,527
Dorea	629	325	3,457,301	2,025,422	3,161	2,338
Parabacteroides	471	266	2,352,723	1,105,076	2,608	975
Ruminococcaceae Unclassified	413	79	2,276,128	1,744,382	2,070	1,731
Methanobrevibacter	141	197	1,711,498	1,051,479	1,861	1,110
Bifidobacterium	119	15	5,166,191	4,805,836	5,382	4,161
Lachnospiraceae Unclassified	97	41	585,820	124,927	480	146
Collinsella	59	54	1,627,144	2,316,022	1,783	2,021
Enterobacteriaceae Unclassified[a]	40	2	147,724	4,434	149	7
Alistipes	32	130	2,710,216	447,729	2,449	439
Eubacteriaceae Unclassified	29	23	85,801	66,193	92	58
Coriobacteriaceae Unclassified	23	3	182,482	7,442	209	8
Erysipelotrichaceae Unclassified	22	10	84,383	29,951	77	34
Clostridiaceae Unclassified	17	4	127,019	18,710	129	22
Bacteroidaceae Unclassified	14	8	45,075	33,885	44	19
Porphyromonadaceae Unclassified	10	3	32,223	10,457	29	11
Providencia	3	0	9,702	0	11	0
Streptococcus	3	1	7,106	4,220	8	1
Lactococcus	3	2	7,425	5,512	5	7
Bifidobacteriaceae Unclassified	3	0	7,194	0	4	0
Rikenellaceae Unclassified	1	0	2,140	0	2	0
Methanobacteriaceae Unclassified	0	1	0	2,025	0	1
Streptococcaceae Unclassified	0	1	0	5,347	0	5
Total	10,525	6,029	94,733,407	59,109,277	88,316	64,453
Percentage binned	89.3	94.3	94.7	96.3		

[a] Unclassified refers to scaffolds that were binned at the family-level but could not be resolved at the genus-level.

Table S7: Genomes in the reference human gut microbe database.

Strain name	NCBI Taxonomy
Actinomyces odontolyticus	Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Actinomycineae; Actinomycetaceae; Actinomyces
Bifidobacterium adolescentis	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium adolescentis ATCC15703	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium angulatum	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium animalis HN019	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium animalis subsp lactis AD011	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium breve	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium catenulatum	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium dentium	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium gallicum	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium longum DJO10A	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium longum NCC2705	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Bifidobacterium pseudocatenulatum	Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium
Collinsella aerofaciens	Actinobacteria; Actinobacteria (class); Coriobacteridae; Coriobacteriales; Coriobacterineae; Coriobacteriaceae; Collinsella
Collinsella intestinalis	Actinobacteria; Actinobacteria (class); Coriobacteridae; Coriobacteriales; Coriobacterineae; Coriobacteriaceae; Collinsella
Collinsella stercoris	Actinobacteria; Actinobacteria (class); Coriobacteridae; Coriobacteriales; Coriobacterineae; Coriobacteriaceae; Collinsella
Bacteroides caccae	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides cellulosilyticus	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides coprocola	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides coprophilus	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides dorei	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides eggerthii	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides finegoldii	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides fragilis 3_1_12	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides fragilis NCTC9343	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides fragilis YCH46	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides intestinalis	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides ovatus	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides plebeius	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides sp 1_1_6	**Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides**
Bacteroides sp D1	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides sp D2	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales;

	Bacteroidaceae; Bacteroides
Bacteroides stercoris	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides thetaiotaomicron 3731	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides thetaiotaomicron 7330	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides thetaiotaomicron VPI5482	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides uniformis	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides vulgatus ATCC8482	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides WH2	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
Bacteroides xylanisolvens XB1A	**Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides**
Parabacteroides distasonis ATCC8503	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
Parabacteroides johnsonii	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
Parabacteroides merdae	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
Prevotella copri	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella
Alistipes putredinis	Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae; Alistipes
Victivallis vadensis ATCCBAA548	Chlamydiae/Verrucomicrobia group; Lentisphaerae; Victivallales; Victivallaceae; Victivallis
Methanobrevibacter smithii ATCC35061	Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanobrevibacter
Methanobrevibacter smithii DSM2374	Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanobrevibacter
Methanobrevibacter smithii DSM2375	Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanobrevibacter
Methanosphaera stadtmanae DSM3091	Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanosphaera
Lactobacillus casei ATCC334	Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus
Lactobacillus delbrueckii subsp bulgaricus ATCC11842	Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus
Lactococcus lactis subsp cremoris MG1363	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Lactococcus
Lactococcus lactis subsp cremoris SK11	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Lactococcus
Lactococcus lactis subsp lactis Il1403	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Lactococcus
Streptococcus infantarius	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus
Streptococcus thermophilus CNRZ1066	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus
Streptococcus thermophilus LMD9	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus
Streptococcus thermophilus LMG18311	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus
Bacteroides capillosus	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium asparagiforme	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium bartlettii	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium bolteae	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium hiranonis	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium hylemonae	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium leptum	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium methylpentosum	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium nexile	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium scindens	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium sp L2	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium sp M62/1	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium sp SS2	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium

Clostridium sporogenes	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Clostridium symbiosum	Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium
Anaerococcus hydrogenalis	Firmicutes; Clostridia; Clostridiales; Clostridiales incertae sedis; Clostridiales Family XI. Incertae Sedis; Anaerococcus
Peptostreptococcus micros	Firmicutes; Clostridia; Clostridiales; Clostridiales incertae sedis; Clostridiales Family XI. Incertae Sedis; Parvimonas
Anaerofustis stercorihominis	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Anaerofustis
Eubacterium eligens	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
Eubacterium hallii	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
Eubacterium rectale ATCC33656	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
Eubacterium ventriosum	Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
Anaerostipes caccae	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes
Bryantella formatexigens	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Bryantella
Butyrivibrio crossotus	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Butyrivibrio
Coprococcus comes	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus
Coprococcus eutactus	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus
Dorea formicigenerans	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea
Dorea longicatena	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea
Roseburia intestinalis L1	Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia
Anaerotruncus colihominis	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Anaerotruncus
Faecalibacterium prausnitzii M21/2	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium
Ruminococcus bromiiL263	**Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus**
Ruminococcus gnavus	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus
Ruminococcus lactaris	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus
Ruminococcus obeum	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus
Ruminococcus torques	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus
Subdoligranulum variabile	Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Subdoligranulum
Blautia hansenii	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Blautia
Ruminococcus hydrogenotrophicus	Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Blautia
Mitsuokella multacida	Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Mitsuokella
Catenibacterium mitsuokai	Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; Catenibacterium
Holdemania filiformis	Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; Holdemania
Clostridium ramosum	Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; unclassified Erysipelotrichaceae
Clostridium spiroforme	Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; unclassified Erysipelotrichaceae
Eubacterium biforme	Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; unclassified Erysipelotrichaceae
Eubacterium dolichum	Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; unclassified Erysipelotrichaceae
Clostridium Innocuum strain SB23	**Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; unclassified Erysipelotrichaceae**
Fusobacterium sp 4_1_13	Fusobacteria; Fusobacteria (class); Fusobacteriales; Fusobacteriaceae; Fusobacterium
Fusobacterium varium ATCC27725	**Fusobacteria; Fusobacteria (class); Fusobacteriales; Fusobacteriaceae; Fusobacterium**
Desulfovibrio piger ATCC29098	Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio
Desulfovibrio piger GOR1	**Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio**
Helicobacter pylori HPAG1	Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter
Citrobacter sp	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Citrobacter
Enterobacter cancerogenus	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter
Escherichia coli str K12 substr MG1655	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia
Escherichia fergusonii ATCC35469	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae;

	Escherichia
Proteus penneri	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Proteus
Providencia alcalifaciens	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Providencia
Providencia rettgeri	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Providencia
Providencia rustigianii	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Providencia
Providencia stuartii	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Providencia
Shigella sp D9	Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella

Legend - Contig selection for PhyloPythia training was performed against all genomes except those in bold. Two additional gut microbial genomes were used for training: *Bacteroides pectinophilus* and *Eubacterium siraeum*.

Table S8: Estimates of gene and gene cluster diversity using Bayesian fits of the log-normal, inverse-Gaussian, log-Student's t, and Sichel distributions.

Dataset	Log-normal	Inverse-Gaussian	Log-Student's t	Sichel
TS28 expressed genes[b]	89486;**90235**;90975	90724;**91516**;92345	84434;**85099**;85789**[a]	77187;**77572**;77969
TS28 expressed clusters[b]	36023;**36268**;36506	35097;**35292**;35498	35340;**35554**;35781**	33223;**33351**;33482
TS28 genes[c]	241113;**242029**;242918	229119;**229746**;230404	241132;**242023**;242919**	240682;**241963**;243603
TS28 clusters[c]	114361;**114886**;115433	106878;**107172**;107489	114374;**114890**;115422	114474;**115216**;116071**
TS29 expressed genes	173737;**177606**;181204	180075;**184535**;189349	169316;**173309**;177310**	123122;**124820**;126715
TS29 expressed clusters	57873;**59389**;60451	50819;**51753**;52758	56854;**58339**;59681**	44725;**45442**;46168
TS29 genes	250842;**252399**;254140	229132;**230164**;231290	250914;**252527**;254204	233035;**234661**;236160**
TS29 clusters	118004;**118886**;119742	104394;**104896**;105398	118046;**119005**;119985	111523;**112522**;113575**

[a] Results are given as lower 2.5% quantile; 50% quantile (**median**); 97.5% quantile of the posterior distribution. **indicates the best-fitting distribution from Deviance Information Criterion (DIC) values (in all cases significant).

[b] expressed genes and gene clusters were observed by sequencing total community cDNA.

[c] genes and gene clusters were observed by sequencing total community DNA.

Table S9: Genes assigned to CAZy categories[a] in microbiome bins.

Individual	Genus	GH	GT	PL	CE	CBM	COH	DOC
TS28	Bacteroides	323	129	22	3	28		
TS29		57	137	28	44	44		
TS28	Ruminococcus	366	148		3	46		11
TS29		345	163		27	27		2
TS28	Faecalibacterium	335	267	1	37	54	1	42
TS29		135	82		9	1		
TS28	Clostridium	18	92	1	13	22		
TS29		68	36	2	2	6		
TS28	Bifidobacterium	117	5		3	18		
TS29		128	48		3	23		
TS28	Eubacterium	1	12	1	12	23		9
TS29		22	13		1	4		8
TS28	Parabacteroides	76	14		7	7		1
TS29		24	12		3	4		
TS28	Dorea	49	38		6	6		
TS29		14	9		2	1		
TS28	Ruminococcaceae Unc[b]	3	14		1	1		1
TS29		28	25		5	4		
TS28	Collinsella	5	9		2	4		
TS29		19	24		4	2		
TS28	Alistipes	13	19		2	3		
TS29			3					
TS28	Lachnospiraceae Unc	6	6					
TS29		1	1					
TS28	Coriobacteriaceae Unc	2	2		1			
TS29								
TS28	Erysipelotrichaceae Unc	1	5					
TS29			6					
TS28	Eubacteriaceae Unc		4					
TS29		1						
TS28	Methanobrevibacter		27		1			
TS29			19		1			
TS28	Porphyromonadaceae Unc	1						
TS29								
TS28	Enterobacteriaceae Unc		1					
TS29								
TS28	Bacteroidaceae Unc							
TS29		1	3					
TOTAL		2,897	1,526	64	246	337	1	74

[a] Categories include: glycoside hydrolases (GH), glycosyl-transferases (GT), polysaccharide lyases (PL), carbohydrate esterases (CE), carbohydrate-binding modules (CBM), cohesins (COH), and dockerins (DOC).

[b] Unc indicates unclassified scaffolds that were binned at the family but not genus level.

Table S10: Genes assigned to CAZy families in microbiome bins.

Genus	Alistipes	Alistipes	Bacteroidaceae Unclassified	Bacteroides	Bacteroides	Bifidobacterium	Bifidobacterium	Clostridium	Clostridium	Collinsella	Collinsella	Coriobacteriaceae Unclassified	Dorea	Dorea	Enterobacteriaceae Unclassified	Erysipelotrichaceae Unclassified	Erysipelotrichaceae Unclassified	Eubacteriaceae Unclassified	Eubacteriaceae Unclassified	Eubacterium	Eubacterium	Faecalibacterium	Faecalibacterium	Lachnospiraceae Unclassified	Lachnospiraceae Unclassified	Methanobrevibacter	Methanobrevibacter	Parabacteroides	Parabacteroides	Porphyromonadaceae Unclassified	Ruminococcaceae Unclassified	Ruminococcaceae Unclassified	Ruminococcus	Ruminococcus
Individual	TS28	TS29	TS29	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS28	TS29	TS28	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS29	TS28	TS28	TS29	TS28	TS29
Abbreviation	TS28Ali	TS29Ali	TS29BacUnc	TS28Bac	TS29Bac	TS28Bif	TS29Bif	TS28Clo	TS29Clo	TS28Col	TS29Col	TS28CorUnc	TS28Dor	TS29Dor	TS28EntUnc	TS28EryUnc	TS29EryUnc	TS28EubUnc	TS29EubUnc	TS28Eub	TS29Eub	TS28Fae	TS29Fae	TS28LacUnc	TS29LacUnc	TS28Met	TS29Met	TS28Par	TS29Par	TS28PorUnc	TS28RumUnc	TS29RumUnc	TS28Rum	TS29Rum
GH1						1	2	7			5		1									27	13										5	13
GH2	3			35	59	5	7	16	2				2	2						7		39	18	1				14	3		5	2	25	27
GH3			1	24	48	9	10	12	4	1			5	1						5		34	24					2	3		2	4	40	28
GH4								3	1		1											4	1								1	1	3	2
GH5				9	18	4	5	5	4		1		1							3		12			1			1					5	3
GH8						1	2													1		1	1										1	
GH9				4	8																	12												
GH10				2	4			1												1		2											2	
GH13	4			8	18	29	25	24	14	2	3	2	10	3						37	15	50	20						1		3	4	70	70
GH15				2	2																								2					
GH16				2	4			4												2		5						3	2					
GH18				3	15	1	2	8	1	2			2	1						1									1			1	9	9
GH20	1			18	19	2	2	6														1						8	1				7	10
GH23	1			6	6		1	3	3		1		2	1		1				1		5	1					2	1		1	2	3	3
GH24	1																																1	
GH25				2	1	3	5	9						2						5	2	21	5	1							2	1	8	7
GH26				1	3		1	1														5									1		3	
GH27				2	3	3	2	1					1	2															1		2	2	3	
GH28				14	13						1		2									11	8										2	
GH29	1			13	7			11	2													2	2								2	1	10	15
GH30				2	4		1	2	2																									
GH31				10	16	5	6	7	4											3		11	4	1				1			1	1	19	17
GH32				6	5	2	3	8	4		4		4							1		3						1	1			2	17	14
GH33				2	9			1																				2	1				2	1
GH35				1	3			3	1																			1			1		4	
GH36				2	7	5	5	5	1				5							4		7	1	1				1					17	13
GH38				2	3	2	2	7	1											1		3	1								1	1	13	1
GH39						1	1	3	1																							1	5	1
GH42				2	4	5	6	2	3													2	1										11	16
GH43				42	50	24	24	3	7				4							5		10	10					4	1		1	1	10	13
GH44																				2		1												
GH48																						1												
GH50					4																													
GH51				8	9	6	7	6	6				2						1	2		2	1	1				1	1			2	8	6
GH53				2	1	1	1													1													3	
GH55				4	4			1																										
GH57	1			1	2																													
GH59																						1												
GH63				4	2								1										1											
GH65	1			2	1			1	1											1		1											1	
GH66					2																													
GH67				2	2																	1	1											
GH73				1	5			2												5		2						1	1				7	7
GH74				1	1															3		1									2			
GH76				1	12				1																			1					1	
GH77				1	3	4	4	3	2		2		4							5	1	17	5					1	1		1		8	13
GH78				8	12	1	1	2					3	2						1		6	5					8		1		1	10	11
GH84				1	2																							1	1				2	1
GH85						1	1																1											
GH88				7	11																	2	1					1						
GH89				1	6			2																				1					3	
GH92				19	30																							11						
GH93																				1														
GH94				2	2			1												1	1	6	3								2		10	15
GH95				3	7			5	2												3	5	1					3			1		9	11
GH97				13	29																							1	2			1		
GH98								1																										1
GH99					1																													
GH101						1	1																										1	1
GH105				9	14			1			1											10	2					1						1
GH106				1	7																							3						
GH108				1																														
GH109				8	4																							1					1	1
GH110				1	1			1																				1			1			
GH111								1																										
GH112						1	1	1	1													10	2										5	13
GH113																				1		1	1	1										1
GH115				8	4																	1	1										2	
GT1				1				2				1								3						1	1							4
GT2	6	2		48	61	30	26	50	18	1	16	1	19	6		1	1	1		54	5	137	40	6	1	21	14	7	5		3	12	78	83
GT3					5																													
GT4	7	1	2	50	37	11	10	14	6	2	2		10	1		2	4	3		31	2	67	25			4	3	4	5		6	6	32	27
GT5				2	1			3	2	2	1		2	1						5	1	7	2								1	1	5	11
GT6				1																		4	1											
GT8				1	1		2	1	1						1					1		1											1	
GT9	1			2	3																													
GT10																1						1											1	
GT11				2	3																	3											3	
GT14				2	1	1																3	3									2		
GT17																																	1	
GT19				1	2																													
GT20				1	1																													
GT25					2																													
GT26			1	4	2					1												4	2						1				2	1
GT28	1			3	4	2	2	5	3	1	2		3	1						7	2	12	1					1			2	1	6	8
GT30	1			2	4																													
GT32				2	3		2	1								1	1			5		2	2					1				2	3	1
GT35	1				1	2	2	9	4	1	2		3							7	2	15	4					1	1		1	1	12	25

GT39																				1		2	1											
GT51	1			4	5	4	4	6	2	1	1		1							6	1	8	1								1		4	3
GT56																						1												
GT66																										1	1							
GT83	1			3	1																													
GT84								1																										
PL1				3	8			1	1													3												
PL6					1																													
PL7																						1												
PL8				3	4																													
PL9				2	1				1													2												
PL10				2	1																													
PL11				4	3															1		3												
PL12				2	3																													
PL13				1	2																													
PL15				3	4																													
PL17					1																	1												
PL21				2																														
CBM2													1																					
CBM3																				1		5												
CBM4																						5	1										3	
CBM5						1	1																											
CBM6				3	5	1	1													1												1		
CBM9								1	1											1													2	
CBM13				1			4				1									1		19	2								1	1	1	1
CBM20				1	3																	1												
CBM22						2	2															2											1	
CBM23																																	1	
CBM26						1	1													2	2													
CBM32				15	15	1	2						1							1		3	3					5	2				17	9
CBM34																				1												1	2	1
CBM35					1	1	1													1		2							1				1	
CBM38					1																													
CBM40																																	2	1
CBM41						2	2																											
CBM48	1			3	7	7	7	3	2	1	1		3	1						12	2	17	4									1	12	14
CBM50	2			2	7	2	2	17	3	3			1							2								2	1				4	1
CBM51					1																													
CBM54								1																										
CBM57				2	4																													
CBM58				1																														
CE1				9	11															3		2	1			1	1	1	1			2	5	1
CE2						1	1															2	2										1	1
CE3																						3											1	
CE4	1			2	2			8	1	2	1	1	4	1						6		11	2								1	2	16	12
CE6				1	12																								1					2
CE7				4	5						1																	1						
CE8				5	3			2			1										1	6	1											
CE9				4	5	2	2	2	1		1		2	1						2		9	3					2				1	7	10
CE11	1			2	2			1																				1						
CE12				3	4															1		4												
CE14																													1					
CE15																												2						1
COH																						1												
DOC1																				9	8	42						1			1		11	2
SUM	37	3	4	532	760	188	202	308	114	20	49	5	99	26	1	6	6	4	1	265	48	746	236	12	2	28	20	105	43	1	47	62	601	564
R^2				0.84		0.97		0.76		0.08			0.66							0.49		0.83				1.00		0.27			0.41		0.93	

Table S11: Genes with high or low relative expression in the TS28 fecal meta-transcriptome.

Gene	cDNA sequences	DNA sequences	Ratio	COG categories	COGs	COG Annotations
TS28Met1158|CDS|CDS	82.2	1.3	217.3	B	COG2036	Histones H3 and H4
Msmi750732|CDS|CDS	82.2	1.3	217.3	B	COG2036	Histones H3 and H4
Msmi740947|CDS|CDS	82.2	1.3	217.3	B	COG2036	Histones H3 and H4
Msmi740186|CDS|CDS	121.2	0.5	801.7	C	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
Msmi740434|CDS|CDS	65.3	0.5	431.8	C	COG1853|COG0446|COG1773|COG0426	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Uncharacterized flavoproteins
Bova1292|CDS|CDS	161.0	2.0	266.2	C	COG1145	Ferredoxin
Msmi751243|CDS|CDS	65.9	0.8	261.4	C	COG1853|COG0446|COG1773|COG0426	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Uncharacterized flavoproteins
Msmi740445|CDS|CDS	59.9	1.3	148.6	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
Msmi751494|CDS|CDS	165.4	4.3	126.2	C	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
Msmi740666|CDS|CDS	59.5	1.8	112.4	C	COG0680	Ni,Fe-hydrogenase maturation factor
TS28Met1385|CDS|CDS	59.5	1.8	112.4	C	COG0680	Ni,Fe-hydrogenase maturation factor
Msmi751010|CDS|CDS	59.5	1.8	112.4	C	COG0680	Ni,Fe-hydrogenase maturation factor
Msmi751009|CDS|CDS	16.9	0.5	111.8	C	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit
TS28Clo06848|CDS|CDS	131.0	5.0	86.6	C	COG1454	Alcohol dehydrogenase, class IV
Msmi750889|CDS|CDS	33.8	1.3	83.9	C	COG0374|COG3259	Ni,Fe-hydrogenase I large subunit|Coenzyme F420-reducing hydrogenase, alpha subunit
Msmi740794|CDS|CDS	37.7	1.7	74.7	C	COG0374|COG3259	Ni,Fe-hydrogenase I large subunit|Coenzyme F420-reducing hydrogenase, alpha subunit
Msmi750591|CDS|CDS	28.8	1.3	71.5	C	COG1151	6Fe-6S prismane cluster-containing protein
TS29Bac03394|CDS|CDS	20.5	1.0	67.8	C	COG0039	Malate/lactate dehydrogenases
Bxyl1753|CDS|CDS	6.6	0.3	65.3	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Msmi741634|CDS|CDS	2.3	0.1	60.8	C	COG0371	Glycerol dehydrogenase and related enzymes
TS28Bac5354|CDS|CDS	339.8	18.5	60.7	C	COG1145	Ferredoxin
CspL20570|CDS|CDS	9.0	0.5	59.5	C	COG1454	Alcohol dehydrogenase, class IV
Msmi740665|CDS|CDS	41.8	2.3	59.2	C	COG0374|COG3259|COG3261	Ni,Fe-hydrogenase I large subunit|Coenzyme F420-reducing hydrogenase, alpha subunit|Ni,Fe-hydrogenase III large subunit
CspSS20152|CDS|CDS	106.2	6.0	58.5	C	COG1592	Rubrerythrin
TS28Fae20658|CDS|CDS	202.2	12.0	55.7	C	COG1592	Rubrerythrin
Bdor3549|CDS|CDS	16.8	1.0	55.7	C	COG0822	NifU homolog involved in Fe-S cluster formation
Msmi750814|CDS|CDS	5.5	0.3	54.6	C	COG0045	Succinyl-CoA synthetase, beta subunit
Bste0134|CDS|CDS	113.0	7.0	53.4	C	COG0039	Malate/lactate dehydrogenases
Hfil0795|CDS|CDS	16.0	1.0	52.9	C	COG1902|COG1053|COG3976	NADH:flavin oxidoreductases, Old Yellow Enzyme family|Succinate dehydrogenase/fumarate reductase, flavoprotein subunit|Uncharacterized protein conserved in bacteria
PRABACTJOHN2409|CDS|CDS	16.0	1.0	52.9	C	COG1592	Rubrerythrin
TS28Met1797|CDS|CDS	15.4	1.0	51.0	C	COG1773|COG1853|COG1592	Rubredoxin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Rubrerythrin
Msmi741534|CDS|CDS	15.4	1.0	51.0	C	COG1592|COG1853|COG1773	Rubrerythrin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Rubredoxin
Msmi750184|CDS|CDS	15.4	1.0	51.0	C	COG1592|COG1853|COG1773	Rubrerythrin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Rubredoxin
Dlon0162|CDS|CDS	7.5	0.5	49.6	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
TS29Rum17368|CDS|CDS	14.0	1.0	46.3	C	COG1151	6Fe-6S prismane cluster-containing protein
TS28Met0317|CDS|CDS	7.0	0.5	46.3	C	COG1013|COG1142	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Fe-S-cluster-containing hydrogenase components 2
TS28RumUnc1774|CDS|CDS	13.5	1.0	44.6	C	COG0355	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)
Msmi751293|CDS|CDS	32.2	2.4	44.0	C	COG1035|COG1145|COG1908	Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin|Coenzyme F420-reducing hydrogenase, delta subunit
Msmi740203|CDS|CDS	15.3	1.2	43.5	C	COG1014|COG1013|COG1142	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Fe-S-cluster-containing hydrogenase components 2
TS28Met0338|CDS|CDS	187.6	14.3	43.3	C	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
TS29Clo1195|CDS|CDS	6.5	0.5	43.0	C	COG1592	Rubrerythrin
Msmi740204|CDS|CDS	6.4	0.5	42.4	C	COG1142|COG0437	Fe-S-cluster-containing hydrogenase components 2|Fe-S-cluster-containing hydrogenase components 1
Msm1348|CDS|rubrerythrin	19.2	1.5	42.3	C	COG1592	Rubrerythrin
Msmi750683|CDS|CDS	12.5	1.0	41.4	C	COG0479|COG2048	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit|Heterodisulfide reductase, subunit B
Msmi740998|CDS|CDS	12.2	1.0	40.3	C	COG0479|COG2048	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit|Heterodisulfide reductase, subunit B
TS29Col1204|CDS|CDS	6.1	0.5	40.2	C	COG1592	Rubrerythrin
Ehal0657|CDS|CDS	12.0	1.0	39.7	C	COG4624|COG3383|COG1034|COG0243	Iron only hydrogenase large subunit, C-terminal domain|Uncharacterized anaerobic dehydrogenase|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Anaerobic dehydrogenases, typically selenocysteine-containing
ShigspD90600|CDS|CDS	6.0	0.5	39.7	C	COG3954	Phosphoribulokinase
Rgna2175|CDS|CDS	6.0	0.5	39.7	C	COG0554	Glycerol kinase

Msmi751475|CDS|CDS	5.8	0.5	38.0	C	COG1142|COG0437	Fe-S-cluster-containing hydrogenase components 2|Fe-S-cluster-containing hydrogenase components 1
Pmer3609|CDS|CDS	23.0	2.0	38.0	C	COG1012	NAD-dependent aldehyde dehydrogenases
Msmi741567|CDS|CDS	5.7	0.5	37.5	C	COG1853|COG0446|COG1773|COG0426	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Uncharacterized flavoproteins
Msmi740384|CDS|CDS	28.7	2.6	36.7	C	COG1035|COG1145|COG1908	Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin|Coenzyme F420-reducing hydrogenase, delta subunit
Msmi740792|CDS|CDS	13.5	1.3	35.7	C	COG1908|COG1941	Coenzyme F420-reducing hydrogenase, delta subunit|Coenzyme F420-reducing hydrogenase, gamma subunit
TS29Eub1165|CDS|CDS	64.7	6.0	35.6	C	COG1454	Alcohol dehydrogenase, class IV
TS28Fae08859|CDS|CDS	106.5	10.0	35.2	C	COG1592	Rubrerythrin
TS29Bac04866|CDS|CDS	10.2	1.0	33.6	C	COG0356	F0F1-type ATP synthase, subunit a
TS29Bac02967|CDS|CDS	3.3	0.3	33.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
CspSS20148|CDS|CDS	10.0	1.0	33.1	C	COG2086	Electron transfer flavoprotein, beta subunit
TS28Par0162|CDS|CDS	5.0	0.5	33.1	C	COG2025	Electron transfer flavoprotein, alpha subunit
TS29Clo3788|CDS|CDS	10.0	1.0	33.1	C	COG1894|COG1905	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|NADH:ubiquinone oxidoreductase 24 kD subunit
Hfil1508|CDS|CDS	10.0	1.0	33.1	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28Bac1171|CDS|CDS	15.0	1.5	33.1	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28RumUnc0596|CDS|CDS	10.0	1.0	33.1	C	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
TS29Bac00720|CDS|CDS	3.3	0.3	33.1	C	COG0056	F0F1-type ATP synthase, alpha subunit
Msmi751230|CDS|CDS	70.6	7.2	32.6	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
Msmi751011|CDS|CDS	46.5	4.8	31.8	C	COG0374|COG3259|COG3261	Ni,Fe-hydrogenase I large subunit|Coenzyme F420-reducing hydrogenase, alpha subunit|Ni,Fe-hydrogenase III large subunit
Bdor3290|CDS|CDS	28.5	3.0	31.4	C	COG1592	Rubrerythrin
Bdor2083|CDS|CDS	37.0	4.0	30.6	C	COG1592|COG1853|COG2025|COG1773	Rubrerythrin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Electron transfer flavoprotein, alpha subunit|Rubredoxin
Msmi740868|CDS|CDS	6.2	0.7	30.6	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
Msmi751092|CDS|CDS	33.6	3.7	30.3	C	COG1927	Coenzyme F420-dependent N(5),N(10)-methenyltetrahydromethanopterin dehydrogenase
Msmi740582|CDS|CDS	33.6	3.7	30.3	C	COG1927	Coenzyme F420-dependent N(5),N(10)-methenyltetrahydromethanopterin dehydrogenase
Bdor4073|CDS|CDS	18.3	2.0	30.3	C	COG0055	F0F1-type ATP synthase, beta subunit
TS29Bac03490|CDS|CDS	3.0	0.3	29.8	C	COG0852|COG0377	NADH:ubiquinone oxidoreductase 27 kD subunit|NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases
TS29Rum14613|CDS|CDS	9.0	1.0	29.8	C	COG2080|COG1529	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
Msmi741675|CDS|CDS	3.6	0.4	29.8	C	COG2037	Formylmethanofuran:tetrahydromethanopterin formyltransferase
Msmi750910|CDS|CDS	3.0	0.3	29.8	C	COG1625	Fe-S oxidoreductase, related to NifB/MoaA family
Msmi751299|CDS|CDS	8.7	1.0	28.8	C	COG1153	Formylmethanofuran dehydrogenase subunit D
Msmi740668|CDS|CDS	29.9	3.5	28.2	C	COG1035|COG1145|COG2221|COG3350	Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin|Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits|Uncharacterized conserved protein
Msmi751047|CDS|CDS	5.9	0.7	27.9	C	COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains
Msmi751008|CDS|CDS	12.6	1.5	27.9	C	COG1035|COG1145|COG2221|COG3350	Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin|Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits|Uncharacterized conserved protein
Dlon2091|CDS|CDS	12.5	1.5	27.6	C	COG1592	Rubrerythrin
Bova1491|CDS|CDS	16.4	2.0	27.2	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Cbol1741|CDS|CDS	8.2	1.0	27.0	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Ccom0561|CDS|CDS	8.0	1.0	26.5	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
TS29Fae09192|CDS|CDS	4.0	0.5	26.5	C	COG2025|COG2086	Electron transfer flavoprotein, alpha subunit|Electron transfer flavoprotein, beta subunit
TS28Ali2359|CDS|CDS	8.0	1.0	26.5	C	COG2025	Electron transfer flavoprotein, alpha subunit
TS29Bac08557|CDS|CDS	8.0	1.0	26.5	C	COG1014|COG1146	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Ferredoxin
Bdor4074|CDS|CDS	8.0	1.0	26.5	C	COG0355	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)
Msmi751592|CDS|CDS	5.2	0.7	26.4	C	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I

Cint819|CDS|CDS	7.7	1.0	25.4	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS29Met0495|CDS|CDS	15.1	2.0	25.3	C	COG3383|COG0243|COG1029	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing|Formylmethanofuran dehydrogenase subunit B
TS28Ali1245|CDS|CDS	83.5	11.0	25.1	C	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Bthe7334651|CDS|CDS	2.5	0.3	24.8	C	COG1882	Pyruvate-formate lyase
Bsp1161141|CDS|CDS	2.5	0.3	24.8	C	COG1882	Pyruvate-formate lyase
Bdor1177|CDS|CDS	29.7	4.0	24.5	C	COG0039	Malate/lactate dehydrogenases
Msmi750684|CDS|CDS	23.3	3.3	23.7	C	COG0247|COG2048|COG1150	Fe-S oxidoreductase|Heterodisulfide reductase, subunit B|Heterodisulfide reductase, subunit C
Msmi740202|CDS|CDS	18.8	2.7	23.3	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS29Bac00287|CDS|CDS	7.0	1.0	23.1	C	COG2869	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrC
Hfil1792|CDS|CDS	7.0	1.0	23.1	C	COG1905|COG1894	NADH:ubiquinone oxidoreductase 24 kD subunit|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit
Msmi740997|CDS|CDS	22.0	3.3	22.4	C	COG0247|COG2048|COG1150	Fe-S oxidoreductase|Heterodisulfide reductase, subunit B|Heterodisulfide reductase, subunit C
TS28RumUnc0593|CDS|CDS	54.0	8.0	22.3	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi740201|CDS|CDS	1.7	0.3	21.8	C	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit
Msmi741543|CDS|CDS	3.8	0.6	21.5	C	COG0221	Inorganic pyrophosphatase
Pmer2622|CDS|CDS	19.0	3.0	20.9	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Ehal0042|CDS|CDS	9.5	1.5	20.9	C	COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains
FpraM2121476|CDS|CDS	6.3	1.0	20.9	C	COG2414	Aldehyde:ferredoxin oxidoreductase
RintL13461|CDS|CDS	25.0	4.0	20.7	C	COG0356	F0F1-type ATP synthase, subunit a
TS29Fae08111|CDS|CDS	3.0	0.5	19.8	C	COG1882	Pyruvate-formate lyase
RintL12400|CDS|CDS	6.0	1.0	19.8	C	COG1151	6Fe-6S prismane cluster-containing protein
Msmi740930|CDS|CDS	4.5	0.8	19.8	C	COG0716	Flavodoxins
Msm0861|CDS|flavodoxin	4.5	0.8	19.8	C	COG0716	Flavodoxins
Msmi750749|CDS|CDS	4.5	0.8	19.8	C	COG0716	Flavodoxins
Csci0616|CDS|CDS	6.0	1.0	19.8	C	COG0280|COG0857	Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
ShigspD92742|CDS|CDS	6.0	1.0	19.8	C	COG0277	FAD/FMN-containing dehydrogenases
Pmer0377|CDS|CDS	20.5	3.5	19.4	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
Msmi750891|CDS|CDS	18.8	3.3	19.2	C	COG1908|COG1941	Coenzyme F420-reducing hydrogenase, delta subunit|Coenzyme F420-reducing hydrogenase, gamma subunit
TS28Met0354|CDS|CDS	18.8	3.3	19.2	C	COG1908|COG1941	Coenzyme F420-reducing hydrogenase, delta subunit|Coenzyme F420-reducing hydrogenase, gamma subunit
Msmi740628|CDS|CDS	5.9	1.0	18.9	C	COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains
TS28RumUnc1463|CDS|CDS	5.5	1.0	18.2	C	COG2878	Predicted NADH:ubiquinone oxidoreductase, subunit RnfB
TS28Fae02269|CDS|CDS	16.5	3.0	18.2	C	COG2080|COG3427	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Uncharacterized conserved protein
Casp6372|CDS|CDS	5.5	1.0	18.2	C	COG1592	Rubrerythrin
Pmer2223|CDS|CDS	5.5	1.0	18.2	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS29Dor1290|CDS|CDS	24.5	4.5	18.0	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
Bdor3235|CDS|CDS	21.5	4.0	17.8	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi751154|CDS|CDS	2.7	0.5	17.6	C	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit
Acol2675|CDS|CDS	8.0	1.5	17.6	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Chyl0524|CDS|CDS	2.7	0.5	17.6	C	COG0822	NifU homolog involved in Fe-S cluster formation
TS28Met0318|CDS|CDS	10.5	2.0	17.4	C	COG1013|COG1142	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Fe-S-cluster-containing hydrogenase components 2
Ehal0970|CDS|CDS	21.0	4.0	17.4	C	COG0554	Glycerol kinase
Even0370|CDS|CDS	5.0	1.0	16.5	C	COG4657|COG2209	Predicted NADH:ubiquinone oxidoreductase, subunit RnfA|Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrE
TS29Rum16193|CDS|CDS	25.0	5.0	16.5	C	COG4624|COG1034|COG3383|COG0243	Iron only hydrogenase large subunit, C-terminal domain|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing

Ceut1181|CDS|CDS	5.0	1.0	16.5	C	COG2086|COG2025	Electron transfer flavoprotein, beta subunit|Electron transfer flavoprotein, alpha subunit
TS29Bac08636|CDS|CDS	5.0	1.0	16.5	C	COG2086	Electron transfer flavoprotein, beta subunit
CspL22527|CDS|CDS	10.0	2.0	16.5	C	COG1592	Rubrerythrin
Ehal1005|CDS|CDS	12.5	2.5	16.5	C	COG1454|COG0371	Alcohol dehydrogenase, class IV|Glycerol dehydrogenase and related enzymes
TS29Fae06617|CDS|CDS	10.0	2.0	16.5	C	COG1227	Inorganic pyrophosphatase/exopolyphosphatase
Rtor1197|CDS|CDS	2.5	0.5	16.5	C	COG1145	Ferredoxin
Msmi751669|CDS|CDS	1.7	0.3	16.5	C	COG0680	Ni,Fe-hydrogenase maturation factor
ShigspD90648|CDS|CDS	5.0	1.0	16.5	C	COG0578	Glycerol-3-phosphate dehydrogenase
Rlac1416|CDS|CDS	5.0	1.0	16.5	C	COG0282	Acetate kinase
TS28Ali2046|CDS|CDS	59.0	12.0	16.3	C	COG1951|COG1838	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain|Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain
Msmi740380|CDS|CDS	11.1	2.3	16.0	C	COG1145	Ferredoxin
TS28Met1386|CDS|CDS	52.5	10.8	16.0	C	COG3259|COG0374|COG3261	Coenzyme F420-reducing hydrogenase, alpha subunit|Ni,Fe-hydrogenase I large subunit|Ni,Fe-hydrogenase III large subunit
Bova4234|CDS|CDS	2.8	0.6	15.6	C	COG1882	Pyruvate-formate lyase
TS28Met0462|CDS|CDS	102.3	21.8	15.5	C	COG0426|COG0446|COG1773|COG1853	Uncharacterized flavoproteins|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
Bdor0110|CDS|CDS	7.0	1.5	15.4	C	COG2086	Electron transfer flavoprotein, beta subunit
Clep1991|CDS|CDS	2.3	0.5	15.4	C	COG1883	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
Msmi750174|CDS|CDS	5.8	1.3	15.3	C	COG0221	Inorganic pyrophosphatase
Bste1806|CDS|CDS	18.5	4.0	15.3	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi750432|CDS|CDS	4.6	1.0	15.2	C	COG0479|COG0247|COG1139|COG0277|COG2048	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit|Fe-S oxidoreductase|Uncharacterized conserved protein containing a ferredoxin-like domain|FAD/FMN-containing dehydrogenases|Heterodisulfide reductase, subunit B
TS29Bac07222|CDS|CDS	4.5	1.0	14.9	C	COG1951|COG1838	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain|Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain
Clep0233|CDS|CDS	9.0	2.0	14.9	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS28Rum13071|CDS|CDS	49.5	11.0	14.9	C	COG0055	F0F1-type ATP synthase, beta subunit
TS29Met0325|CDS|CDS	4.4	1.0	14.6	C	COG4074|COG4007	H2-forming N5,N10-methylenetetrahydromethanopterin dehydrogenase|Predicted dehydrogenase related to H2-forming N5,N10-methylenetetrahydromethanopterin dehydrogenase
Msmi751478|CDS|CDS	7.3	1.7	14.6	C	COG1014|COG1144	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
TS28Met0320|CDS|CDS	7.3	1.7	14.6	C	COG1014|COG1144	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
TS28Rum13272|CDS|CDS	26.0	6.0	14.3	C	COG2069	CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe-S protein)
TS29Bac00722|CDS|CDS	13.0	3.0	14.3	C	COG0711	F0F1-type ATP synthase, subunit b
ShigspD92811|CDS|CDS	4.3	1.0	14.3	C	COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing
Bdor2463|CDS|CDS	17.0	4.0	14.1	C	COG1726	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrA
Msmi740984|CDS|CDS	3.5	0.8	13.9	C	COG0535|COG2710	Predicted Fe-S oxidoreductases|Nitrogenase molybdenum-iron protein, alpha and beta chains
Pmer1521|CDS|CDS	21.0	5.0	13.9	C	COG0039	Malate/lactate dehydrogenases
Msmi750982|CDS|CDS	4.9	1.2	13.7	C	COG2037	Formylmethanofuran:tetrahydromethanopterin formyltransferase
Rtor0314|CDS|CDS	27.0	6.5	13.7	C	COG1592	Rubrerythrin
TS28Bac7105|CDS|CDS	84.7	20.5	13.7	C	COG0039	Malate/lactate dehydrogenases
Cbol5612|CDS|CDS	8.0	2.0	13.2	C	COG3808	Inorganic pyrophosphatase
Pmer3423|CDS|CDS	20.0	5.0	13.2	C	COG2086	Electron transfer flavoprotein, beta subunit
Csci3049|CDS|CDS	4.0	1.0	13.2	C	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family
Bryfor0567|CDS|CDS	4.0	1.0	13.2	C	COG1853|COG0446|COG1773|COG0426	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Uncharacterized flavoproteins
DpigATC1526|CDS|CDS	2.0	0.5	13.2	C	COG1757	Na+/H+ antiporter
DpigGOR12032|CDS|CDS	2.0	0.5	13.2	C	COG1757	Na+/H+ antiporter
Csym1675|CDS|CDS	8.0	2.0	13.2	C	COG1625	Fe-S oxidoreductase, related to NifB/MoaA family
Msmi750596|CDS|CDS	1.3	0.3	13.2	C	COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases
Pmer1757|CDS|CDS	2.0	0.5	13.2	C	COG1139	Uncharacterized conserved protein containing a ferredoxin-like domain
TS29Dor2147|CDS|CDS	4.0	1.0	13.2	C	COG1014|COG4231|COG1146	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits|Ferredoxin
TS29Fae09988|CDS|CDS	2.0	0.5	13.2	C	COG0667|COG1453	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)|Predicted oxidoreductases of the aldo/keto reductase family
Cbol4815|CDS|CDS	4.0	1.0	13.2	C	COG0554	Glycerol kinase
b0727|CDS|dihydrolipoyltranssuccinase	4.0	1.0	13.2	C	COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes
TS29RumUnc1452|CDS|CDS	2.0	0.5	13.2	C	COG0348	Polyferredoxin
TS28Rum06565|CDS|CDS	8.0	2.0	13.2	C	COG0280	Phosphotransacetylase
BactD20745|CDS|CDS	2.0	0.5	13.2	C	COG0045	Succinyl-CoA synthetase, beta subunit
Bova1894|CDS|CDS	2.0	0.5	13.2	C	COG0045	Succinyl-CoA synthetase, beta subunit

Msmi741609|CDS|CDS	5.8	1.5	12.9	C	COG2033	Desulfoferrodoxin
Msmi750106|CDS|CDS	5.8	1.5	12.9	C	COG2033	Desulfoferrodoxin
TS28Met0585|CDS|CDS	5.8	1.5	12.9	C	COG2033	Desulfoferrodoxin
Msmi750151|CDS|CDS	13.5	3.5	12.8	C	COG1853|COG0446|COG1773|COG0426	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Uncharacterized flavoproteins
Pmer2122|CDS|CDS	38.5	10.0	12.7	C	COG1048	Aconitase A
Bste1812|CDS|CDS	17.3	4.5	12.7	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Ali1921|CDS|CDS	23.0	6.0	12.7	C	COG0039	Malate/lactate dehydrogenases
DpigGOR11331|CDS|CDS	7.0	1.8	12.6	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Pmer2746|CDS|CDS	19.0	5.0	12.6	C	COG1271	Cytochrome bd-type quinol oxidase, subunit 1
Bfin3327|CDS|CDS	11.3	3.0	12.5	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Bdor4119|CDS|CDS	18.5	5.0	12.2	C	COG1979|COG1454	Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family|Alcohol dehydrogenase, class IV
TS28Fae21632|CDS|CDS	11.0	3.0	12.1	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
BactD11824|CDS|CDS	1.8	0.5	12.1	C	COG0224	F0F1-type ATP synthase, gamma subunit
TS28Bac1044|CDS|CDS	5.5	1.5	12.1	C	COG0039	Malate/lactate dehydrogenases
BactD11151|CDS|CDS	2.4	0.7	12.0	C	COG0039	Malate/lactate dehydrogenases
Bxyl1549|CDS|CDS	2.4	0.7	12.0	C	COG0039	Malate/lactate dehydrogenases
TS29Bac00404|CDS|CDS	2.4	0.7	12.0	C	COG0039	Malate/lactate dehydrogenases
TS29Rum03322|CDS|CDS	28.5	8.0	11.8	C	COG0554	Glycerol kinase
TS29Met0210|CDS|CDS	2.6	0.7	11.7	C	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I
Buni1807|CDS|CDS	7.0	2.0	11.6	C	COG2869	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrC
TS29Bac07428|CDS|CDS	7.0	2.0	11.6	C	COG1883	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
TS28Clo06483|CDS|CDS	3.5	1.0	11.6	C	COG1145	Ferredoxin
CspM6210241|CDS|CDS	17.5	5.0	11.6	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Casp3082|CDS|CDS	7.0	2.0	11.6	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
TS28Par1667|CDS|CDS	7.0	2.0	11.6	C	COG0240	Glycerol-3-phosphate dehydrogenase
Pmer2954|CDS|CDS	7.0	2.0	11.6	C	COG0039	Malate/lactate dehydrogenases
Msmi750516|CDS|CDS	2.3	0.7	11.6	C	COG0240	Glycerol-3-phosphate dehydrogenase
Msmi751292|CDS|CDS	26.6	7.6	11.5	C	COG3383|COG0243	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
Msmi740385|CDS|CDS	26.6	7.6	11.5	C	COG3383|COG0243	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
Bxyl0179|CDS|CDS	1.7	0.5	11.5	C	COG1032	Fe-S oxidoreductase
TS28Met1367|CDS|CDS	9.5	2.8	11.4	C	COG0716	Flavodoxins
Msmi740667|CDS|CDS	22.2	6.7	11.0	C	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit
TS28Met1384|CDS|CDS	22.2	6.7	11.0	C	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit
TS29Bac04589|CDS|CDS	3.3	1.0	11.0	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
TS29Bac10441|CDS|CDS	1.7	0.5	11.0	C	COG3808	Inorganic pyrophosphatase
Bdor2178|CDS|CDS	3.3	1.0	11.0	C	COG1394	Archaeal/vacuolar-type H+-ATPase subunit D
Clep0151|CDS|CDS	5.0	1.5	11.0	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
Pmer2912|CDS|CDS	36.0	11.0	10.8	C	COG4249|COG3005|COG1262	Uncharacterized protein containing caspase domain|Nitrate/TMAO reductases, membrane-bound tetraheme cytochrome c subunit|Uncharacterized conserved protein
Msmi740377|CDS|CDS	18.8	5.8	10.7	C	COG3383|COG0243|COG1029	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing|Formylmethanofuran dehydrogenase subunit B
TS28Met1302|CDS|CDS	23.3	7.3	10.6	C	COG2048|COG0247|COG1150	Heterodisulfide reductase, subunit B|Fe-S oxidoreductase|Heterodisulfide reductase, subunit C
Ehal0870|CDS|CDS	11.0	3.5	10.4	C	COG1592	Rubrerythrin
TS29Bac08242|CDS|CDS	4.7	1.5	10.3	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28Met0619|CDS|CDS	5.0	1.6	10.2	C	COG0377|COG3260	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases|Ni,Fe-hydrogenase III small subunit
Msmi750034|CDS|CDS	5.0	1.6	10.2	C	COG0377|COG3260	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases|Ni,Fe-hydrogenase III small subunit
TS28Fae15593|CDS|CDS	43.3	14.0	10.2	C	COG1592	Rubrerythrin
Buni3211|CDS|CDS	1.5	0.5	10.1	C	COG0479	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit
TS29Bac07678|CDS|CDS	1.5	0.5	10.1	C	COG0479	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit
TS28Met0473|CDS|CDS	97.6	32.2	10.0	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
TS28Eub8500|CDS|CDS	2.0	67.0	0.1	C	COG1319	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs
TS28Fae14018|CDS|CDS	1.0	33.5	0.1	C	COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases

TS28Clo10196|CDS|CDS	1.0	34.0	0.1	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
TS28Fae12159|CDS|CDS	1.0	34.0	0.1	C	COG0778	Nitroreductase
TS28Clo10316|CDS|CDS	0.5	17.0	0.1	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Par1621|CDS|CDS	0.3	11.5	0.1	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Bova2002|CDS|CDS	0.2	7.3	0.1	C	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit
TS28Eub1117|CDS|CDS	1.5	55.0	0.1	C	COG0224	F0F1-type ATP synthase, gamma subunit
TS28Bac6247|CDS|CDS	0.5	18.5	0.1	C	COG0731|COG4004	Fe-S oxidoreductases|Uncharacterized protein conserved in archaea
TS29Rum13450|CDS|CDS	0.8	28.8	0.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Fae18800|CDS|CDS	1.0	38.5	0.1	C	COG0372	Citrate synthase
TS28Eub7359|CDS|CDS	0.5	19.5	0.1	C	COG0426|COG0446|COG1773|COG1853	Uncharacterized flavoproteins|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
TS28Fae16148|CDS|CDS	1.0	40.8	0.1	C	COG1882	Pyruvate-formate lyase
TS28Dor0088|CDS|CDS	0.5	20.5	0.1	C	COG1151	6Fe-6S prismane cluster-containing protein
TS28Fae22085|CDS|CDS	1.8	72.0	0.1	C	COG0372	Citrate synthase
TS29Rum16842|CDS|CDS	2.0	82.5	0.1	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
TS28Clo01200|CDS|CDS	3.0	135.0	0.1	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS28Met1153|CDS|CDS	0.3	11.3	0.1	C	COG0656|COG0667|COG1453|COG4989	Aldo/keto reductases, related to diketogulonate reductase|Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)|Predicted oxidoreductases of the aldo/keto reductase family|Predicted oxidoreductase
Bdor1394|CDS|CDS	0.5	23.0	0.1	C	COG1012|COG4230	NAD-dependent aldehyde dehydrogenases|Delta 1-pyrroline-5-carboxylate dehydrogenase
TS28Fae12060|CDS|CDS	0.5	23.2	0.1	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS28Eub8485|CDS|CDS	2.3	111.2	0.1	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
Robe0063|CDS|CDS	0.2	9.8	0.1	C	COG2033	Desulfoferrodoxin
TS28Met1825|CDS|CDS	0.3	13.1	0.1	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS28Dor1817|CDS|CDS	0.5	27.5	0.1	C	COG1882	Pyruvate-formate lyase
Dfor1725|CDS|CDS	0.3	14.0	0.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Eub5066|CDS|CDS	1.0	56.8	0.1	C	COG1035	Coenzyme F420-reducing hydrogenase, beta subunit
TS29Rum20820|CDS|CDS	1.0	59.5	0.1	C	COG1454	Alcohol dehydrogenase, class IV
TS28Eub5183|CDS|CDS	0.7	41.0	0.1	C	COG0656|COG0667	Aldo/keto reductases, related to diketogulonate reductase|Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
TS28Eub0062|CDS|CDS	0.5	32.0	0.1	C	COG1882	Pyruvate-formate lyase
TS28Rum14899|CDS|CDS	0.5	32.5	0.1	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
TS28Eub1116|CDS|CDS	1.5	99.5	0.0	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Eub7098|CDS|CDS	0.5	35.5	0.0	C	COG4659	Predicted NADH:ubiquinone oxidoreductase, subunit RnfG
Bpse1690|CDS|CDS	0.3	18.0	0.0	C	COG2352	Phosphoenolpyruvate carboxylase
TS28Eub4871|CDS|CDS	0.3	21.0	0.0	C	COG0056|COG4933	F0F1-type ATP synthase, alpha subunit|Uncharacterized conserved protein
TS28Fae21205|CDS|CDS	1.0	80.3	0.0	C	COG1757	Na+/H+ antiporter
TS28Rum12477|CDS|CDS	0.3	27.0	0.0	C	COG2080|COG1529	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
Robe3772|CDS|CDS	1.0	82.0	0.0	C	COG1882	Pyruvate-formate lyase
TS28Rum15837|CDS|CDS	0.3	28.3	0.0	C	COG1882	Pyruvate-formate lyase
TS29Rum16870|CDS|CDS	0.3	28.5	0.0	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Rum11776|CDS|CDS	0.3	29.0	0.0	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Clo01515|CDS|CDS	2.0	183.0	0.0	C	COG0282	Acetate kinase
TS28Fae17599|CDS|CDS	1.0	92.0	0.0	C	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family
Ccom0015|CDS|CDS	0.3	33.0	0.0	C	COG0372	Citrate synthase
TS29Bif0989|CDS|CDS	0.3	25.5	0.0	C	COG2352	Phosphoenolpyruvate carboxylase
TS28Clo00972|CDS|CDS	1.0	108.0	0.0	C	COG0822	NifU homolog involved in Fe-S cluster formation
TS28Eub8710|CDS|CDS	0.5	55.0	0.0	C	COG0055	F0F1-type ATP synthase, beta subunit
TS28Fae22484|CDS|CDS	0.3	37.5	0.0	C	COG1301	Na+/H+-dicarboxylate symporters
TS28Fae08978|CDS|CDS	0.5	58.0	0.0	C	COG0281	Malic enzyme
TS28Eub8712|CDS|CDS	0.5	86.5	0.0	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Eub5054|CDS|CDS	0.6	115.8	0.0	C	COG1882	Pyruvate-formate lyase
RintL10790|CDS|CDS	0.3	73.8	0.0	C	COG0372	Citrate synthase
TS28Bif3548|CDS|CDS	0.3	60.5	0.0	C	COG2352	Phosphoenolpyruvate carboxylase
FpraM2121978|CDS|CDS	7.0	0.5	46.3	C|F	COG1529|COG2080|COG4631	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs|Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Xanthine dehydrogenase, molybdopterin-binding subunit B
Robe0280|CDS|CDS	3.0	0.5	19.8	C|F	COG1319|COG4630	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs|Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A
Bdor0776|CDS|CDS	15.3	3.3	15.2	C|G	COG1070|COG1069	Sugar (pentulose and hexulose) kinases|Ribulose kinase
Msmi741308|CDS|CDS	14.1	0.3	139.7	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Msm1733|CDS|rubrerythrin	13.8	0.3	136.4	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Msmi750375|CDS|CDS	19.6	1.2	55.5	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Bste1935|CDS|CDS	22.5	3.0	24.8	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
TS28Clo07003|CDS|CDS	58.0	8.0	24.0	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
Pmer2198|CDS|CDS	26.0	4.0	21.5	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Bdor1728|CDS|CDS	29.0	4.5	21.3	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Bxyl2120|CDS|CDS	1.5	0.3	19.8	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
BVU1137|CDS|rubrerythrin	85.5	15.5	18.2	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
TS28Fae00075|CDS|CDS	5.0	1.0	16.5	C|I	COG5016|COG0511	Pyruvate/oxaloacetate carboxyltransferase|Biotin carboxyl carrier protein
Acol0748|CDS|CDS	5.0	1.0	16.5	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
TS28Met0851|CDS|CDS	19.6	4.2	15.5	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase

TS28Ali2358|CDS|CDS	129.0	32.0	13.3	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
Bste1701|CDS|CDS	2.0	0.5	13.2	C|I	COG0280|COG2030|COG0857	Phosphotransacetylase|Acyl dehydratase|BioD-like N-terminal domain of phosphotransacetylase
Bcap0876|CDS|CDS	11.0	3.0	12.1	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
CspM6212612|CDS|CDS	18.0	5.0	11.9	C|I	COG2025|COG1960	Electron transfer flavoprotein, alpha subunit|Acyl-CoA dehydrogenases
Ccom0934|CDS|CDS	7.0	2.0	11.6	C|I	COG2025|COG1960	Electron transfer flavoprotein, alpha subunit|Acyl-CoA dehydrogenases
Robe2722|CDS|CDS	0.8	25.8	0.1	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Dlon2489|CDS|CDS	0.8	50.3	0.0	C|I	COG1592|COG1853|COG1607	Rubrerythrin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Acyl-CoA hydrolase
TS28Dor1597|CDS|CDS	0.5	27.5	0.1	C|J	COG0060|COG1032	Isoleucyl-tRNA synthetase|Fe-S oxidoreductase
TS28Fae18589|CDS|CDS	0.5	19.0	0.1	C|K	COG0427|COG0454	Acetyl-CoA hydrolase|Histone acetyltransferase HPA2 and related acetyltransferases
TS29Rum18637|CDS|CDS	1.5	62.5	0.1	C|K	COG1227|COG4109	Inorganic pyrophosphatase/exopolyphosphatase|Predicted transcriptional regulator containing CBS domains
TS28Eub8526|CDS|CDS	0.5	89.5	0.0	C|K	COG1227|COG4109	Inorganic pyrophosphatase/exopolyphosphatase|Predicted transcriptional regulator containing CBS domains
Msmi751486|CDS|CDS	14.5	0.3	191.8	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
BactD12232|CDS|CDS	21.5	0.5	142.2	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
BactD13066|CDS|CDS	9.7	0.3	95.9	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
Bxyl3872|CDS|CDS	9.7	0.3	95.9	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
Msmi740194|CDS|CDS	14.5	1.3	38.4	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Dfor0624|CDS|CDS	31.0	3.0	34.2	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Ccom1705|CDS|CDS	10.0	1.0	33.1	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Pmer3165|CDS|CDS	17.5	2.0	28.9	C|O	COG0778|COG1225	Nitroreductase|Peroxiredoxin
Dfor0623|CDS|CDS	6.5	1.0	21.5	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Dfor2070|CDS|CDS	12.0	2.0	19.8	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Cbol2856|CDS|CDS	6.0	1.0	19.8	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Bxyl4091|CDS|CDS	8.5	1.5	18.7	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
Bfin3687|CDS|CDS	5.6	1.0	18.6	C|O	COG0526|COG3634|COG0492	Thiol-disulfide isomerase and thioredoxins|Alkyl hydroperoxide reductase, large subunit|Thioredoxin reductase
ShigspD91265|CDS|CDS	5.5	1.0	18.2	C|O	COG4232|COG4233	Thiol:disulfide interchange protein|Uncharacterized protein predicted to be involved in C-type cytochrome biogenesis
Dfor2069|CDS|CDS	8.5	2.0	14.1	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Bste2939|CDS|CDS	8.0	2.0	13.2	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Rtor1258|CDS|CDS	4.0	1.0	13.2	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Begg0694|CDS|CDS	4.0	1.0	13.2	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Bdor0648|CDS|CDS	13.5	3.5	12.8	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Bdor2834|CDS|CDS	10.5	3.0	11.6	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
Pmer2351|CDS|CDS	26.0	8.0	10.7	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Bdor1370|CDS|CDS	24.5	8.0	10.1	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
TS28Rum05867|CDS|CDS	0.3	13.2	0.1	C|P	COG0426|COG0446|COG1773|COG1853|COG1251|COG2146	Uncharacterized flavoproteins|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|NAD(P)H-nitrite reductase|Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases
TS29Rum12353|CDS|CDS	19.8	4.0	16.3	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS29Rum18424|CDS|CDS	4.0	1.0	13.2	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
Robe3277|CDS|CDS	2.0	0.5	13.2	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS29Rum00111|CDS|CDS	3.8	1.0	12.4	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
Pmer2833|CDS|CDS	5.0	1.5	11.0	C|Q	COG0282|COG4869	Acetate kinase|Propanediol utilization protein
Clep0939|CDS|CDS	10.0	3.0	11.0	C|V|O	COG1132|COG4988|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
Msmi751409|CDS|CDS	17.0	0.5	112.4	D	COG0206	Cell division GTPase
Ehal1927|CDS|CDS	8.0	0.5	52.9	D	COG0772	Bacterial cell division membrane protein
Acac2925|CDS|CDS	9.0	1.0	29.8	D	COG1077	Actin-like ATPase involved in cell morphogenesis
Bthe3730956|CDS|CDS	2.3	0.3	23.1	D	COG1192	ATPases involved in chromosome partitioning
TS29Bac09389|CDS|CDS	2.3	0.3	23.1	D	COG0772	Bacterial cell division membrane protein
Cspi1479|CDS|CDS	7.0	1.0	23.1	D	COG0206	Cell division GTPase
TS29Rum13370|CDS|CDS	6.5	1.0	21.5	D	COG3640	CO dehydrogenase maturation factor
Cste1263|CDS|CDS	6.0	1.0	19.8	D	COG1196	Chromosome segregation ATPases
TS29Rum17370|CDS|CDS	5.0	1.0	16.5	D	COG3640	CO dehydrogenase maturation factor
Rbro0823|CDS|CDS	3.3	0.8	13.2	D	COG0772	Bacterial cell division membrane protein
Rbro0827|CDS|CDS	2.0	0.5	13.2	D	COG0206	Cell division GTPase
Bdor2885|CDS|CDS	19.3	5.0	12.8	D	COG1077	Actin-like ATPase involved in cell morphogenesis
TS29Fae08269|CDS|CDS	3.8	1.0	12.4	D	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control
Pmer0601|CDS|CDS	15.0	4.0	12.4	D	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control
Msmi740271|CDS|CDS	14.3	4.2	11.4	D	COG0206	Cell division GTPase
TS28Clo00864|CDS|CDS	11.0	377.0	0.1	D	COG1196	Chromosome segregation ATPases

TS28Rum00313|CDS|CDS	0.7	23.5	0.1	D	COG0206	Cell division GTPase
TS28Bif3337|CDS|CDS	0.3	9.0	0.1	D	COG1674	DNA segregation ATPase FtsK/SpoIIIE and related proteins
TS28Fae18143|CDS|CDS	1.5	55.0	0.1	D	COG1192	ATPases involved in chromosome partitioning
TS29Fae00047|CDS|CDS	1.5	55.0	0.1	D	COG1192	ATPases involved in chromosome partitioning
FpraM2122628|CDS|CDS	0.3	13.0	0.1	D	COG1196	Chromosome segregation ATPases
TS28Eub3834|CDS|CDS	1.5	64.0	0.1	D	COG5279	Uncharacterized protein involved in cytokinesis, contains TGc (transglutaminase/protease-like) domain
TS28Fae22190|CDS|CDS	1.0	44.0	0.1	D	COG0772	Bacterial cell division membrane protein
TS29Rum13418|CDS|CDS	1.0	49.0	0.1	D	COG5279	Uncharacterized protein involved in cytokinesis, contains TGc (transglutaminase/protease-like) domain
TS28Rum01062|CDS|CDS	1.0	56.8	0.1	D	COG2184	Protein involved in cell division
TS28Dor1185|CDS|CDS	0.5	34.5	0.0	D	COG1196	Chromosome segregation ATPases
TS28Fae15959|CDS|CDS	0.5	35.0	0.0	D	COG0445	NAD/FAD-utilizing enzyme apparently involved in cell division
TS28Rum08889|CDS|CDS	0.5	36.0	0.0	D	COG1196	Chromosome segregation ATPases
TS28Bif3406|CDS|CDS	0.6	42.6	0.0	D	COG1196	Chromosome segregation ATPases
TS28Clo01533|CDS|CDS	1.0	78.0	0.0	D	COG3599	Cell division initiation protein
TS28Eub7153|CDS|CDS	0.5	62.5	0.0	D	COG0206	Cell division GTPase
Cnex1324|CDS|CDS	16.5	1.0	54.6	D|U|W	COG5295|COG1674	Autotransporter adhesin|DNA segregation ATPase FtsK/SpoIIIE and related proteins
Rgna2457|CDS|CDS	0.3	47.7	0.0	D|V	COG1136|COG2884|COG2177	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ATPase involved in cell division|Cell division protein
Rumhyd1512|CDS|CDS	1.0	65.0	0.1	D|V|Q	COG1136|COG4181|COG2884	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component|Predicted ATPase involved in cell division
Rlac0718|CDS|CDS	0.3	25.2	0.0	D|V|Q	COG1136|COG4181|COG2884	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component|Predicted ATPase involved in cell division
CspL21888|CDS|CDS	0.3	25.2	0.0	D|V|Q	COG1136|COG4181|COG2884	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component|Predicted ATPase involved in cell division
Pmer0936|CDS|CDS	20.5	0.5	135.6	E	COG0006	Xaa-Pro aminopeptidase
Bste0970|CDS|CDS	30.5	1.0	100.9	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS28Clo07223|CDS|CDS	148.0	6.0	81.6	E	COG0040	ATP phosphoribosyltransferase
Csci1219|CDS|CDS	22.0	1.0	72.8	E	COG1115	Na+/alanine symporter
ShigspD90687|CDS|CDS	11.0	0.5	72.8	E	COG0747	ABC-type dipeptide transport system, periplasmic component
Msmi741263|CDS|CDS	5.7	0.3	56.2	E	COG0107|COG0106|COG1411	Imidazoleglycerol-phosphate synthase|Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase|Uncharacterized protein related to proFAR isomerase (HisA)
Rbro0692|CDS|CDS	8.0	0.5	52.9	E	COG0082	Chorismate synthase
Msmi741505|CDS|CDS	3.9	0.3	51.4	E	COG2061	ACT-domain-containing protein, predicted allosteric regulator of homoserine dehydrogenase
Csym4390|CDS|CDS	14.5	1.0	48.0	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS29Fae02228|CDS|CDS	4.7	0.3	46.3	E	COG1115	Na+/alanine symporter
Rlac2184|CDS|CDS	14.0	1.0	46.3	E	COG0560	Phosphoserine phosphatase
ShigspD90704|CDS|CDS	7.0	0.5	46.3	E	COG0339	Zn-dependent oligopeptidases
TS29Fae06344|CDS|CDS	6.5	0.5	43.0	E	COG4992	Ornithine/acetylornithine aminotransferase
Msmi740580|CDS|CDS	6.5	0.5	43.0	E	COG0241|COG0131	Histidinol phosphatase and related phosphatases|Imidazoleglycerol-phosphate dehydratase
Msmi750207|CDS|CDS	2.9	0.3	38.1	E	COG2061	ACT-domain-containing protein, predicted allosteric regulator of homoserine dehydrogenase
ShigspD91594|CDS|CDS	11.5	1.0	38.0	E	COG0070	Glutamate synthase domain 3
ShigspD91973|CDS|CDS	5.5	0.5	36.4	E	COG2166|COG0520	SufE protein probably involved in Fe-S center assembly|Selenocysteine lyase
Msmi751157|CDS|CDS	2.7	0.3	35.7	E	COG0040	ATP phosphoribosyltransferase
TS29Rum15162|CDS|CDS	5.0	0.5	33.1	E	COG0703	Shikimate kinase
CspM6212980|CDS|CDS	55.8	6.0	30.8	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Even0062|CDS|CDS	18.0	2.0	29.8	E	COG0141|COG0079	Histidinol dehydrogenase|Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase
TS28Par1626|CDS|CDS	8.3	1.0	27.6	E	COG0031	Cysteine synthase
Msmi741112|CDS|CDS	4.8	0.6	27.2	E	COG0082	Chorismate synthase
TS29Bac10313|CDS|CDS	4.0	0.5	26.5	E	COG2195	Di- and tripeptidases
Csym2934|CDS|CDS	8.0	1.0	26.5	E	COG2049|COG1984	Allophanate hydrolase subunit 1|Allophanate hydrolase subunit 2
Bxyl1135|CDS|CDS	7.0	1.0	23.1	E	COG1770|COG1505	Protease II|Serine proteases of the peptidase family S9A
Hfil2320|CDS|CDS	7.0	1.0	23.1	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
ShigspD90224|CDS|CDS	7.0	1.0	23.1	E	COG1171	Threonine dehydratase
TS29Fae08373|CDS|CDS	3.5	0.5	23.1	E	COG1164	Oligoendopeptidase F
Acol3089|CDS|CDS	7.0	1.0	23.1	E	COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
Chyl3376|CDS|CDS	7.0	1.0	23.1	E	COG1063|COG1064	Threonine dehydrogenase and related Zn-dependent dehydrogenases|Zn-dependent alcohol dehydrogenases
Msmi750208|CDS|CDS	7.0	1.0	23.1	E	COG0460	Homoserine dehydrogenase
Rgna0316|CDS|CDS	7.0	1.0	23.1	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
TS29Fae03807|CDS|CDS	3.3	0.5	22.0	E	COG0107	Imidazoleglycerol-phosphate synthase
TS29Bac01406|CDS|CDS	6.5	1.0	21.5	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
Buni3612|CDS|CDS	6.5	1.0	21.5	E	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases
ShigspD90675|CDS|CDS	6.5	1.0	21.5	E	COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component
Dlon0626|CDS|CDS	25.5	4.0	21.1	E	COG0686	Alanine dehydrogenase
TS29Bac11385|CDS|CDS	5.0	0.8	19.8	E	COG1509	Lysine 2,3-aminomutase
TS29Bac00610|CDS|CDS	3.0	0.5	19.8	E	COG2502	Asparagine synthetase A
Aput2348|CDS|CDS	6.0	1.0	19.8	E	COG1410	Methionine synthase I, cobalamin-binding domain

TS29Clo1411|CDS|CDS	12.0	2.0	19.8	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
Ccom0724|CDS|CDS	6.0	1.0	19.8	E	COG0560	Phosphoserine phosphatase
Ccom0570|CDS|CDS	3.0	0.5	19.8	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
Dfor2261|CDS|CDS	12.0	2.0	19.8	E	COG0031	Cysteine synthase
TS28Bac3160|CDS|CDS	3.0	0.5	19.8	E	COG0006	Xaa-Pro aminopeptidase
TS29Bac11144|CDS|CDS	5.9	1.0	19.5	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Clo08986|CDS|CDS	22.0	4.0	18.2	E	COG2309	Leucyl aminopeptidase (aminopeptidase T)
BactD12877|CDS|CDS	11.0	2.0	18.2	E	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases
Bdor0185|CDS|CDS	52.7	10.0	17.4	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Msmi751306|CDS|CDS	5.7	1.1	16.9	E	COG0174	Glutamine synthetase
ShigspD91251|CDS|CDS	2.5	0.5	16.5	E	COG1982	Arginine/lysine/ornithine decarboxylases
Dlon1964|CDS|CDS	5.0	1.0	16.5	E	COG1775	Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB
Dfor0629|CDS|CDS	25.0	5.0	16.5	E	COG1115	Na+/alanine symporter
TS29Rum13140|CDS|CDS	2.5	0.5	16.5	E	COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
Ehal0230|CDS|CDS	2.5	0.5	16.5	E	COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
Aput0521|CDS|CDS	5.0	1.0	16.5	E	COG1003	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain
Acol0348|CDS|CDS	5.0	1.0	16.5	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases
TS29Rum03801|CDS|CDS	5.0	1.0	16.5	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
FpraM2122241|CDS|CDS	2.5	0.5	16.5	E	COG0112	Glycine/serine hydroxymethyltransferase
Casp5373|CDS|CDS	5.0	1.0	16.5	E	COG0110|COG1605	Acetyltransferase (isoleucine patch superfamily)|Chorismate mutase
TS28Bac8210|CDS|CDS	2.5	0.5	16.5	E	COG0066	3-isopropylmalate dehydratase small subunit
TS28Rum02192|CDS|CDS	11.7	2.3	16.5	E	COG0031	Cysteine synthase
Msmi751231|CDS|CDS	6.7	1.3	16.5	E	COG0112	Glycine/serine hydroxymethyltransferase
Msmi740412|CDS|CDS	10.8	2.2	16.4	E	COG0019	Diaminopimelate decarboxylase
Bdor0887|CDS|CDS	47.0	9.8	15.8	E	COG0527	Aspartokinases
Bdor0438|CDS|CDS	4.7	1.0	15.4	E	COG1280	Putative threonine efflux protein
RintL13590|CDS|CDS	14.0	3.0	15.4	E	COG1045|COG2151	Serine acetyltransferase|Predicted metal-sulfur cluster biosynthetic enzyme
Hfil2341|CDS|CDS	4.7	1.0	15.4	E	COG0747	ABC-type dipeptide transport system, periplasmic component
TS29Rum12053|CDS|CDS	9.0	2.0	14.9	E	COG2151|COG1045	Predicted metal-sulfur cluster biosynthetic enzyme|Serine acetyltransferase
ShigspD91918|CDS|CDS	4.5	1.0	14.9	E	COG1171	Threonine dehydratase
TS29Rum17372|CDS|CDS	9.0	2.0	14.9	E	COG0685	5,10-methylenetetrahydrofolate reductase
TS28Par0149|CDS|CDS	4.5	1.0	14.9	E	COG0509	Glycine cleavage system H protein (lipoate-binding)
Pmer0208|CDS|CDS	4.5	1.0	14.9	E	COG0509	Glycine cleavage system H protein (lipoate-binding)
TS28Fae10494|CDS|CDS	9.0	2.0	14.9	E	COG0019|COG0527	Diaminopimelate decarboxylase|Aspartokinases
TS29Fae06291|CDS|CDS	6.5	1.5	14.3	E	COG0169|COG0703	Shikimate 5-dehydrogenase|Shikimate kinase
TS29Bac05416|CDS|CDS	8.5	2.0	14.1	E	COG1350|COG0133	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)|Tryptophan synthase beta chain
TS29Bif2456|CDS|CDS	3.5	0.8	13.9	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
BactD14232|CDS|CDS	9.8	2.3	13.8	E	COG0673|COG1063	Predicted dehydrogenases and related proteins|Threonine dehydrogenase and related Zn-dependent dehydrogenases
Bdor2206|CDS|CDS	25.0	6.0	13.8	E	COG0174	Glutamine synthetase
Pmer1998|CDS|CDS	12.3	3.0	13.6	E	COG0031	Cysteine synthase
TS29RumUnc0053|CDS|CDS	4.0	1.0	13.2	E	COG4992	Ornithine/acetylornithine aminotransferase
Ccom0576|CDS|CDS	8.0	2.0	13.2	E	COG4992	Ornithine/acetylornithine aminotransferase
Cbol4568|CDS|CDS	4.0	1.0	13.2	E	COG4608|COG1123	ABC-type oligopeptide transport system, ATPase component|ATPase components of various ABC-type transport systems, contain duplicated ATPase
RintL13046|CDS|CDS	4.0	1.0	13.2	E	COG2957	Peptidylarginine deiminase and related enzymes
Acol3304|CDS|CDS	8.0	2.0	13.2	E	COG2873	O-acetylhomoserine sulfhydrylase
TS29Fae05550|CDS|CDS	2.0	0.5	13.2	E	COG2502	Asparagine synthetase A
Cram0425|CDS|CDS	4.0	1.0	13.2	E	COG1748	Saccharopine dehydrogenase and related proteins
Bste1007|CDS|CDS	8.0	2.0	13.2	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
ShigspD90484|CDS|CDS	2.0	0.5	13.2	E	COG1446	Asparaginase
b0828|CDS|L-asparaginase	2.0	0.5	13.2	E	COG1446	Asparaginase
Csym2155|CDS|CDS	4.0	1.0	13.2	E	COG1114	Branched-chain amino acid permeases
Bdor3564|CDS|CDS	24.0	6.0	13.2	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases
Even1832|CDS|CDS	8.0	2.0	13.2	E	COG0560	Phosphoserine phosphatase
Rbro1276|CDS|CDS	4.0	1.0	13.2	E	COG0498	Threonine synthase
Dlon0672|CDS|CDS	4.0	1.0	13.2	E	COG0436|COG1168	Aspartate/tyrosine/aromatic aminotransferase|Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities
TS29Rum18876|CDS|CDS	4.0	1.0	13.2	E	COG0410|COG0411	ABC-type branched-chain amino acid transport systems, ATPase component|ABC-type branched-chain amino acid transport systems, ATPase component
TS28Rum01620|CDS|CDS	4.0	1.0	13.2	E	COG0345	Pyrroline-5-carboxylate reductase
Bste2240|CDS|CDS	4.0	1.0	13.2	E	COG0078	Ornithine carbamoyltransferase
Acac0231|CDS|CDS	4.0	1.0	13.2	E	COG0078	Ornithine carbamoyltransferase
Aput0169|CDS|CDS	4.0	1.0	13.2	E	COG0019|COG1166	Diaminopimelate decarboxylase|Arginine decarboxylase (spermidine biosynthesis)
ShigspD90048|CDS|CDS	2.0	0.5	13.2	E	COG0002	Acetylglutamate semialdehyde dehydrogenase
Bcap3085|CDS|CDS	30.5	8.0	12.6	E	COG4992	Ornithine/acetylornithine aminotransferase
Msmi740560|CDS|CDS	1.9	0.5	12.2	E	COG0440	Acetolactate synthase, small (regulatory) subunit
Msmi750974|CDS|CDS	4.9	1.3	12.2	E	COG0137	Argininosuccinate synthase
Msmi741518|CDS|CDS	4.5	1.3	11.9	E	COG2021	Homoserine acetyltransferase
ShigspD92349|CDS|CDS	3.5	1.0	11.6	E	COG3075	Anaerobic glycerol-3-phosphate dehydrogenase
Csym2030|CDS|CDS	7.0	2.0	11.6	E	COG1775	Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB
Pmer2705|CDS|CDS	7.0	2.0	11.6	E	COG1280	Putative threonine efflux protein

FpraM2120523|CDS|CDS	4.7	1.3	11.6	E	COG1115	Na+/alanine symporter
Cbol2811|CDS|CDS	7.0	2.0	11.6	E	COG0078	Ornithine carbamoyltransferase
TS28Bac6391|CDS|CDS	50.7	14.5	11.6	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Pmer2888|CDS|CDS	11.0	3.2	11.5	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Col1292|CDS|CDS	52.0	15.0	11.5	E	COG0548|COG1364	Acetylglutamate kinase|N-acetylglutamate synthase (N-acetylornithine aminotransferase)
Bdor1187|CDS|CDS	20.5	6.0	11.3	E	COG0404	Glycine cleavage system T protein (aminomethyltransferase)
TS29Met0793|CDS|CDS	4.8	1.4	11.2	E	COG0082	Chorismate synthase
Msmi751359|CDS|CDS	4.8	1.4	11.2	E	COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase
Bdor1186|CDS|CDS	23.5	7.0	11.1	E	COG2195	Di- and tripeptidases
TS29Fae02910|CDS|CDS	3.3	1.0	11.0	E	COG1362	Aspartyl aminopeptidase
Bpse1580|CDS|CDS	3.3	1.0	11.0	E	COG0110|COG1605	Acetyltransferase (isoleucine patch superfamily)|Chorismate mutase
Bste2827|CDS|CDS	16.0	5.0	10.6	E	COG0337|COG0703	3-dehydroquinate synthetase|Shikimate kinase
Rtor1749|CDS|CDS	10.7	3.3	10.6	E	COG0031	Cysteine synthase
TS28Rum14136|CDS|CDS	44.0	14.0	10.4	E	COG0747	ABC-type dipeptide transport system, periplasmic component
Bdor3565|CDS|CDS	37.7	12.0	10.4	E	COG0082	Chorismate synthase
Rbro0803|CDS|CDS	4.2	1.3	10.3	E	COG3869	Arginine kinase
FpraM2120451|CDS|CDS	25.0	8.0	10.3	E	COG2856	Predicted Zn peptidase
Bova0498|CDS|CDS	12.5	4.0	10.3	E	COG0006	Xaa-Pro aminopeptidase
BactD20947|CDS|CDS	3.1	1.0	10.3	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Msmi751520|CDS|CDS	8.8	2.8	10.2	E	COG1410|COG5012	Methionine synthase I, cobalamin-binding domain|Predicted cobalamin binding protein
Msmi740959|CDS|CDS	10.0	3.3	10.2	E	COG0527	Aspartokinases
Msmi750720|CDS|CDS	10.0	3.3	10.2	E	COG0527	Aspartokinases
TS28Fae16493|CDS|CDS	2.0	66.8	0.1	E	COG1123|COG4608	ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type oligopeptide transport system, ATPase component
TS28Eub4040|CDS|CDS	4.0	134.5	0.1	E	COG0136|COG0165|COG1246	Aspartate-semialdehyde dehydrogenase|Argininosuccinate lyase|N-acetylglutamate synthase and related acetyltransferases
TS28Fae02068|CDS|CDS	0.5	17.0	0.1	E	COG1176	ABC-type spermidine/putrescine transport system, permease component I
TS28Bif3955|CDS|CDS	2.0	68.0	0.1	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
TS28Rum12316|CDS|CDS	1.0	34.0	0.1	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Eub4646|CDS|CDS	1.0	34.0	0.1	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Fae00621|CDS|CDS	0.5	17.5	0.1	E	COG0786	Na+/glutamate symporter
TS28Clo00908|CDS|CDS	4.0	144.0	0.1	E	COG2309	Leucyl aminopeptidase (aminopeptidase T)
TS28Rum10436|CDS|CDS	0.5	18.0	0.1	E	COG1364	N-acetylglutamate synthase (N-acetylornithine aminotransferase)
TS28Rum12473|CDS|CDS	0.5	18.0	0.1	E	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases
TS28Fae19782|CDS|CDS	1.0	36.0	0.1	E	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases
TS28Eub0362|CDS|CDS	0.5	18.0	0.1	E	COG0078	Ornithine carbamoyltransferase
TS28Fae18506|CDS|CDS	0.5	18.0	0.1	E	COG0031	Cysteine synthase
TS28Bif2402|CDS|CDS	1.3	48.2	0.1	E	COG0620	Methionine synthase II (cobalamin-independent)
TS28Eub6318|CDS|CDS	1.5	55.0	0.1	E	COG0070	Glutamate synthase domain 3
TS28Rum12491|CDS|CDS	0.3	12.3	0.1	E	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases
TS29Fae01323|CDS|CDS	0.4	16.0	0.1	E	COG1123|COG4608	ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type oligopeptide transport system, ATPase component
TS28Eub7013|CDS|CDS	4.0	150.5	0.1	E	COG3968|COG0174	Uncharacterized protein related to glutamine synthetase|Glutamine synthetase
TS28Dor1361|CDS|CDS	0.5	19.0	0.1	E	COG2195	Di- and tripeptidases
TS28Fae04728|CDS|CDS	1.0	38.0	0.1	E	COG1115	Na+/alanine symporter
TS28Eub5168|CDS|CDS	1.0	39.0	0.1	E	COG0337|COG0703	3-dehydroquinate synthetase|Shikimate kinase
TS28Fae10723|CDS|CDS	0.5	19.5	0.1	E	COG0002	Acetylglutamate semialdehyde dehydrogenase
TS28Met1793|CDS|CDS	0.5	19.7	0.1	E	COG0165	Argininosuccinate lyase
TS28Eub5088|CDS|CDS	1.5	60.5	0.1	E	COG0112	Glycine/serine hydroxymethyltransferase
TS29Bif3947|CDS|CDS	0.3	10.2	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS28Fae10127|CDS|CDS	0.8	30.5	0.1	E	COG0040	ATP phosphoribosyltransferase
TS28Fae20332|CDS|CDS	2.0	81.5	0.1	E	COG1982	Arginine/lysine/ornithine decarboxylases
TS28Met1421|CDS|CDS	0.3	10.3	0.1	E	COG0118	Glutamine amidotransferase
TS28Met0011|CDS|CDS	0.8	31.0	0.1	E	COG0747	ABC-type dipeptide transport system, periplasmic component
TS28Fae00332|CDS|CDS	0.5	22.0	0.1	E	COG0002	Acetylglutamate semialdehyde dehydrogenase
TS28Eub8330|CDS|CDS	2.5	111.5	0.1	E	COG1115	Na+/alanine symporter
TS28Eub7177|CDS|CDS	6.0	268.5	0.1	E	COG0070	Glutamate synthase domain 3
TS28Bac7238|CDS|CDS	0.3	15.0	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS28Eub7543|CDS|CDS	1.5	69.5	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS29Rum00378|CDS|CDS	1.0	47.5	0.1	E	COG2957	Peptidylarginine deiminase and related enzymes
TS28Eub4474|CDS|CDS	0.6	29.0	0.1	E	COG3340	Peptidase E
TS28Eub8531|CDS|CDS	1.0	48.5	0.1	E	COG0107	Imidazoleglycerol-phosphate synthase
TS28Fae16580|CDS|CDS	2.0	102.0	0.1	E	COG2317	Zn-dependent carboxypeptidase
TS28Fae16508|CDS|CDS	1.0	51.0	0.1	E	COG0031	Cysteine synthase
TS28Clo01140|CDS|CDS	2.0	104.0	0.1	E	COG2755	Lysophospholipase L1 and related esterases
TS29Rum00069|CDS|CDS	1.0	52.0	0.1	E	COG1115	Na+/alanine symporter
TS28Eub7471|CDS|CDS	1.0	52.5	0.1	E	COG0141	Histidinol dehydrogenase
TS28Clo01167|CDS|CDS	3.0	159.0	0.1	E	COG0520|COG2166	Selenocysteine lyase|SufE protein probably involved in Fe-S center assembly
TS28Fae12510|CDS|CDS	1.0	54.3	0.1	E	COG0337|COG0703	3-dehydroquinate synthetase|Shikimate kinase
TS28Fae00309|CDS|CDS	0.5	28.5	0.1	E	COG2317	Zn-dependent carboxypeptidase
TS28Rum12290|CDS|CDS	0.5	28.5	0.1	E	COG1410|COG0685|COG0646	Methionine synthase I, cobalamin-binding domain|5,10-methylenetetrahydrofolate reductase|Methionine synthase I (cobalamin-dependent), methyltransferase domain
TS28Fae20285|CDS|CDS	1.0	57.0	0.1	E	COG0014	Gamma-glutamyl phosphate reductase
TS28Clo00524|CDS|CDS	3.0	172.0	0.1	E	COG3579	Aminopeptidase C
TS28Eub0092|CDS|CDS	1.0	58.8	0.1	E	COG2873	O-acetylhomoserine sulfhydrylase

Buni0698|CDS|CDS	0.1	5.5	0.1	E	COG0019|COG1166	Diaminopimelate decarboxylase|Arginine decarboxylase (spermidine biosynthesis)
TS28Fae12395|CDS|CDS	0.3	21.3	0.1	E	COG3048	D-serine dehydratase
TS28Fae16847|CDS|CDS	1.0	66.0	0.1	E	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases
TS28Rum08384|CDS|CDS	0.5	33.0	0.1	E	COG0460	Homoserine dehydrogenase
TS28Fae08445|CDS|CDS	1.0	67.0	0.0	E	COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog
Bpse1713|CDS|CDS	0.5	35.5	0.0	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
TS28Eub8339|CDS|CDS	0.5	35.5	0.0	E	COG0260	Leucyl aminopeptidase
TS28Clo00974|CDS|CDS	2.0	147.0	0.0	E	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases
TS28Met1521|CDS|CDS	0.3	19.3	0.0	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
TS28Fae19459|CDS|CDS	0.5	39.0	0.0	E	COG0040	ATP phosphoribosyltransferase
TS28Fae19783|CDS|CDS	1.0	79.0	0.0	E	COG0070	Glutamate synthase domain 3
TS28Fae08988|CDS|CDS	0.5	40.0	0.0	E	COG0031	Cysteine synthase
TS28Fae22037|CDS|CDS	1.0	84.0	0.0	E	COG1305	Transglutaminase-like enzymes, putative cysteine proteases
TS28Eub8892|CDS|CDS	1.5	129.0	0.0	E	COG1410	Methionine synthase I, cobalamin-binding domain
TS28Eub6262|CDS|CDS	0.3	22.0	0.0	E	COG1115	Na+/alanine symporter
TS28Met1855|CDS|CDS	0.3	22.2	0.0	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
TS28Eub8766|CDS|CDS	0.7	60.0	0.0	E	COG0137	Argininosuccinate synthase
TS28Fae16126|CDS|CDS	0.3	30.5	0.0	E	COG4177	ABC-type branched-chain amino acid transport system, permease component
TS28Eub3848|CDS|CDS	2.5	233.5	0.0	E	COG0070	Glutamate synthase domain 3
TS28Eub4118|CDS|CDS	0.5	52.0	0.0	E	COG0019	Diaminopimelate decarboxylase
TS28Eub8543|CDS|CDS	0.5	52.5	0.0	E	COG0031	Cysteine synthase
TS28Fae12262|CDS|CDS	0.4	46.0	0.0	E	COG0421	Spermidine synthase
TS28Eub8882|CDS|CDS	1.0	122.8	0.0	E	COG1305|COG1721	Transglutaminase-like enzymes, putative cysteine proteases|Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)
TS28Bif3581|CDS|CDS	0.5	69.0	0.0	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
TS28Eub6499|CDS|CDS	0.5	73.5	0.0	E	COG1115	Na+/alanine symporter
TS28Fae15789|CDS|CDS	0.2	33.0	0.0	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
TS28Fae20498|CDS|CDS	0.3	84.5	0.0	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases
Msmi751273|CDS|CDS	104.5	0.3	1,036.7	E|C	COG1063|COG1064|COG0604	Threonine dehydrogenase and related Zn-dependent dehydrogenases|Zn-dependent alcohol dehydrogenases|NADPH:quinone reductase and related Zn-dependent oxidoreductases
Msmi740404|CDS|CDS	105.8	0.8	419.6	E|C	COG1063|COG1064|COG0604	Threonine dehydrogenase and related Zn-dependent dehydrogenases|Zn-dependent alcohol dehydrogenases|NADPH:quinone reductase and related Zn-dependent oxidoreductases
Cspi1642|CDS|CDS	206.0	3.0	227.1	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS29Bac09082|CDS|CDS	8.0	0.5	52.9	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS28Met0718|CDS|CDS	179.3	16.8	35.2	E|C	COG1064|COG1063|COG0604	Zn-dependent alcohol dehydrogenases|Threonine dehydrogenase and related Zn-dependent dehydrogenases|NADPH:quinone reductase and related Zn-dependent oxidoreductases
TS29Fae08554|CDS|CDS	4.0	0.5	26.5	E|C	COG0578|COG0579|COG0665	Glycerol-3-phosphate dehydrogenase|Predicted dehydrogenase|Glycine/D-amino acid oxidases (deaminating)
Bste2233|CDS|CDS	10.3	1.5	22.8	E|C	COG0665|COG0579|COG0578	Glycine/D-amino acid oxidases (deaminating)|Predicted dehydrogenase|Glycerol-3-phosphate dehydrogenase
Bste2622|CDS|CDS	12.5	2.0	20.7	E|C	COG0473|COG0538	Isocitrate/isopropylmalate dehydrogenase|Isocitrate dehydrogenases
CspSS22014|CDS|CDS	8.0	2.5	10.6	E|C	COG0665|COG0579|COG0578	Glycine/D-amino acid oxidases (deaminating)|Predicted dehydrogenase|Glycerol-3-phosphate dehydrogenase
Dfor2257|CDS|CDS	0.3	9.0	0.1	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS28Fae22487|CDS|CDS	0.5	19.5	0.1	E|C	COG0473|COG0538	Isocitrate/isopropylmalate dehydrogenase|Isocitrate dehydrogenases
TS28Clo05930|CDS|CDS	0.3	15.0	0.1	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS28Fae00442|CDS|CDS	0.3	22.2	0.0	E|C	COG0493|COG1902|COG1249	NADPH-dependent glutamate synthase beta chain and related oxidoreductases|NADH:flavin oxidoreductases, Old Yellow Enzyme family|Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS28Eub8736|CDS|CDS	0.5	46.0	0.0	E|C	COG0473	Isocitrate/isopropylmalate dehydrogenase
TS28Bac0889|CDS|CDS	5.5	1.0	18.2	E|C|H	COG0111|COG1052	Phosphoglycerate dehydrogenase and related dehydrogenases|Lactate dehydrogenase and related dehydrogenases
TS28Par1075|CDS|CDS	15.0	3.0	16.5	E|C|H	COG0111|COG1052	Phosphoglycerate dehydrogenase and related dehydrogenases|Lactate dehydrogenase and related dehydrogenases
TS28Clo03090|CDS|CDS	0.5	17.5	0.1	E|C|H	COG1148|COG4624|COG0493|COG0543|COG1034|COG1142|COG1894|COG1145|COG1143|COG1319	Heterodisulfide reductase, subunit A and related polyferredoxins|Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin|Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)|Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs

TS28Fae14640|CDS|CDS	1.0	46.5	0.1	E|C|H	COG1148|COG4624|COG0493|COG0543|COG1034|COG1142|COG1894|COG1145|COG1143|COG1144	Heterodisulfide reductase, subunit A and related polyferredoxins|Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin|Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
TS28Eub8446|CDS|CDS	1.0	50.5	0.1	E|C|H	COG4624|COG0493|COG0543|COG1034|COG1142|COG1894	Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit
TS28Fae17638|CDS|CDS	1.0	60.0	0.1	E|C|H	COG0111|COG1052	Phosphoglycerate dehydrogenase and related dehydrogenases|Lactate dehydrogenase and related dehydrogenases
TS28Eub4390|CDS|CDS	0.5	59.0	0.0	E|C|H	COG0493|COG0543|COG1034|COG1142|COG1894	NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit
TS28Fae03904|CDS|CDS	0.3	32.0	0.0	E|C|H	COG1148|COG4624|COG0493|COG0543|COG1034|COG1142|COG1894|COG1145|COG1143|COG1144	Heterodisulfide reductase, subunit A and related polyferredoxins|Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin|Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
Msmi750470|CDS|CDS	6.3	0.3	83.8	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
Msmi750095|CDS|CDS	10.5	1.3	25.9	E|F	COG0283|COG0128|COG0287|COG0710	Cytidylate kinase|5-enolpyruvylshikimate-3-phosphate synthase|Prephenate dehydrogenase|3-dehydroquinate dehydratase
Cspi0127|CDS|CDS	18.0	3.0	19.8	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
Bpse0543|CDS|CDS	5.0	1.0	16.5	E|F	COG0283|COG0128|COG0287	Cytidylate kinase|5-enolpyruvylshikimate-3-phosphate synthase|Prephenate dehydrogenase
Bste2836|CDS|CDS	2.0	0.5	13.2	E|F	COG0283|COG0128|COG0287	Cytidylate kinase|5-enolpyruvylshikimate-3-phosphate synthase|Prephenate dehydrogenase
TS28Rum01448|CDS|CDS	1.8	69.5	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS28Eub1148|CDS|CDS	0.5	21.0	0.1	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
TS28Bif4271|CDS|CDS	1.3	59.8	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS28Eub3855|CDS|CDS	3.7	206.0	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
Clep1399|CDS|CDS	0.5	29.3	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS28Fae16889|CDS|CDS	0.5	37.0	0.0	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
TS28Eub1593|CDS|CDS	0.5	54.5	0.0	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
RintL10507|CDS|CDS	10.0	1.0	33.1	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
TS28Par1495|CDS|CDS	10.5	1.5	23.1	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
TS29Bac11100|CDS|CDS	5.5	1.0	18.2	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
Bxyl4222|CDS|CDS	5.5	1.0	18.2	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
TS28Eub2774|CDS|CDS	5.5	1.0	18.2	E|G	COG0129|COG0676	Dihydroxyacid dehydratase/phosphogluconate dehydratase|Uncharacterized enzymes related to aldose 1-epimerase
TS29Fae04485|CDS|CDS	2.5	0.5	16.5	E|G	COG2610	H+/gluconate symporter and related permeases
TS28Clo04570|CDS|CDS	12.0	3.0	13.2	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
Csym3061|CDS|CDS	8.0	2.0	13.2	E|G	COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase
Even1370|CDS|CDS	7.0	2.0	11.6	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
TS28Bac4048|CDS|CDS	0.5	23.5	0.1	E|G	COG2755|COG3401|COG4677	Lysophospholipase L1 and related esterases|Fibronectin type 3 domain-containing protein|Pectin methylesterase
TS28Fae21406|CDS|CDS	0.5	35.5	0.0	E|G	COG2610	H+/gluconate symporter and related permeases
TS28Col0748|CDS|CDS	0.2	19.0	0.0	E|G	COG3842|COG3839	ABC-type spermidine/putrescine transport systems, ATPase components|ABC-type sugar transport systems, ATPase components
TS29Bac00733|CDS|CDS	358.0	0.5	2,367.8	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS28Rum14282|CDS|CDS	3.0	141.5	0.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS28Rum16342|CDS|CDS	1.0	66.0	0.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
Msmi741008|CDS|CDS	15.1	1.8	27.2	E|G|U	COG2730|COG3291|COG5563|COG3210|COG1305	Endoglucanase|FOG: PKD repeat|Predicted integral membrane proteins containing uncharacterized repeats|Large exoproteins involved in heme utilization or adhesion|Transglutaminase-like enzymes, putative cysteine proteases
Msmi741564|CDS|CDS	14.8	1.2	41.8	E|G|U|W	COG2730|COG3291|COG5563|COG3210|COG1305|COG5295	Endoglucanase|FOG: PKD repeat|Predicted integral membrane proteins containing uncharacterized repeats|Large exoproteins involved in heme utilization or adhesion|Transglutaminase-like enzymes, putative cysteine proteases|Autotransporter adhesin

<table>
<tr><td>Msmi750154|CDS|CDS</td><td>6.9</td><td>0.7</td><td>34.3</td><td>E|G|U|W</td><td>COG2730|COG3291|COG5563|COG3210|COG1305|COG5295</td><td>Endoglucanase|FOG: PKD repeat|Predicted integral membrane proteins containing uncharacterized repeats|Large exoproteins involved in heme utilization or adhesion|Transglutaminase-like enzymes, putative cysteine proteases|Autotransporter adhesin</td></tr>
<tr><td>Msmi750673|CDS|CDS</td><td>15.1</td><td>4.8</td><td>10.3</td><td>E|G|U|W</td><td>COG2730|COG3291|COG5563|COG3210|COG1305|COG5295</td><td>Endoglucanase|FOG: PKD repeat|Predicted integral membrane proteins containing uncharacterized repeats|Large exoproteins involved in heme utilization or adhesion|Transglutaminase-like enzymes, putative cysteine proteases|Autotransporter adhesin</td></tr>
<tr><td>Msmi751575|CDS|CDS</td><td>12.9</td><td>1.1</td><td>39.5</td><td>E|H</td><td>COG0111</td><td>Phosphoglycerate dehydrogenase and related dehydrogenases</td></tr>
<tr><td>Dfor0946|CDS|CDS</td><td>8.0</td><td>1.0</td><td>26.5</td><td>E|H</td><td>COG0111|COG1760</td><td>Phosphoglycerate dehydrogenase and related dehydrogenases|L-serine deaminase</td></tr>
<tr><td>TS29Fae08234|CDS|CDS</td><td>4.0</td><td>0.5</td><td>26.5</td><td>E|H</td><td>COG0028</td><td>Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]</td></tr>
<tr><td>ShigspD92659|CDS|CDS</td><td>3.8</td><td>0.5</td><td>25.4</td><td>E|H</td><td>COG0512|COG0147</td><td>Anthranilate/para-aminobenzoate synthases component II|Anthranilate/para-aminobenzoate synthases component I</td></tr>
<tr><td>Msmi751383|CDS|CDS</td><td>6.8</td><td>0.9</td><td>24.7</td><td>E|H</td><td>COG0079|COG1492</td><td>Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase|Cobyric acid synthase</td></tr>
<tr><td>Msmi740079|CDS|CDS</td><td>16.8</td><td>2.4</td><td>22.9</td><td>E|H</td><td>COG0111</td><td>Phosphoglycerate dehydrogenase and related dehydrogenases</td></tr>
<tr><td>ShigspD90227|CDS|CDS</td><td>6.5</td><td>1.0</td><td>21.5</td><td>E|H</td><td>COG0028</td><td>Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]</td></tr>
<tr><td>TS29Bac09079|CDS|CDS</td><td>2.0</td><td>0.3</td><td>19.8</td><td>E|H</td><td>COG0059</td><td>Ketol-acid reductoisomerase</td></tr>
<tr><td>ShigspD91565|CDS|CDS</td><td>5.8</td><td>1.0</td><td>19.3</td><td>E|H</td><td>COG0591|COG4145</td><td>Na+/proline symporter|Na+/panthothenate symporter</td></tr>
<tr><td>Chyl0578|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>E|H</td><td>COG0059</td><td>Ketol-acid reductoisomerase</td></tr>
<tr><td>Msmi740299|CDS|CDS</td><td>6.8</td><td>1.4</td><td>16.0</td><td>E|H</td><td>COG0079|COG1492</td><td>Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase|Cobyric acid synthase</td></tr>
<tr><td>TS28Fae15995|CDS|CDS</td><td>18.0</td><td>4.0</td><td>14.9</td><td>E|H</td><td>COG1932</td><td>Phosphoserine aminotransferase</td></tr>
<tr><td>TS29Bac09019|CDS|CDS</td><td>4.4</td><td>1.0</td><td>14.6</td><td>E|H</td><td>COG1932</td><td>Phosphoserine aminotransferase</td></tr>
<tr><td>BactD21340|CDS|CDS</td><td>1.4</td><td>0.3</td><td>13.9</td><td>E|H</td><td>COG0028</td><td>Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]</td></tr>
<tr><td>Acol2402|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>E|H</td><td>COG0111</td><td>Phosphoglycerate dehydrogenase and related dehydrogenases</td></tr>
<tr><td>TS28Dor1091|CDS|CDS</td><td>0.5</td><td>18.0</td><td>0.1</td><td>E|H</td><td>COG0028|COG3962</td><td>Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]|Acetolactate synthase</td></tr>
<tr><td>Dlon1512|CDS|CDS</td><td>0.5</td><td>18.0</td><td>0.1</td><td>E|H</td><td>COG0028|COG3962</td><td>Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]|Acetolactate synthase</td></tr>
<tr><td>TS28Eub7935|CDS|CDS</td><td>1.5</td><td>56.5</td><td>0.1</td><td>E|H</td><td>COG0115</td><td>Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase</td></tr>
<tr><td>TS28Eub6197|CDS|CDS</td><td>1.0</td><td>41.7</td><td>0.1</td><td>E|H</td><td>COG0059</td><td>Ketol-acid reductoisomerase</td></tr>
<tr><td>TS28Fae00213|CDS|CDS</td><td>0.4</td><td>17.0</td><td>0.1</td><td>E|H</td><td>COG0059</td><td>Ketol-acid reductoisomerase</td></tr>
<tr><td>TS29Fae10364|CDS|CDS</td><td>1.0</td><td>44.5</td><td>0.1</td><td>E|H</td><td>COG0175</td><td>3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes</td></tr>
<tr><td>TS28Fae07632|CDS|CDS</td><td>0.5</td><td>24.2</td><td>0.1</td><td>E|H</td><td>COG0059</td><td>Ketol-acid reductoisomerase</td></tr>
<tr><td>TS28Rum15403|CDS|CDS</td><td>0.5</td><td>24.5</td><td>0.1</td><td>E|H</td><td>COG0079|COG1492|COG2158|COG1797</td><td>Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase|Cobyric acid synthase|Uncharacterized protein containing a Zn-finger-like domain|Cobyrinic acid a,c-diamide synthase</td></tr>
<tr><td>TS28Fae20464|CDS|CDS</td><td>0.9</td><td>78.7</td><td>0.0</td><td>E|H</td><td>COG0059</td><td>Ketol-acid reductoisomerase</td></tr>
<tr><td>TS28Eub4391|CDS|CDS</td><td>0.5</td><td>56.5</td><td>0.0</td><td>E|H</td><td>COG0079|COG1492|COG2158</td><td>Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase|Cobyric acid synthase|Uncharacterized protein containing a Zn-finger-like domain</td></tr>
<tr><td>Even0016|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>E|H|C</td><td>COG1894|COG4624|COG1034|COG0493|COG1142|COG0543</td><td>NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Iron only hydrogenase large subunit, C-terminal domain|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|Fe-S-cluster-containing hydrogenase components 2|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases</td></tr>
<tr><td>Casp1736|CDS|CDS</td><td>9.0</td><td>2.5</td><td>11.9</td><td>E|H|C</td><td>COG1894|COG4624|COG1034|COG0493|COG1142|COG0543</td><td>NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Iron only hydrogenase large subunit, C-terminal domain|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|Fe-S-cluster-containing hydrogenase components 2|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases</td></tr>
<tr><td>Dlon1448|CDS|CDS</td><td>2.0</td><td>0.5</td><td>13.2</td><td>E|I</td><td>COG3581|COG3580|COG1924|COG1775</td><td>Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria|Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)|Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB</td></tr>
<tr><td>TS29Rum03420|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>E|J</td><td>COG0124|COG3705</td><td>Histidyl-tRNA synthetase|ATP phosphoribosyltransferase involved in histidine biosynthesis</td></tr>
<tr><td>TS28Clo00472|CDS|CDS</td><td>1.0</td><td>40.0</td><td>0.1</td><td>E|K</td><td>COG1725|COG1167</td><td>Predicted transcriptional regulators|Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs</td></tr>
<tr><td>Bste2832|CDS|CDS</td><td>10.0</td><td>3.0</td><td>11.0</td><td>E|K|M|U|Q</td><td>COG0793|COG3291|COG1506|COG4946|COG0823|COG1228|COG3710</td><td>Periplasmic protease|FOG: PKD repeat|Dipeptidyl aminopeptidases/acylaminoacyl-peptidases|Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system|Periplasmic component of the Tol biopolymer transport system|Imidazolonepropionase and related amidohydrolases|DNA-binding winged-HTH domains</td></tr>
</table>

TS28Clo01679|CDS|CDS	3.0	247.0	0.0	E|K|T	COG0642|COG2202|COG0834|COG3452|COG2770|COG0784|COG3614|COG4252|COG2198|COG2203|COG3300|COG3437|COG3706|COG3447	Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|Predicted transmembrane sensor domain|FOG: HPt domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted integral membrane sensor domain
TS28Clo00473|CDS|CDS	1.0	65.0	0.1	E|L|V	COG1131|COG1125|COG3666|COG4152	ABC-type multidrug transport system, ATPase component|ABC-type proline/glycine betaine transport systems, ATPase components|Transposase and inactivated derivatives|ABC-type uncharacterized transport system, ATPase component
Msmi740960|CDS|CDS	5.0	0.3	66.1	E|M	COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase
Msmi750719|CDS|CDS	6.7	0.6	37.8	E|M	COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase
TS28RumUnc0889|CDS|CDS	18.0	3.0	19.8	E|P	COG0601|COG4174	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components|ABC-type uncharacterized transport system, permease component
TS28RumUnc0891|CDS|CDS	17.0	4.0	14.1	E|P	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
TS28Clo01454|CDS|CDS	2.0	72.0	0.1	E|P	COG1121|COG1125|COG1122	ABC-type Mn/Zn transport systems, ATPase component|ABC-type proline/glycine betaine transport systems, ATPase components|ABC-type cobalt transport system, ATPase component
TS28Fae16492|CDS|CDS	2.0	128.5	0.1	E|P	COG0444|COG1123	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component|ATPase components of various ABC-type transport systems, contain duplicated ATPase
TS28Col1410|CDS|CDS	0.3	52.0	0.0	E|P|V	COG1131|COG1123|COG3842|COG1122	ABC-type multidrug transport system, ATPase component|ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type spermidine/putrescine transport systems, ATPase components|ABC-type cobalt transport system, ATPase component
TS28Eub8604|CDS|CDS	0.5	62.0	0.0	E|Q	COG3191	L-aminopeptidase/D-esterase
TS28RumUnc0955|CDS|CDS	13.0	2.0	21.5	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS29Fae00833|CDS|CDS	3.5	1.0	11.6	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS28Met1664|CDS|CDS	22.8	7.1	10.6	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS28Fae20816|CDS|CDS	1.0	38.0	0.1	E|T	COG0834|COG0765|COG4160	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component|ABC-type arginine/histidine transport system, permease component
TS28Rum00298|CDS|CDS	0.5	23.5	0.1	E|T	COG0834|COG0765|COG4160	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component|ABC-type arginine/histidine transport system, permease component
TS28Fae16623|CDS|CDS	1.0	53.5	0.1	E|T	COG0834|COG0765	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component
TS28Fae19983|CDS|CDS	0.3	38.5	0.0	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS29Bac10849|CDS|CDS	4.0	1.0	13.2	E|V	COG2755|COG1680|COG3876	Lysophospholipase L1 and related esterases|Beta-lactamase class C and other penicillin binding proteins|Uncharacterized protein conserved in bacteria
Cint665|CDS|CDS	12.7	0.5	83.8	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
Msmi750496|CDS|CDS	27.4	1.9	47.3	F	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain
Msmi741181|CDS|CDS	27.4	1.9	47.3	F	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain
TS29Fae00691|CDS|CDS	6.5	0.5	43.0	F	COG0151	Phosphoribosylamine-glycine ligase
Cspi0866|CDS|CDS	12.0	1.0	39.7	F	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase
Msmi751253|CDS|CDS	5.8	0.5	38.0	F	COG0503|COG0461	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins|Orotate phosphoribosyltransferase
Msmi740424|CDS|CDS	5.8	0.5	38.0	F	COG0503|COG0461	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins|Orotate phosphoribosyltransferase
Aput0106|CDS|CDS	11.0	1.0	36.4	F	COG0504	CTP synthase (UTP-ammonia lyase)
HPAG10269|CDS|chlorohydrolase	11.0	1.0	36.4	F	COG0402	Cytosine deaminase and related metal-dependent hydrolases
TS28Met0451|CDS|CDS	5.3	0.5	34.7	F	COG0461|COG0503	Orotate phosphoribosyltransferase|Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins
TS28Met1239|CDS|CDS	5.2	0.5	34.2	F	COG0461	Orotate phosphoribosyltransferase
Chyl1127|CDS|CDS	9.0	1.0	29.8	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
Ebif0507|CDS|CDS	8.0	1.0	26.5	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
Msmi741499|CDS|CDS	11.9	1.5	26.3	F	COG0504	CTP synthase (UTP-ammonia lyase)
Cbol4268|CDS|CDS	7.0	1.0	23.1	F	COG0138|COG0299	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)|Folate-dependent phosphoribosylglycinamide formyltransferase PurN
TS29Bac08157|CDS|CDS	4.3	0.7	21.5	F	COG0572	Uridine kinase
Msmi751353|CDS|CDS	3.3	0.5	21.5	F	COG0717	Deoxycytidine deaminase
TS29Bac02632|CDS|CDS	6.5	1.0	21.5	F	COG0105	Nucleoside diphosphate kinase
Msmi750750|CDS|CDS	3.1	0.5	20.4	F	COG1781	Aspartate carbamoyltransferase, regulatory subunit
Bcat0750|CDS|CDS	6.0	1.0	19.8	F	COG2233	Xanthine/uracil permeases

Bste1926|CDS|CDS	3.0	0.5	19.8	F	COG1864	DNA/RNA endonuclease G, NUC1
Acod1257|CDS|CDS	6.0	1.0	19.8	F	COG1457	Purine-cytosine permease and related proteins
Cspi1715|CDS|CDS	6.0	1.0	19.8	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
Pmer0612|CDS|CDS	18.0	3.0	19.8	F	COG0295	Cytidine deaminase
TS28Bac0921|CDS|CDS	3.0	0.5	19.8	F	COG0232	dGTP triphosphohydrolase
ShigspD91916|CDS|CDS	6.0	1.0	19.8	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
Pmer1473|CDS|CDS	8.3	1.5	18.4	F	COG0775|COG2820	Nucleoside phosphorylase|Uridine phosphorylase
TS29Eub1678|CDS|CDS	2.7	0.5	17.6	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS29Fae06044|CDS|CDS	10.6	2.0	17.5	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS29Bac05330|CDS|CDS	2.5	0.5	16.5	F	COG2759	Formyltetrahydrofolate synthetase
TS29Rum07475|CDS|CDS	2.5	0.5	16.5	F	COG2233	Xanthine/uracil permeases
Cbol3219|CDS|CDS	5.0	1.0	16.5	F	COG0461	Orotate phosphoribosyltransferase
Bryfor3729|CDS|CDS	5.0	1.0	16.5	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
Msmi750498|CDS|CDS	6.7	1.3	16.5	F	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase
Msmi751115|CDS|CDS	8.4	1.8	15.9	F	COG0151|COG0152	Phosphoribosylamine-glycine ligase|Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase
Bdor2354|CDS|CDS	9.5	2.0	15.7	F	COG0540	Aspartate carbamoyltransferase, catalytic chain
Msmi750620|CDS|CDS	9.3	2.0	15.4	F	COG1102	Cytidylate kinase
TS28Par0793|CDS|CDS	6.8	1.5	15.1	F	COG0150	Phosphoribosylaminoimidazole (AIR) synthetase
TS28Fae06915|CDS|CDS	9.0	2.0	14.9	F	COG2820	Uridine phosphorylase
Begg1811|CDS|CDS	18.0	4.0	14.9	F	COG0572	Uridine kinase
Even0516|CDS|CDS	4.5	1.0	14.9	F	COG0563	Adenylate kinase and related kinases
Msmi750709|CDS|CDS	2.8	0.7	14.1	F	COG0461	Orotate phosphoribosyltransferase
Bova2806|CDS|CDS	2.7	0.7	13.4	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS28Fae10285|CDS|CDS	8.0	2.0	13.2	F	COG0528	Uridylate kinase
Bste1720|CDS|CDS	16.0	4.0	13.2	F	COG0041|COG0151	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase|Phosphoribosylamine-glycine ligase
TS28Met1124|CDS|CDS	29.4	7.9	12.3	F	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain
TS28Bac3162|CDS|CDS	4.3	1.2	12.3	F	COG0572	Uridine kinase
TS28Rum01303|CDS|CDS	63.0	17.0	12.3	F	COG2759	Formyltetrahydrofolate synthetase
Bste1042|CDS|CDS	11.0	3.0	12.1	F	COG0540	Aspartate carbamoyltransferase, catalytic chain
TS29Rum13298|CDS|CDS	3.7	1.0	12.1	F	COG0151|COG0041	Phosphoribosylamine-glycine ligase|Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase
TS28Rum03196|CDS|CDS	3.7	1.0	12.1	F	COG0151|COG0041	Phosphoribosylamine-glycine ligase|Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase
Rtor0045|CDS|CDS	3.7	1.0	12.1	F	COG0041|COG0151	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase|Phosphoribosylamine-glycine ligase
Rumhyd0001|CDS|CDS	7.0	2.0	11.6	F	COG2759	Formyltetrahydrofolate synthetase
Bdor2353|CDS|CDS	7.0	2.0	11.6	F	COG1781	Aspartate carbamoyltransferase, regulatory subunit
TS28Rum11371|CDS|CDS	26.0	8.0	10.7	F	COG2065	Pyrimidine operon attenuation protein/uracil phosphoribosyltransferase
TS29Fae00686|CDS|CDS	6.5	2.0	10.7	F	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase
Bdor2886|CDS|CDS	30.3	9.5	10.6	F	COG0138	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)
TS28Fae07641|CDS|CDS	19.0	6.0	10.5	F	COG0035	Uracil phosphoribosyltransferase
TS28Ali2042|CDS|CDS	161.0	51.0	10.4	F	COG0528	Uridylate kinase
TS28Ali1949|CDS|CDS	164.0	52.0	10.4	F	COG1864	DNA/RNA endonuclease G, NUC1
Msmi750213|CDS|CDS	7.8	2.5	10.3	F	COG0504	CTP synthase (UTP-ammonia lyase)
Robe3904|CDS|CDS	0.5	16.7	0.1	F	COG0015	Adenylosuccinate lyase
TS28Eub7581|CDS|CDS	1.0	34.0	0.1	F	COG0461	Orotate phosphoribosyltransferase
Bpse1102|CDS|CDS	0.3	8.7	0.1	F	COG0167	Dihydroorotate dehydrogenase
TS28Dor1853|CDS|CDS	0.5	17.5	0.1	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS28Fae10590|CDS|CDS	1.0	35.0	0.1	F	COG0295|COG0813	Cytidine deaminase|Purine-nucleoside phosphorylase
TS28Clo01211|CDS|CDS	6.0	213.0	0.1	F	COG2759	Formyltetrahydrofolate synthetase
TS28Fae08721|CDS|CDS	0.3	10.0	0.1	F	COG0232	dGTP triphosphohydrolase
TS28Fae15732|CDS|CDS	1.0	41.0	0.1	F	COG0519	GMP synthase, PP-ATPase domain/subunit
CspSS22435|CDS|CDS	1.0	44.5	0.1	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS29Bif1205|CDS|CDS	0.3	11.7	0.1	F	COG0167	Dihydroorotate dehydrogenase
TS28Bac3472|CDS|CDS	0.2	11.0	0.1	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS28Eub7003|CDS|CDS	2.0	103.0	0.1	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS28Met0467|CDS|CDS	0.7	37.0	0.1	F	COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS28Clo00527|CDS|CDS	1.0	53.0	0.1	F	COG0756	dUTPase
TS28Fae18262|CDS|CDS	1.0	56.0	0.1	F	COG0563	Adenylate kinase and related kinases
TS28Eub5187|CDS|CDS	1.5	94.0	0.1	F	COG1001	Adenine deaminase
Dlon2581|CDS|CDS	0.5	33.5	0.0	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS28Eub0954|CDS|CDS	0.5	33.5	0.0	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
TS28Fae16694|CDS|CDS	0.5	34.3	0.0	F	COG0104	Adenylosuccinate synthase
TS28Eub3869|CDS|CDS	1.3	102.5	0.0	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS28Bif3806|CDS|CDS	0.3	25.7	0.0	F	COG0167	Dihydroorotate dehydrogenase
Eeli1739|CDS|CDS	0.1	13.0	0.0	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS28Clo00504|CDS|CDS	1.0	108.5	0.0	F	COG1816	Adenosine deaminase
TS28Fae20643|CDS|CDS	0.3	27.3	0.0	F	COG0232	dGTP triphosphohydrolase

TS28Bif4810|CDS|CDS	0.3	38.9	0.0	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS28Eub3856|CDS|CDS	0.3	78.0	0.0	F	COG0504	CTP synthase (UTP-ammonia lyase)
Robe3819|CDS|CDS	0.1	37.3	0.0	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS28Rum12474|CDS|CDS	0.7	35.0	0.1	F|C	COG2080|COG1529|COG4631	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs|Xanthine dehydrogenase, molybdopterin-binding subunit B
TS28Fae21470|CDS|CDS	0.5	23.0	0.1	F|C|H	COG0167|COG0543|COG1146	Dihydroorotate dehydrogenase|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Ferredoxin
TS29Fae06953|CDS|CDS	5.0	1.0	16.5	F|H	COG0283|COG1160|COG0414	Cytidylate kinase|Predicted GTPases|Panthothenate synthetase
TS28Bac4451|CDS|CDS	5.0	1.0	16.5	F|J	COG0127|COG0689	Xanthosine triphosphate pyrophosphatase|RNase PH
TS28Clo01410|CDS|CDS	1.0	241.0	0.0	F|J	COG0441|COG0572	Threonyl-tRNA synthetase|Uridine kinase
TS28Fae12958|CDS|CDS	1.0	41.5	0.1	F|J|D	COG0037|COG0634|COG0590	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control|Hypoxanthine-guanine phosphoribosyltransferase|Cytosine/adenosine deaminases
TS28Dor2839|CDS|CDS	14.0	4.0	11.6	F|J|L	COG1194|COG1051|COG1670|COG0494	A/G-specific DNA glycosylase|ADP-ribose pyrophosphatase|Acetyltransferases, including N-acetylases of ribosomal proteins|NTP pyrophosphohydrolases including oxidative damage repair enzymes
TS29Fae08488|CDS|CDS	2.5	0.5	16.5	F|K	COG2207|COG2169|COG3708|COG4977	AraC-type DNA-binding domain-containing proteins|Adenosine deaminase|Uncharacterized protein conserved in bacteria|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS29Fae01179|CDS|CDS	7.0	1.5	15.4	F|K|T	COG4753|COG2207|COG4936|COG2169|COG3708|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Predicted sensor domain|Adenosine deaminase|Uncharacterized protein conserved in bacteria|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS28Fae21176|CDS|CDS	1.5	54.5	0.1	F|K|T	COG5002|COG2202|COG0745|COG4753|COG2207|COG2204|COG0784|COG3437|COG3279|COG4936|COG3706|COG2197|COG2169	Signal transduction histidine kinase|FOG: PAS/PAC domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|FOG: CheY-like receiver|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Response regulator of the LytR/AlgR family|Predicted sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Adenosine deaminase
TS28Bac8321|CDS|CDS	22.0	5.0	14.6	F|T	COG0737|COG3103	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases|SH3 domain protein
Chyl2219|CDS|CDS	1,920.3	1.0	6,350.3	G	COG1879	ABC-type sugar transport system, periplasmic component
BactD23013|CDS|CDS	334.8	1.0	1,107.1	G	COG0524	Sugar kinases, ribokinase family
Bova1522|CDS|CDS	334.8	2.0	553.5	G	COG0524	Sugar kinases, ribokinase family
TS28Rum15781|CDS|CDS	763.0	12.0	210.3	G	COG2017	Galactose mutarotase and related enzymes
Dlon0471|CDS|CDS	49.0	1.0	162.0	G	COG1653	ABC-type sugar transport system, periplasmic component
Ccom2466|CDS|CDS	181.0	4.0	149.6	G	COG3345	Alpha-galactosidase
Ehal2019|CDS|CDS	15.5	0.5	102.5	G	COG0448	ADP-glucose pyrophosphorylase
TS29Fae06721|CDS|CDS	12.5	0.5	82.7	G	COG1874	Beta-galactosidase
TS29Bac10833|CDS|CDS	8.0	0.3	79.4	G	COG3934	Endo-beta-mannanase
TS29Eub1284|CDS|CDS	33.5	1.5	73.9	G	COG2182	Maltose-binding periplasmic proteins/domains
Acol3408|CDS|CDS	20.0	1.0	66.1	G	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases
TS29Rum05495|CDS|CDS	6.0	0.3	59.5	G	COG4409	Neuraminidase (sialidase)
Casp2021|CDS|CDS	61.5	3.5	58.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29Rum02336|CDS|CDS	5.7	0.3	56.2	G	COG1879	ABC-type sugar transport system, periplasmic component
TS29Fae00079|CDS|CDS	8.4	0.5	55.7	G	COG0296	1,4-alpha-glucan branching enzyme
BVU3512|CDS|6-phosphofructokinase	2.8	0.2	55.6	G	COG0205	6-phosphofructokinase
Hfil3422|CDS|CDS	15.0	1.0	49.6	G	COG1879	ABC-type sugar transport system, periplasmic component
TS29Fae08283|CDS|CDS	7.5	0.5	49.6	G	COG0149	Triosephosphate isomerase
TS28Ali2244|CDS|CDS	75.0	5.0	49.6	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bxyl3893|CDS|CDS	4.5	0.3	44.6	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
Ehal0749|CDS|CDS	73.0	5.5	43.9	G	COG0296	1,4-alpha-glucan branching enzyme
TS29Rum03526|CDS|CDS	21.0	1.7	41.7	G	COG1653	ABC-type sugar transport system, periplasmic component
ShigspD90525|CDS|CDS	6.2	0.5	40.8	G	COG4677	Pectin methylesterase
TS29Bac10838|CDS|CDS	4.0	0.3	39.7	G	COG3250	Beta-galactosidase/beta-glucuronidase
CspL21752|CDS|CDS	12.0	1.0	39.7	G	COG1803	Methylglyoxal synthase
Msmi751420|CDS|CDS	7.9	0.7	39.3	G	COG1980	Archaeal fructose 1,6-bisphosphatase
CspM6212397|CDS|CDS	11.2	1.0	37.0	G	COG0574|COG1080|COG4668|COG3412	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria
TS29Bac08447|CDS|CDS	5.5	0.5	36.4	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
Buni1688|CDS|CDS	5.5	0.5	36.4	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase

<table>
<tr><td>Bdor1424|CDS|CDS</td><td>31.4</td><td>3.0</td><td>34.6</td><td>G</td><td>COG0057</td><td>Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase</td></tr>
<tr><td>TS28Dor1642|CDS|CDS</td><td>10.0</td><td>1.0</td><td>33.1</td><td>G</td><td>COG1925</td><td>Phosphotransferase system, HPr-related proteins</td></tr>
<tr><td>Acol0367|CDS|CDS</td><td>10.0</td><td>1.0</td><td>33.1</td><td>G</td><td>COG1879</td><td>ABC-type sugar transport system, periplasmic component</td></tr>
<tr><td>TS29Fae04582|CDS|CDS</td><td>5.0</td><td>0.5</td><td>33.1</td><td>G</td><td>COG1082</td><td>Sugar phosphate isomerases/epimerases</td></tr>
<tr><td>Csym3668|CDS|CDS</td><td>10.0</td><td>1.0</td><td>33.1</td><td>G</td><td>COG0448</td><td>ADP-glucose pyrophosphorylase</td></tr>
<tr><td>b0688|CDS|phosphoglucomutase</td><td>9.4</td><td>1.0</td><td>31.1</td><td>G</td><td>COG1109|COG0033</td><td>Phosphomannomutase|Phosphoglucomutase</td></tr>
<tr><td>Cbol0676|CDS|CDS</td><td>9.3</td><td>1.0</td><td>30.9</td><td>G</td><td>COG0448</td><td>ADP-glucose pyrophosphorylase</td></tr>
<tr><td>TS29Bac00193|CDS|CDS</td><td>3.1</td><td>0.3</td><td>30.7</td><td>G</td><td>COG1830</td><td>DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes</td></tr>
<tr><td>TS28Eub8790|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG4209</td><td>ABC-type polysaccharide transport system, permease component</td></tr>
<tr><td>Bste2756|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG3717</td><td>5-keto 4-deoxyuronate isomerase</td></tr>
<tr><td>TS29Fae01192|CDS|CDS</td><td>4.5</td><td>0.5</td><td>29.8</td><td>G</td><td>COG3250</td><td>Beta-galactosidase/beta-glucuronidase</td></tr>
<tr><td>TS29Rum03806|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG1879|COG4213</td><td>ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component</td></tr>
<tr><td>ShigspD92138|CDS|CDS</td><td>4.5</td><td>0.5</td><td>29.8</td><td>G</td><td>COG1879|COG1172|COG4158|COG4214</td><td>ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component|ABC-type xylose transport system, permease component</td></tr>
<tr><td>RintL13136|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG1820</td><td>N-acetylglucosamine-6-phosphate deacetylase</td></tr>
<tr><td>TS29Fae07187|CDS|CDS</td><td>4.5</td><td>0.5</td><td>29.8</td><td>G</td><td>COG1472</td><td>Beta-glucosidase-related glycosidases</td></tr>
<tr><td>Clep1252|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG1082</td><td>Sugar phosphate isomerases/epimerases</td></tr>
<tr><td>Bxyl0043|CDS|CDS</td><td>4.5</td><td>0.5</td><td>29.8</td><td>G</td><td>COG0800</td><td>2-keto-3-deoxy-6-phosphogluconate aldolase</td></tr>
<tr><td>FpraM2120142|CDS|CDS</td><td>3.0</td><td>0.3</td><td>29.8</td><td>G</td><td>COG0448</td><td>ADP-glucose pyrophosphorylase</td></tr>
<tr><td>TS28Par1403|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG0363</td><td>6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase</td></tr>
<tr><td>Bryfor3653|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>G</td><td>COG0057</td><td>Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase</td></tr>
<tr><td>Bdor3671|CDS|CDS</td><td>1.8</td><td>0.2</td><td>29.2</td><td>G</td><td>COG1803</td><td>Methylglyoxal synthase</td></tr>
<tr><td>ShigspD90765|CDS|CDS</td><td>8.5</td><td>1.0</td><td>28.1</td><td>G</td><td>COG1070</td><td>Sugar (pentulose and hexulose) kinases</td></tr>
<tr><td>TS28Ali2049|CDS|CDS</td><td>165.0</td><td>20.0</td><td>27.3</td><td>G</td><td>COG0191</td><td>Fructose/tagatose bisphosphate aldolase</td></tr>
<tr><td>Cspi0396|CDS|CDS</td><td>16.1</td><td>2.0</td><td>26.6</td><td>G</td><td>COG1501</td><td>Alpha-glucosidases, family 31 of glycosyl hydrolases</td></tr>
<tr><td>BactD12525|CDS|CDS</td><td>4.0</td><td>0.5</td><td>26.5</td><td>G</td><td>COG3507</td><td>Beta-xylosidase</td></tr>
<tr><td>TS29Fae01183|CDS|CDS</td><td>4.0</td><td>0.5</td><td>26.5</td><td>G</td><td>COG3090|COG1593</td><td>TRAP-type C4-dicarboxylate transport system, small permease component|TRAP-type C4-dicarboxylate transport system, large permease component</td></tr>
<tr><td>Bpse1884|CDS|CDS</td><td>2.7</td><td>0.3</td><td>26.5</td><td>G</td><td>COG1653</td><td>ABC-type sugar transport system, periplasmic component</td></tr>
<tr><td>Dlon1704|CDS|CDS</td><td>4.0</td><td>0.5</td><td>26.5</td><td>G</td><td>COG1015</td><td>Phosphopentomutase</td></tr>
<tr><td>b3526|CDS|ketodeoxygluconokinase</td><td>4.0</td><td>0.5</td><td>26.5</td><td>G</td><td>COG0524|COG3718</td><td>Sugar kinases, ribokinase family|Uncharacterized enzyme involved in inositol metabolism</td></tr>
<tr><td>TS29Rum12278|CDS|CDS</td><td>8.0</td><td>1.0</td><td>26.5</td><td>G</td><td>COG0524</td><td>Sugar kinases, ribokinase family</td></tr>
<tr><td>Rtor0337|CDS|CDS</td><td>45.0</td><td>5.7</td><td>26.3</td><td>G</td><td>COG1653</td><td>ABC-type sugar transport system, periplasmic component</td></tr>
<tr><td>CspM6212277|CDS|CDS</td><td>7.8</td><td>1.0</td><td>25.9</td><td>G</td><td>COG1879</td><td>ABC-type sugar transport system, periplasmic component</td></tr>
<tr><td>Msmi741412|CDS|CDS</td><td>3.9</td><td>0.5</td><td>25.9</td><td>G</td><td>COG1830</td><td>DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes</td></tr>
<tr><td>Svar1991|CDS|CDS</td><td>7.8</td><td>1.0</td><td>25.6</td><td>G</td><td>COG1129</td><td>ABC-type sugar transport system, ATPase component</td></tr>
<tr><td>Rgna1586|CDS|CDS</td><td>7.5</td><td>1.0</td><td>24.8</td><td>G</td><td>COG3408</td><td>Glycogen debranching enzyme</td></tr>
<tr><td>TS29Rum12478|CDS|CDS</td><td>7.5</td><td>1.0</td><td>24.8</td><td>G</td><td>COG3408</td><td>Glycogen debranching enzyme</td></tr>
<tr><td>ShigspD90655|CDS|CDS</td><td>7.5</td><td>1.0</td><td>24.8</td><td>G</td><td>COG0448</td><td>ADP-glucose pyrophosphorylase</td></tr>
<tr><td>Pmer3099|CDS|CDS</td><td>52.0</td><td>7.0</td><td>24.6</td><td>G</td><td>COG0148</td><td>Enolase</td></tr>
<tr><td>BactD13756|CDS|CDS</td><td>7.4</td><td>1.0</td><td>24.3</td><td>G</td><td>COG0696</td><td>Phosphoglyceromutase</td></tr>
<tr><td>Cspi0450|CDS|CDS</td><td>7.1</td><td>1.0</td><td>23.3</td><td>G</td><td>COG1501</td><td>Alpha-glucosidases, family 31 of glycosyl hydrolases</td></tr>
<tr><td>Cbol0656|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG3839</td><td>ABC-type sugar transport systems, ATPase components</td></tr>
<tr><td>BactD23254|CDS|CDS</td><td>3.5</td><td>0.5</td><td>23.1</td><td>G</td><td>COG3537</td><td>Putative alpha-1,2-mannosidase</td></tr>
<tr><td>TS28Bac0491|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG2407</td><td>L-fucose isomerase and related proteins</td></tr>
<tr><td>TS29Bac02903|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG2115</td><td>Xylose isomerase</td></tr>
<tr><td>Cspi0065|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG1523</td><td>Type II secretory pathway, pullulanase PulA and related glycosidases</td></tr>
<tr><td>TS29Bac04374|CDS|CDS</td><td>4.7</td><td>0.7</td><td>23.1</td><td>G</td><td>COG1501</td><td>Alpha-glucosidases, family 31 of glycosyl hydrolases</td></tr>
<tr><td>Acol2156|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG0800</td><td>2-keto-3-deoxy-6-phosphogluconate aldolase</td></tr>
<tr><td>TS28Clo04898|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG0574</td><td>Phosphoenolpyruvate synthase/pyruvate phosphate dikinase</td></tr>
<tr><td>TS29Fae08749|CDS|CDS</td><td>3.5</td><td>0.5</td><td>23.1</td><td>G</td><td>COG0406</td><td>Fructose-2,6-bisphosphatase</td></tr>
<tr><td>Ehal1651|CDS|CDS</td><td>3.5</td><td>0.5</td><td>23.1</td><td>G</td><td>COG0297</td><td>Glycogen synthase</td></tr>
<tr><td>ShigspD90640|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>G</td><td>COG0058</td><td>Glucan phosphorylase</td></tr>
<tr><td>Hfil0155|CDS|CDS</td><td>6.7</td><td>1.0</td><td>22.0</td><td>G</td><td>COG0057</td><td>Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase</td></tr>
<tr><td>BactD23513|CDS|CDS</td><td>6.5</td><td>1.0</td><td>21.5</td><td>G</td><td>COG3525</td><td>N-acetyl-beta-hexosaminidase</td></tr>
<tr><td>Bste0424|CDS|CDS</td><td>13.0</td><td>2.0</td><td>21.5</td><td>G</td><td>COG2407</td><td>L-fucose isomerase and related proteins</td></tr>
<tr><td>Bdor3986|CDS|CDS</td><td>31.7</td><td>5.0</td><td>20.9</td><td>G</td><td>COG0297</td><td>Glycogen synthase</td></tr>
<tr><td>Bste1250|CDS|CDS</td><td>18.8</td><td>3.0</td><td>20.8</td><td>G</td><td>COG0588</td><td>Phosphoglycerate mutase 1</td></tr>
<tr><td>Rtor0339|CDS|CDS</td><td>12.5</td><td>2.0</td><td>20.7</td><td>G</td><td>COG0395|COG3833</td><td>ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component</td></tr>
<tr><td>CspM6211083|CDS|CDS</td><td>15.4</td><td>2.5</td><td>20.4</td><td>G</td><td>COG0057</td><td>Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase</td></tr>
<tr><td>Pmer3326|CDS|CDS</td><td>24.5</td><td>4.0</td><td>20.3</td><td>G</td><td>COG0363</td><td>6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase</td></tr>
<tr><td>Csci2431|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>G</td><td>COG2407</td><td>L-fucose isomerase and related proteins</td></tr>
<tr><td>Hfil1237|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>G</td><td>COG1820</td><td>N-acetylglucosamine-6-phosphate deacetylase</td></tr>
<tr><td>TS29Rum17478|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>G</td><td>COG1653</td><td>ABC-type sugar transport system, periplasmic component</td></tr>
<tr><td>Bova3871|CDS|CDS</td><td>3.0</td><td>0.5</td><td>19.8</td><td>G</td><td>COG0297</td><td>Glycogen synthase</td></tr>
<tr><td>Aput1142|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>G</td><td>COG0057</td><td>Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase</td></tr>
<tr><td>Sinf0639|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>G</td><td>COG0057</td><td>Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase</td></tr>
<tr><td>TS28Rum08489|CDS|CDS</td><td>45.0</td><td>7.7</td><td>19.4</td><td>G</td><td>COG1653</td><td>ABC-type sugar transport system, periplasmic component</td></tr>
<tr><td>Clep1000|CDS|CDS</td><td>34.7</td><td>6.0</td><td>19.1</td><td>G</td><td>COG0395|COG3833</td><td>ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component</td></tr>
<tr><td>TS29Bac01188|CDS|CDS</td><td>17.0</td><td>3.0</td><td>18.7</td><td>G</td><td>COG4632</td><td>Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase</td></tr>
</table>

Even1637|CDS|CDS	8.3	1.5	18.4	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bxyl2682|CDS|CDS	8.3	1.5	18.2	G	COG3507	Beta-xylosidase
Rbro0909|CDS|CDS	5.5	1.0	18.2	G	COG0296	1,4-alpha-glucan branching enzyme
TS29Rum17483|CDS|CDS	33.0	6.0	18.2	G	COG0191	Fructose/tagatose bisphosphate aldolase
Bova1771|CDS|CDS	2.7	0.5	17.9	G	COG1820	N-acetylglucosamine-6-phosphate deacetylase
Rtor1578|CDS|CDS	21.5	4.0	17.8	G	COG3716	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IID
Bxyl0567|CDS|CDS	2.7	0.5	17.6	G	COG3537	Putative alpha-1,2-mannosidase
BactD13483|CDS|CDS	2.7	0.5	17.6	G	COG3537	Putative alpha-1,2-mannosidase
FpraM2120367|CDS|CDS	8.0	1.5	17.6	G	COG0205	6-phosphofructokinase
BactD12576|CDS|CDS	5.3	1.0	17.4	G	COG3507	Beta-xylosidase
Cmet0760|CDS|CDS	15.7	3.0	17.3	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Rbro0630|CDS|CDS	43.5	8.5	16.9	G	COG2182	Maltose-binding periplasmic proteins/domains
FpraM2120350|CDS|CDS	12.7	2.5	16.8	G	COG1175|COG4209	ABC-type sugar transport systems, permease components|ABC-type polysaccharide transport system, permease component
Ehal1451|CDS|CDS	20.3	4.0	16.7	G	COG1879	ABC-type sugar transport system, periplasmic component
Bdor0615|CDS|CDS	80.7	16.0	16.7	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
Bdor3919|CDS|CDS	40.2	8.0	16.6	G	COG3408	Glycogen debranching enzyme
TS28Par1526|CDS|CDS	2.5	0.5	16.5	G	COG4409	Neuraminidase (sialidase)
CspSS21430|CDS|CDS	10.0	2.0	16.5	G	COG3775	Phosphotransferase system, galactitol-specific IIC component
Bdor2375|CDS|CDS	15.0	3.0	16.5	G	COG2731	Beta-galactosidase, beta subunit
TS29RumUnc0460|CDS|CDS	5.0	1.0	16.5	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bac03753|CDS|CDS	2.5	0.5	16.5	G	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)
Cmit0823|CDS|CDS	5.0	1.0	16.5	G	COG0574|COG1080|COG4668|COG3412|COG2190	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components
ShigspD90553|CDS|CDS	5.0	1.0	16.5	G	COG0383	Alpha-mannosidase
TS29Rum12314|CDS|CDS	1.7	0.3	16.5	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
TS28EntUnc146|CDS|CDS	10.0	2.0	16.5	G	COG0205	6-phosphofructokinase
Ccom0805|CDS|CDS	5.0	1.0	16.5	G	COG0205	6-phosphofructokinase
Pmer3227|CDS|CDS	10.0	2.0	16.5	G	COG0191	Fructose/tagatose bisphosphate aldolase
Bfin0903|CDS|CDS	2.4	0.5	16.1	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Bthe3732371|CDS|CDS	2.4	0.5	16.1	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
BactD12630|CDS|CDS	2.4	0.5	16.1	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Bthe7331681|CDS|CDS	2.4	0.5	16.1	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Bthe3730341|CDS|CDS	1.2	0.3	16.0	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bthe7332104|CDS|CDS	1.2	0.3	16.0	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Rgna0763|CDS|CDS	29.0	6.0	16.0	G	COG1070	Sugar (pentulose and hexulose) kinases
TS28Rum08487|CDS|CDS	9.5	2.0	15.7	G	COG0395|COG3833	ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component
TS28Eub0689|CDS|CDS	73.0	15.5	15.6	G	COG0296	1,4-alpha-glucan branching enzyme
Cbol1156|CDS|CDS	7.0	1.5	15.4	G	COG1129	ABC-type sugar transport system, ATPase component
RintL10955|CDS|CDS	14.0	3.0	15.4	G	COG0448	ADP-glucose pyrophosphorylase
STER1366|CDS|beta-galactosidase	2.3	0.5	15.4	G	COG3250	Beta-galactosidase/beta-glucuronidase
str1397|CDS|beta-galactosidase	2.3	0.5	15.4	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Fae01620|CDS|CDS	6.9	1.5	15.2	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28RumUnc0992|CDS|CDS	23.0	5.0	15.2	G	COG2152	Predicted glycosylase
TS29Rum10837|CDS|CDS	59.0	13.0	15.0	G	COG1653	ABC-type sugar transport system, periplasmic component
Bdor0616|CDS|CDS	19.7	4.3	15.0	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
Bste1086|CDS|CDS	45.3	10.0	15.0	G	COG0296	1,4-alpha-glucan branching enzyme
ShigspD90233|CDS|CDS	4.5	1.0	14.9	G	COG1879|COG1129	ABC-type sugar transport system, periplasmic component|ABC-type sugar transport system, ATPase component
Msmi750304|CDS|CDS	6.7	1.5	14.9	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
FpraM2120140|CDS|CDS	3.0	0.7	14.9	G	COG0297	Glycogen synthase
TS28Clo04564|CDS|CDS	9.0	2.0	14.9	G	COG0296	1,4-alpha-glucan branching enzyme
Clep0321|CDS|CDS	6.7	1.5	14.7	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29Fae05698|CDS|CDS	2.9	0.7	14.6	G	COG1653	ABC-type sugar transport system, periplasmic component
Pmer3620|CDS|CDS	2.5	0.6	14.4	G	COG0588	Phosphoglycerate mutase 1
Bdor3664|CDS|CDS	2.5	0.6	14.4	G	COG0588	Phosphoglycerate mutase 1
TS28Rum12793|CDS|CDS	4.3	1.0	14.3	G	COG0524	Sugar kinases, ribokinase family
TS29Bac08446|CDS|CDS	6.5	1.5	14.3	G	COG0364	Glucose-6-phosphate 1-dehydrogenase
FpraM2121137|CDS|CDS	4.3	1.0	14.3	G	COG3250	Beta-galactosidase/beta-glucuronidase
Cspi1588|CDS|CDS	4.3	1.0	14.3	G	COG1501|COG4724	Alpha-glucosidases, family 31 of glycosyl hydrolases|Endo-beta-N-acetylglucosaminidase D
Msmi750975|CDS|CDS	2.9	0.7	14.3	G	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)
TS29Fae05950|CDS|CDS	8.5	2.0	14.1	G	COG2017	Galactose mutarotase and related enzymes
TS29Fae04148|CDS|CDS	6.3	1.5	14.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
BactD13152|CDS|CDS	21.0	5.0	13.9	G	COG2160	L-arabinose isomerase
Rgna1672|CDS|CDS	4.2	1.0	13.9	G	COG0149	Triosephosphate isomerase
Bdor1042|CDS|CDS	69.5	17.0	13.5	G	COG3250	Beta-galactosidase/beta-glucuronidase
Bdor3247|CDS|CDS	24.2	6.0	13.3	G	COG0153	Galactokinase
Rtor1813|CDS|CDS	4.0	1.0	13.2	G	COG4668|COG1925	Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphotransferase system, HPr-related proteins
TS29Bac08546|CDS|CDS	8.0	2.0	13.2	G	COG3525	N-acetyl-beta-hexosaminidase

BactD11424|CDS|CDS	2.0	0.5	13.2	G	COG3507	Beta-xylosidase
Rtor1576|CDS|CDS	26.0	6.5	13.2	G	COG3444	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB
ShigspD91590|CDS|CDS	4.0	1.0	13.2	G	COG3010	Putative N-acetylmannosamine-6-phosphate epimerase
TS28Rum02188|CDS|CDS	2.0	0.5	13.2	G	COG2893	Phosphotransferase system, mannose/fructose-specific component IIA
Pmer1552|CDS|CDS	4.0	1.0	13.2	G	COG2731	Beta-galactosidase, beta subunit
BactD12493|CDS|CDS	2.0	0.5	13.2	G	COG2730	Endoglucanase
TS29Bac11104|CDS|CDS	4.0	1.0	13.2	G	COG2271	Sugar phosphate permease
BactD23255|CDS|CDS	4.0	1.0	13.2	G	COG2152	Predicted glycosylase
Casp2745|CDS|CDS	4.0	1.0	13.2	G	COG1879	ABC-type sugar transport system, periplasmic component
TS29Rum08551|CDS|CDS	2.0	0.5	13.2	G	COG1653	ABC-type sugar transport system, periplasmic component
Rgna1196|CDS|CDS	2.0	0.5	13.2	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum11964|CDS|CDS	2.0	0.5	13.2	G	COG1653	ABC-type sugar transport system, periplasmic component
RintL10911|CDS|CDS	4.0	1.0	13.2	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Bac11287|CDS|CDS	4.0	1.0	13.2	G	COG1472	Beta-glucosidase-related glycosidases
Bste3064|CDS|CDS	4.0	1.0	13.2	G	COG1109	Phosphomannomutase
TS29Rum02613|CDS|CDS	8.0	2.0	13.2	G	COG0448	ADP-glucose pyrophosphorylase
Ccom0832|CDS|CDS	4.0	1.0	13.2	G	COG0448	ADP-glucose pyrophosphorylase
TS28Dor0774|CDS|CDS	4.0	1.0	13.2	G	COG0395	ABC-type sugar transport system, permease component
Robe0171|CDS|CDS	2.0	0.5	13.2	G	COG0296	1,4-alpha-glucan branching enzyme
TS29Bac08270|CDS|CDS	2.0	0.5	13.2	G	COG0205	6-phosphofructokinase
Ehal1631|CDS|CDS	4.0	1.0	13.2	G	COG0191	Fructose/tagatose bisphosphate aldolase
Dlon0373|CDS|CDS	4.0	1.0	13.2	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
Csci2583|CDS|CDS	4.0	1.0	13.2	G	COG0058	Glucan phosphorylase
Cbol4778|CDS|CDS	4.0	1.0	13.2	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Rbro0910|CDS|CDS	27.3	7.0	12.9	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Msmi750809|CDS|CDS	2.2	0.6	12.7	G	COG0149	Triosephosphate isomerase
TS29Rum06752|CDS|CDS	2.5	0.7	12.4	G	COG2190|COG1264	Phosphotransferase system IIA components|Phosphotransferase system IIB components
Bdor0266|CDS|CDS	25.7	7.0	12.1	G	COG0191	Fructose/tagatose bisphosphate aldolase
Bste2964|CDS|CDS	20.0	5.5	12.0	G	COG3537	Putative alpha-1,2-mannosidase
CspSS22702|CDS|CDS	18.0	5.0	11.9	G	COG2893|COG3444	Phosphotransferase system, mannose/fructose-specific component IIA|Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB
Dfor2762|CDS|CDS	21.5	6.0	11.8	G	COG0448	ADP-glucose pyrophosphorylase
Cspi0227|CDS|CDS	10.7	3.0	11.8	G	COG3250|COG1501|COG3525	Beta-galactosidase/beta-glucuronidase|Alpha-glucosidases, family 31 of glycosyl hydrolases|N-acetyl-beta-hexosaminidase
TS28Par2005|CDS|CDS	7.0	2.0	11.6	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Bac1548|CDS|CDS	11.7	3.3	11.6	G	COG3459	Cellobiose phosphorylase
TS29Rum18173|CDS|CDS	14.0	4.0	11.6	G	COG2407	L-fucose isomerase and related proteins
Ehal0447|CDS|CDS	3.5	1.0	11.6	G	COG2376	Dihydroxyacetone kinase
TS29Eub1129|CDS|CDS	2.3	0.7	11.6	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum13175|CDS|CDS	14.0	4.0	11.6	G	COG1472	Beta-glucosidase-related glycosidases
BactD12739|CDS|CDS	7.0	2.0	11.6	G	COG0297	Glycogen synthase
Pmer0815|CDS|CDS	7.0	2.0	11.6	G	COG0297	Glycogen synthase
BactD10952|CDS|CDS	1.8	0.5	11.6	G	COG0191	Fructose/tagatose bisphosphate aldolase
Hfil1390|CDS|CDS	3.5	1.0	11.6	G	COG0176|COG0166	Transaldolase|Glucose-6-phosphate isomerase
TS28Dor0107|CDS|CDS	73.0	21.0	11.5	G	COG1653	ABC-type sugar transport system, periplasmic component
BactD13148|CDS|CDS	6.3	1.8	11.4	G	COG0021	Transketolase
Bdor0591|CDS|CDS	30.3	9.0	11.1	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Bac7962|CDS|CDS	57.2	17.0	11.1	G	COG0297	Glycogen synthase
Rtor2421|CDS|CDS	15.0	4.5	11.0	G	COG5263|COG4193	FOG: Glucan-binding domain (YG repeat)|Beta- N-acetylglucosaminidase
Acol0978|CDS|CDS	5.0	1.5	11.0	G	COG1129	ABC-type sugar transport system, ATPase component
RintL10388|CDS|CDS	6.5	2.0	10.7	G	COG1653	ABC-type sugar transport system, periplasmic component
Csym1961|CDS|CDS	13.0	4.0	10.7	G	COG0574|COG1080|COG4668|COG3412	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria
Pmer1909|CDS|CDS	32.0	10.0	10.6	G	COG0021	Transketolase
Svar1735|CDS|CDS	48.8	15.3	10.5	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bste0539|CDS|CDS	19.0	6.0	10.5	G	COG1109	Phosphomannomutase
TS28Rum04748|CDS|CDS	17.0	5.5	10.2	G	COG1879	ABC-type sugar transport system, periplasmic component
Bpse1035|CDS|CDS	1.8	58.0	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS29Bif2248|CDS|CDS	0.3	8.3	0.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Fae00649|CDS|CDS	1.0	33.3	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Rum20811|CDS|CDS	1.0	34.0	0.1	G	COG3534	Alpha-L-arabinofuranosidase
Bdor1382|CDS|CDS	1.0	34.0	0.1	G	COG2017	Galactose mutarotase and related enzymes
Rbro0327|CDS|CDS	0.3	11.3	0.1	G	COG0366|COG1523	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases
EUBREC0500|CDS|alpha-glucosidase	3.0	103.5	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS28Rum11134|CDS|CDS	0.5	17.3	0.1	G	COG0205	6-phosphofructokinase
Rtor0320|CDS|CDS	0.3	11.7	0.1	G	COG0058	Glucan phosphorylase
TS28Rum02648|CDS|CDS	0.3	11.7	0.1	G	COG0058	Glucan phosphorylase
TS28Eub0515|CDS|CDS	2.0	71.5	0.1	G	COG0448	ADP-glucose pyrophosphorylase
TS28Bif0083|CDS|CDS	1.3	47.8	0.1	G	COG2211	Na+/melibiose symporter and related transporters
TS28Eub8022|CDS|CDS	2.0	72.0	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Bac7725|CDS|CDS	1.0	36.0	0.1	G	COG0366|COG1523	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases
TS28Bac1179|CDS|CDS	0.3	12.0	0.1	G	COG3635	Predicted phosphoglycerate mutase, AP superfamily
TS28Bif3556|CDS|CDS	2.6	94.0	0.1	G	COG0058	Glucan phosphorylase
TS28Eub1225|CDS|CDS	1.5	55.0	0.1	G	COG0297	Glycogen synthase
TS28Fae00258|CDS|CDS	1.0	37.0	0.1	G	COG2190|COG1264|COG1263	Phosphotransferase system IIA components|Phosphotransferase system IIB components|Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific
TS28Eub7636|CDS|CDS	1.0	37.0	0.1	G	COG0395	ABC-type sugar transport system, permease component

TS28Eub5173|CDS|CDS	2.0	74.0	0.1	G	COG0366|COG3281	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis
TS28Fae05601|CDS|CDS	1.0	37.0	0.1	G	COG0366|COG1523|COG3281|COG1640	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis|4-alpha-glucanotransferase
TS28Eub6115|CDS|CDS	0.5	18.5	0.1	G	COG0296	1,4-alpha-glucan branching enzyme
Ehal1866|CDS|CDS	0.5	18.5	0.1	G	COG0296	1,4-alpha-glucan branching enzyme
TS28Rum16058|CDS|CDS	2.0	75.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Rum13932|CDS|CDS	0.5	19.0	0.1	G	COG1129|COG3845	ABC-type sugar transport system, ATPase component|ABC-type uncharacterized transport systems, ATPase components
TS29Rum13502|CDS|CDS	1.0	38.0	0.1	G	COG0366|COG3281	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis
EUBREC2816|CDS|cellobiose-phosphorylase	4.0	153.0	0.1	G	COG3459	Cellobiose phosphorylase
TS28Rum11780|CDS|CDS	0.5	19.2	0.1	G	COG1874	Beta-galactosidase
Bpse1278|CDS|CDS	1.0	39.3	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Eub0693|CDS|CDS	1.5	60.0	0.1	G	COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component
TS28Rum09583|CDS|CDS	1.0	40.0	0.1	G	COG1593|COG4666	TRAP-type C4-dicarboxylate transport system, large permease component|TRAP-type uncharacterized transport system, fused permease components
TS29Rum16554|CDS|CDS	1.0	40.0	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS28Rum05120|CDS|CDS	0.2	8.0	0.1	G	COG1129	ABC-type sugar transport system, ATPase component
RintL12748|CDS|CDS	0.8	30.2	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Clo00906|CDS|CDS	9.0	363.0	0.1	G	COG3957	Phosphoketolase
TS28Fae20065|CDS|CDS	0.7	27.5	0.1	G	COG0395|COG3833	ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component
FpraM2120647|CDS|CDS	0.5	21.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Rum14204|CDS|CDS	0.5	21.0	0.1	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
TS28Eub7588|CDS|CDS	1.0	42.0	0.1	G	COG0021|COG3959	Transketolase|Transketolase, N-terminal subunit
TS28Eub8795|CDS|CDS	3.0	126.5	0.1	G	COG0058	Glucan phosphorylase
TS28Clo01420|CDS|CDS	5.0	212.0	0.1	G	COG0696	Phosphoglyceromutase
TS28Rum02687|CDS|CDS	0.8	34.0	0.1	G	COG3459	Cellobiose phosphorylase
TS28Rum14378|CDS|CDS	0.5	21.5	0.1	G	COG2301	Citrate lyase beta subunit
TS28Eub6169|CDS|CDS	2.5	108.5	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Rum00971|CDS|CDS	2.0	87.0	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
Buni0566|CDS|CDS	0.3	14.5	0.1	G	COG0296	1,4-alpha-glucan branching enzyme
TS29Fae01009|CDS|CDS	0.5	22.0	0.1	G	COG3345	Alpha-galactosidase
TS28Fae13899|CDS|CDS	0.5	22.0	0.1	G	COG1129|COG3845	ABC-type sugar transport system, ATPase component|ABC-type uncharacterized transport systems, ATPase components
TS28Rum00924|CDS|CDS	0.5	22.0	0.1	G	COG0448	ADP-glucose pyrophosphorylase
TS28Fae18822|CDS|CDS	1.0	44.5	0.1	G	COG0058	Glucan phosphorylase
TS28Fae21235|CDS|CDS	2.0	89.5	0.1	G	COG2211	Na+/melibiose symporter and related transporters
TS28Fae21294|CDS|CDS	1.0	45.0	0.1	G	COG0063|COG0062	Predicted sugar kinase|Uncharacterized conserved protein
TS28Bif1744|CDS|CDS	1.7	75.5	0.1	G	COG0366	Glycosidases
TS28Eub7889|CDS|CDS	2.5	114.0	0.1	G	COG0366	Glycosidases
TS28Fae17601|CDS|CDS	2.0	91.5	0.1	G	COG2211	Na+/melibiose symporter and related transporters
TS28Fae15649|CDS|CDS	1.0	46.0	0.1	G	COG3345	Alpha-galactosidase
TS29Fae05447|CDS|CDS	1.0	46.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Bif1654|CDS|CDS	0.5	23.0	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS28Clo01024|CDS|CDS	5.0	230.0	0.1	G	COG0406	Fructose-2,6-bisphosphatase
FpraM2121881|CDS|CDS	1.1	50.0	0.1	G	COG2190|COG1264|COG1263	Phosphotransferase system IIA components|Phosphotransferase system IIB components|Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific
TS28Eub6845|CDS|CDS	1.0	46.5	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS28Rum09738|CDS|CDS	1.0	47.0	0.1	G	COG3345	Alpha-galactosidase
TS28Dor0178|CDS|CDS	0.5	23.5	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Eub6218|CDS|CDS	1.0	47.0	0.1	G	COG0063	Predicted sugar kinase
TS29Rum11778|CDS|CDS	2.0	95.5	0.1	G	COG1874	Beta-galactosidase
TS28Fae17531|CDS|CDS	0.5	24.0	0.1	G	COG1482	Phosphomannose isomerase
TS28Eub5384|CDS|CDS	1.0	49.0	0.1	G	COG0366|COG3408|COG3281	Glycosidases|Glycogen debranching enzyme|Uncharacterized protein, probably involved in trehalose biosynthesis
TS28Fae20033|CDS|CDS	1.0	49.0	0.1	G	COG0205	6-phosphofructokinase
TS28Rum16036|CDS|CDS	2.5	124.5	0.1	G	COG0058	Glucan phosphorylase
FpraM2121911|CDS|CDS	0.2	10.0	0.1	G	COG3855	Uncharacterized protein conserved in bacteria
TS28Clo00598|CDS|CDS	2.0	101.5	0.1	G	COG0524	Sugar kinases, ribokinase family
TS29Rum16571|CDS|CDS	0.5	26.0	0.1	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
TS28Rum07758|CDS|CDS	1.0	52.0	0.1	G	COG0366|COG1523|COG1640	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases|4-alpha-glucanotransferase
TS28Rum14101|CDS|CDS	0.3	17.5	0.1	G	COG0176	Transaldolase
TS29Rum20666|CDS|CDS	0.3	17.5	0.1	G	COG0176	Transaldolase
TS28Bac6863|CDS|CDS	0.3	18.5	0.1	G	COG1523	Type II secretory pathway, pullulanase PulA and related glycosidases
TS28Rum12294|CDS|CDS	0.7	37.0	0.1	G	COG0205	6-phosphofructokinase
TS28Clo01412|CDS|CDS	3.0	167.0	0.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Eub7077|CDS|CDS	0.3	14.0	0.1	G	COG3408	Glycogen debranching enzyme
TS28Fae13794|CDS|CDS	0.5	29.0	0.1	G	COG2152	Predicted glycosylase
TS28Clo01413|CDS|CDS	3.0	174.0	0.1	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
TS28Bif2348|CDS|CDS	0.3	19.3	0.1	G	COG0448	ADP-glucose pyrophosphorylase
TS28Fae14434|CDS|CDS	1.0	59.0	0.1	G	COG4806	L-rhamnose isomerase
TS28Eub7902|CDS|CDS	1.5	89.0	0.1	G	COG3855	Uncharacterized protein conserved in bacteria
TS28Fae18322|CDS|CDS	0.3	21.0	0.1	G	COG3717	5-keto 4-deoxyuronate isomerase
TS28Eub8799|CDS|CDS	1.0	64.5	0.1	G	COG0205	6-phosphofructokinase
TS28Eub0705|CDS|CDS	1.0	64.5	0.1	G	COG0148	Enolase
TS28Bac0445|CDS|CDS	1.0	66.0	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS28Fae14446|CDS|CDS	2.0	132.5	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Bif1192|CDS|CDS	0.3	16.7	0.0	G	COG0366	Glycosidases
TS28Fae11102|CDS|CDS	0.5	33.5	0.0	G	COG4668|COG2213	Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphotransferase system, mannitol-specific IIBC component

TS28Dor0270|CDS|CDS	0.5	33.5	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS28Fae21320|CDS|CDS	0.5	34.2	0.0	G	COG3507	Beta-xylosidase
TS29Bif0340|CDS|CDS	0.3	23.0	0.0	G	COG0366	Glycosidases
TS28Eub6222|CDS|CDS	1.0	70.0	0.0	G	COG0297	Glycogen synthase
TS29Rum13471|CDS|CDS	1.0	72.0	0.0	G	COG3459	Cellobiose phosphorylase
TS28Eub6543|CDS|CDS	2.0	147.5	0.0	G	COG1523	Type II secretory pathway, pullulanase PulA and related glycosidases
TS28Fae21446|CDS|CDS	0.5	37.0	0.0	G	COG3345	Alpha-galactosidase
TS28Fae18435|CDS|CDS	0.5	37.5	0.0	G	COG0058	Glucan phosphorylase
TS28Fae06035|CDS|CDS	0.5	38.0	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Rum03130|CDS|CDS	0.3	25.5	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS28Bif3089|CDS|CDS	0.3	19.3	0.0	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29Bif0273|CDS|CDS	0.3	26.0	0.0	G	COG1874	Beta-galactosidase
TS28Rum11332|CDS|CDS	0.3	26.0	0.0	G	COG1129|COG3845	ABC-type sugar transport system, ATPase component|ABC-type uncharacterized transport systems, ATPase components
TS29Bif0584|CDS|CDS	0.3	19.7	0.0	G	COG0366	Glycosidases
TS28Clo01086|CDS|CDS	2.0	162.0	0.0	G	COG4632	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase
TS28Rum12499|CDS|CDS	0.3	22.0	0.0	G	COG0205	6-phosphofructokinase
Rtor1047|CDS|CDS	0.5	44.5	0.0	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Eub6433|CDS|CDS	1.0	89.0	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS28Eub8026|CDS|CDS	0.5	45.5	0.0	G	COG3345	Alpha-galactosidase
Robe3230|CDS|CDS	0.3	31.0	0.0	G	COG2160	L-arabinose isomerase
TS28Fae13618|CDS|CDS	0.3	31.0	0.0	G	COG1904	Glucuronate isomerase
TS28Bac5054|CDS|CDS	0.3	31.0	0.0	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Bpse1316|CDS|CDS	0.3	24.0	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS28Rum12056|CDS|CDS	0.7	64.3	0.0	G	COG0058	Glucan phosphorylase
TS28Fae17619|CDS|CDS	1.0	97.5	0.0	G	COG0366|COG3281|COG1640	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis|4-alpha-glucanotransferase
Bpse1332|CDS|CDS	0.3	34.5	0.0	G	COG1874	Beta-galactosidase
TS28Bif1656|CDS|CDS	0.3	36.5	0.0	G	COG1874	Beta-galactosidase
Ehal1351|CDS|CDS	0.8	86.8	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Eub8470|CDS|CDS	1.0	118.0	0.0	G	COG0574|COG4668|COG1080|COG3412	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria
TS28Eub0949|CDS|CDS	0.5	62.0	0.0	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
EUBREC2820|CDS|beta-glucosidase	1.0	126.0	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS28Eub5752|CDS|CDS	0.2	22.0	0.0	G	COG0574|COG4668|COG1080|COG3412|COG2190	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components
EUBREC0489|CDS|alpha-galactosidase	0.5	69.5	0.0	G	COG3345	Alpha-galactosidase
TS28Eub6357|CDS|CDS	0.5	76.0	0.0	G	COG1523	Type II secretory pathway, pullulanase PulA and related glycosidases
TS28Clo01491|CDS|CDS	2.0	320.0	0.0	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS29Bif0101|CDS|CDS	0.2	37.5	0.0	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Eub6849|CDS|CDS	0.5	94.0	0.0	G	COG0153	Galactokinase
TS28Eub1268|CDS|CDS	0.7	140.0	0.0	G	COG3459	Cellobiose phosphorylase
TS28Bif0093|CDS|CDS	0.2	47.5	0.0	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Bif1731|CDS|CDS	0.3	96.0	0.0	G	COG0366	Glycosidases
TS28Eub8454|CDS|CDS	0.3	100.3	0.0	G	COG0366|COG1523	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases
TS28Bif0039|CDS|CDS	0.3	88.0	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS28Fae16517|CDS|CDS	1.0	35.0	0.1	G|F|K|T	COG4753|COG2207|COG3437|COG4936|COG2169|COG3708|COG3664|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted sensor domain|Adenosine deaminase|Uncharacterized protein conserved in bacteria|Beta-xylosidase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS28Clo01353|CDS|CDS	2.0	86.0	0.1	G|H	COG0698|COG2227	Ribose 5-phosphate isomerase RpiB|2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase
Bdor2526|CDS|CDS	19.3	4.0	16.0	G|I	COG1597|COG1803	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase|Methylglyoxal synthase
TS28Fae12497|CDS|CDS	0.7	58.0	0.0	G|I|H	COG0021|COG1154|COG3958	Transketolase|Deoxyxylulose-5-phosphate synthase|Transketolase, C-terminal subunit
TS28Fae06004|CDS|CDS	7.0	1.0	23.1	G|K	COG1879|COG1609	ABC-type sugar transport system, periplasmic component|Transcriptional regulators
TS29Rum00106|CDS|CDS	2.0	0.5	13.2	G|K	COG1349	Transcriptional regulators of sugar metabolism
TS28Eub0176|CDS|CDS	0.5	21.0	0.1	G|K	COG2207|COG3664	AraC-type DNA-binding domain-containing proteins|Beta-xylosidase
TS28Met1378|CDS|CDS	0.3	11.3	0.1	G|K	COG1548	Predicted transcriptional regulator/sugar kinase
TS28Fae20061|CDS|CDS	0.5	24.0	0.1	G|K	COG1940	Transcriptional regulator/sugar kinase
TS28Eub5184|CDS|CDS	0.5	40.5	0.0	G|K	COG1349	Transcriptional regulators of sugar metabolism

TS29Bac09752|CDS|CDS	7.0	1.0	23.1	G|K|T	COG0642|COG5002|COG2202|COG0745|COG4753|COG2207|COG0784|COG3437|COG3706|COG4251|COG2197|COG1879	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|FOG: CheY-like receiver|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|ABC-type sugar transport system, periplasmic component
TS29Bac11499|CDS|CDS	4.3	1.0	14.3	G|K|T	COG0642|COG5002|COG2202|COG0745|COG4753|COG2207|COG2770|COG0784|COG2198|COG2203|COG2972|COG5001|COG3706|COG4251|COG1879|COG2114	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|FOG: HAMP domain|FOG: CheY-like receiver|FOG: HPt domain|FOG: GAF domain|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)
TS28Rum12127|CDS|CDS	1.0	48.0	0.1	G|K|T	COG4219|COG4632	Antirepressor regulating drug resistance, predicted signal transduction N-terminal membrane component|Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase
TS28Eub4898|CDS|CDS	0.5	41.0	0.0	G|K|T	COG4753|COG2207|COG3664	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Beta-xylosidase
TS29Fae08636|CDS|CDS	7.5	1.0	24.8	G|M	COG1134	ABC-type polysaccharide/polyol phosphate transport system, ATPase component
TS29Bac05444|CDS|CDS	2.3	0.5	15.4	G|M	COG3507|COG5498|COG3940	Beta-xylosidase|Predicted glycosyl hydrolase|Predicted beta-xylosidase
TS29Fae06667|CDS|CDS	6.8	1.5	15.1	G|M	COG3594|COG0463|COG0726|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Predicted xylanase/chitin deacetylase|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS29Fae05734|CDS|CDS	1.3	0.3	13.2	G|M	COG3594|COG0463|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS28Clo03965|CDS|CDS	0.5	19.0	0.1	G|M	COG1086	Predicted nucleoside-diphosphate sugar epimerases
TS28Rum14200|CDS|CDS	0.5	21.0	0.1	G|M	COG4249|COG0726|COG1215|COG3858	Uncharacterized protein containing caspase domain|Predicted xylanase/chitin deacetylase|Glycosyltransferases, probably involved in cell wall biogenesis|Predicted glycosyl hydrolase
TS28Fae01858|CDS|CDS	0.3	11.0	0.1	G|M	COG3594|COG0463|COG0726|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Predicted xylanase/chitin deacetylase|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS29Rum20836|CDS|CDS	0.5	24.0	0.1	G|M	COG0451	Nucleoside-diphosphate-sugar epimerases
TS28Fae03201|CDS|CDS	0.3	19.0	0.1	G|M	COG0451|COG1088	Nucleoside-diphosphate-sugar epimerases|dTDP-D-glucose 4,6-dehydratase
TS28Clo01150|CDS|CDS	2.0	120.0	0.1	G|M	COG3594|COG0463|COG1887|COG1442|COG4641	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases|Uncharacterized protein conserved in bacteria
TS28Fae22076|CDS|CDS	0.5	30.5	0.1	G|M	COG3594|COG0463|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS28Eub7897|CDS|CDS	0.8	68.0	0.0	G|M	COG0451|COG3475	Nucleoside-diphosphate-sugar epimerases|LPS biosynthesis protein
TS29Fae05174|CDS|CDS	10.0	2.0	16.5	G|M|K	COG4464|COG1316	Capsular polysaccharide biosynthesis protein|Transcriptional regulator
TS28Met1454|CDS|CDS	1.3	90.8	0.0	G|O|M|U|W	COG4932|COG5295|COG3210|COG2730|COG4870	Predicted outer membrane protein|Autotransporter adhesin|Large exoproteins involved in heme utilization or adhesion|Endoglucanase|Cysteine protease
TS28Par0448|CDS|CDS	23.5	6.0	13.0	G|P	COG0483|COG1218	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family|3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase

TS29Fae08312|CDS|CDS	4.5	0.5	29.8	G|T	COG4668|COG1080|COG3412|COG1762|COG1925	Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)|Phosphotransferase system, HPr-related proteins
TS28Eub8515|CDS|CDS	3.0	112.5	0.1	G|T	COG0469|COG3848	Pyruvate kinase|Phosphohistidine swiveling domain
TS28Bif4599|CDS|CDS	0.3	9.5	0.1	G|T	COG0469|COG3848	Pyruvate kinase|Phosphohistidine swiveling domain
TS29Bif3200|CDS|CDS	0.3	9.5	0.1	G|T	COG0469|COG3848	Pyruvate kinase|Phosphohistidine swiveling domain
TS28Fae07042|CDS|CDS	1.0	43.0	0.1	G|T	COG1762|COG1445|COG3925	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)|Phosphotransferase system fructose-specific component IIB|N-terminal domain of the phosphotransferase system fructose-specific component IIB
TS28Dor0661|CDS|CDS	0.5	27.5	0.1	G|T	COG4668|COG1080|COG3412|COG3605	Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Signal transduction protein containing GAF and PtsI domains
TS28Eub7599|CDS|CDS	1.0	98.0	0.0	G|T	COG1762|COG1445|COG3925	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)|Phosphotransferase system fructose-specific component IIB|N-terminal domain of the phosphotransferase system fructose-specific component IIB
TS28Eub7537|CDS|CDS	1.0	116.5	0.0	G|T	COG4668|COG1080|COG3412|COG3605|COG2190	Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Signal transduction protein containing GAF and PtsI domains|Phosphotransferase system IIA components
TS28Met1692|CDS|CDS	3.0	109.5	0.1	G|U|W	COG5295|COG3210|COG2730	Autotransporter adhesin|Large exoproteins involved in heme utilization or adhesion|Endoglucanase
TS29Fae05459|CDS|CDS	40.0	4.0	33.1	G|V	COG1680|COG1472	Beta-lactamase class C and other penicillin binding proteins|Beta-glucosidase-related glycosidases
TS28Clo01706|CDS|CDS	5.0	205.0	0.1	G|V	COG1680|COG1472	Beta-lactamase class C and other penicillin binding proteins|Beta-glucosidase-related glycosidases
TS28Eub7778|CDS|CDS	1.0	52.0	0.1	G|V	COG1680|COG1472	Beta-lactamase class C and other penicillin binding proteins|Beta-glucosidase-related glycosidases
Msmi750907|CDS|CDS	177.2	0.7	879.2	H	COG4056	Methyl coenzyme M reductase, subunit C
Msmi740775|CDS|CDS	54.0	0.3	714.3	H	COG4055	Methyl coenzyme M reductase, subunit D
Msmi740777|CDS|CDS	100.8	0.5	666.3	H	COG4057	Methyl coenzyme M reductase, gamma subunit
Msmi751004|CDS|CDS	171.5	2.5	226.9	H	COG1572|COG1429	Uncharacterized conserved protein|Cobalamin biosynthesis protein CobN and related Mg-chelatases
Msmi740774|CDS|CDS	167.3	3.8	147.5	H	COG4054	Methyl coenzyme M reductase, beta subunit
Msmi750900|CDS|CDS	58.0	1.7	115.0	H	COG4063	Tetrahydromethanopterin S-methyltransferase, subunit A
TS28Met0363|CDS|CDS	58.0	1.7	115.0	H	COG4063	Tetrahydromethanopterin S-methyltransferase, subunit A
Msmi740783|CDS|CDS	58.0	1.7	115.0	H	COG4063	Tetrahydromethanopterin S-methyltransferase, subunit A
Msmi750908|CDS|CDS	76.0	2.3	111.7	H	COG4055	Methyl coenzyme M reductase, subunit D
Msmi750909|CDS|CDS	163.9	4.9	110.2	H	COG4054	Methyl coenzyme M reductase, beta subunit
TS28Met0361|CDS|CDS	48.8	1.5	107.5	H	COG4064	Tetrahydromethanopterin S-methyltransferase, subunit G
Msmi740785|CDS|CDS	48.8	1.5	107.5	H	COG4064	Tetrahydromethanopterin S-methyltransferase, subunit G
Msmi750898|CDS|CDS	48.8	1.5	107.5	H	COG4064	Tetrahydromethanopterin S-methyltransferase, subunit G
Msmi740782|CDS|CDS	9.5	0.3	94.2	H	COG4062	Tetrahydromethanopterin S-methyltransferase, subunit B
Msmi751280|CDS|CDS	8.6	0.3	85.2	H	COG0422	Thiamine biosynthesis protein ThiC
Msmi750776|CDS|CDS	12.7	0.5	84.0	H	COG0181	Porphobilinogen deaminase
Msmi740778|CDS|CDS	137.9	5.5	82.9	H	COG4058	Methyl coenzyme M reductase, alpha subunit
TS28Met0369|CDS|CDS	112.4	4.5	82.6	H	COG4057	Methyl coenzyme M reductase, gamma subunit
Msmi750906|CDS|CDS	112.4	4.5	82.6	H	COG4057	Methyl coenzyme M reductase, gamma subunit
TS28Met0370|CDS|CDS	231.8	9.7	79.3	H	COG4056	Methyl coenzyme M reductase, subunit C
Msmi750905|CDS|CDS	145.6	7.3	65.7	H	COG4058	Methyl coenzyme M reductase, alpha subunit
Msmi740786|CDS|CDS	18.8	1.0	62.0	H	COG1962|COG4063	Tetrahydromethanopterin S-methyltransferase, subunit H|Tetrahydromethanopterin S-methyltransferase, subunit A
TS29Rum11885|CDS|CDS	101.5	6.0	55.9	H	COG0502|COG0161	Biotin synthase and related enzymes|Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
TS28Met0371|CDS|CDS	84.0	5.3	52.9	H	COG4055	Methyl coenzyme M reductase, subunit D
Msmi740942|CDS|CDS	3.8	0.3	50.3	H	COG0535|COG4001|COG2896|COG1964	Predicted Fe-S oxidoreductases|Predicted metal-binding protein|Molybdenum cofactor biosynthesis enzyme|Predicted Fe-S oxidoreductases
Msmi741182|CDS|CDS	4.5	0.3	44.6	H	COG1648|COG0007|COG1587	Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)|Uroporphyrinogen-III methylase|Uroporphyrinogen-III synthase
Msmi750395|CDS|CDS	3.3	0.3	43.0	H	COG1541	Coenzyme F390 synthetase
Msmi751182|CDS|CDS	6.5	0.5	42.9	H	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases
TS28Met0372|CDS|CDS	183.9	15.1	40.3	H	COG4054	Methyl coenzyme M reductase, beta subunit
Msmi750902|CDS|CDS	37.8	3.2	39.4	H	COG4061	Tetrahydromethanopterin S-methyltransferase, subunit C
Msmi751148|CDS|CDS	3.9	0.3	38.9	H	COG0807|COG0108	GTP cyclohydrolase II|3,4-dihydroxy-2-butanone 4-phosphate synthase
Acol1926|CDS|CDS	11.0	1.0	36.4	H	COG1488	Nicotinic acid phosphoribosyltransferase
Msmi750823|CDS|CDS	5.9	0.6	33.5	H	COG0368	Cobalamin-5-phosphate synthase
Robe3392|CDS|CDS	4.5	0.5	29.8	H	COG2145	Hydroxyethylthiazole kinase, sugar kinase family
Even0300|CDS|CDS	9.0	1.0	29.8	H	COG1541	Coenzyme F390 synthetase
TS29Bac01470|CDS|CDS	4.5	0.5	29.8	H	COG0196	FAD synthase
Msmi740781|CDS|CDS	36.3	4.2	28.8	H	COG4061	Tetrahydromethanopterin S-methyltransferase, subunit C
Msmi740780|CDS|CDS	13.7	1.6	28.5	H	COG4060	Tetrahydromethanopterin S-methyltransferase, subunit D
FpraM2122120|CDS|CDS	4.0	0.5	26.5	H	COG2038|COG2087	NaMN:DMB phosphoribosyltransferase|Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase
CspSS20131|CDS|CDS	4.0	0.5	26.5	H	COG0414	Panthothenate synthetase
TS28Met0368|CDS|CDS	199.6	26.3	25.1	H	COG4058	Methyl coenzyme M reductase, alpha subunit
Msmi740494|CDS|CDS	6.2	0.8	24.4	H	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases
TS29Rum17238|CDS|CDS	3.5	0.5	23.1	H	COG2091	Phosphopantetheinyl transferase
Msmi740149|CDS|CDS	1.8	0.3	23.1	H	COG1541	Coenzyme F390 synthetase
Robe0308|CDS|CDS	3.5	0.5	23.1	H	COG1060|COG0502	Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes|Biotin synthase and related enzymes

Bdor2192|CDS|CDS	9.7	1.5	21.3	H	COG0352	Thiamine monophosphate synthase
Msmi750897|CDS|CDS	19.3	3.0	21.2	H	COG1962|COG4063	Tetrahydromethanopterin S-methyltransferase, subunit H|Tetrahydromethanopterin S-methyltransferase, subunit A
Msmi740779|CDS|CDS	23.5	3.7	21.2	H	COG4059	Tetrahydromethanopterin S-methyltransferase, subunit E
TS29Bac08313|CDS|CDS	2.1	0.3	20.7	H	COG1995	Pyridoxal phosphate biosynthesis protein
TS28Fae04994|CDS|CDS	31.0	5.0	20.5	H	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes
TS29Bac06524|CDS|CDS	3.0	0.5	19.8	H	COG1541	Coenzyme F390 synthetase
Bxyl1481|CDS|CDS	3.0	0.5	19.8	H	COG1541	Coenzyme F390 synthetase
BactD21769|CDS|CDS	6.0	1.0	19.8	H	COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase
Bdor3877|CDS|CDS	12.0	2.0	19.8	H	COG0413	Ketopantoate hydroxymethyltransferase
TS28Met0360|CDS|CDS	41.3	7.0	19.5	H	COG1962|COG4063	Tetrahydromethanopterin S-methyltransferase, subunit H|Tetrahydromethanopterin S-methyltransferase, subunit A
Msmi750904|CDS|CDS	25.8	4.7	18.3	H	COG4059	Tetrahydromethanopterin S-methyltransferase, subunit E
TS29Rum13305|CDS|CDS	11.0	2.0	18.2	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
TS28RumUnc0430|CDS|CDS	16.0	3.0	17.6	H	COG2099|COG1903	Precorrin-6x reductase|Cobalamin biosynthesis protein CbiD
Msmi750901|CDS|CDS	9.5	1.8	17.1	H	COG4062	Tetrahydromethanopterin S-methyltransferase, subunit B
TS28Met0364|CDS|CDS	9.5	1.8	17.1	H	COG4062	Tetrahydromethanopterin S-methyltransferase, subunit B
RintL10043|CDS|CDS	5.0	1.0	16.5	H	COG1713	Predicted HD superfamily hydrolase involved in NAD metabolism
TS28Clo08770|CDS|CDS	5.0	1.0	16.5	H	COG1541	Coenzyme F390 synthetase
TS29Clo1886|CDS|CDS	5.0	1.0	16.5	H	COG1541	Coenzyme F390 synthetase
FpraM2122123|CDS|CDS	2.5	0.5	16.5	H	COG1492	Cobyric acid synthase
Msmi750939|CDS|CDS	1.7	0.3	16.5	H	COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase
Bdor3977|CDS|CDS	5.0	1.0	16.5	H	COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase
Dlon1060|CDS|CDS	2.5	0.5	16.5	H	COG0352	Thiamine monophosphate synthase
Ccom2106|CDS|CDS	5.0	1.0	16.5	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
Csci2222|CDS|CDS	5.0	1.0	16.5	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
BactD21558|CDS|CDS	2.5	0.5	16.5	H	COG0157	Nicotinate-nucleotide pyrophosphorylase
TS28Met0365|CDS|CDS	37.8	7.7	16.3	H	COG4061	Tetrahydromethanopterin S-methyltransferase, subunit C
ShigspD90518|CDS|CDS	4.7	1.0	15.4	H	COG2896	Molybdenum cofactor biosynthesis enzyme
Dlon0780|CDS|CDS	7.0	1.5	15.4	H	COG1995	Pyridoxal phosphate biosynthesis protein
TS28Met0367|CDS|CDS	25.8	5.7	15.1	H	COG4059	Tetrahydromethanopterin S-methyltransferase, subunit E
Bdor1162|CDS|CDS	10.0	2.3	14.2	H	COG0854	Pyridoxal phosphate biosynthesis protein
TS28Met1696|CDS|CDS	402.5	95.5	13.9	H	COG1572|COG1429	Uncharacterized conserved protein|Cobalamin biosynthesis protein CobN and related Mg-chelatases
Ehal0015|CDS|CDS	2.0	0.5	13.2	H	COG2099|COG1903	Precorrin-6x reductase|Cobalamin biosynthesis protein CbiD
Acol3252|CDS|CDS	4.0	1.0	13.2	H	COG1564	Thiamine pyrophosphokinase
Msmi751146|CDS|CDS	2.0	0.5	13.2	H	COG1492	Cobyric acid synthase
Msmi750903|CDS|CDS	20.5	5.3	12.9	H	COG4060	Tetrahydromethanopterin S-methyltransferase, subunit D
Msmi750737|CDS|CDS	7.3	1.9	12.6	H	COG0535|COG4001|COG2896|COG1964	Predicted Fe-S oxidoreductases|Predicted metal-binding protein|Molybdenum cofactor biosynthesis enzyme|Predicted Fe-S oxidoreductases
TS28Fae15028|CDS|CDS	19.0	5.0	12.6	H	COG2109	ATP:corrinoid adenosyltransferase
TS28Rum16295|CDS|CDS	101.5	27.0	12.4	H	COG0502|COG0161	Biotin synthase and related enzymes|Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
BL1685|CDS|SulD	1.8	0.5	11.6	H	COG1539|COG0801	Dihydroneopterin aldolase|7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase
TS29Fae02334|CDS|CDS	3.5	1.0	11.6	H	COG0854|COG0319	Pyridoxal phosphate biosynthesis protein|Predicted metal-dependent hydrolase
Pmer1540|CDS|CDS	7.0	2.0	11.6	H	COG0095	Lipoate-protein ligase A
BactD12340|CDS|CDS	1.7	0.5	11.0	H	COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase
Rtor1499|CDS|CDS	16.5	5.0	10.9	H	COG2109	ATP:corrinoid adenosyltransferase
Bdor0237|CDS|CDS	6.5	2.0	10.7	H	COG1057|COG1713	Nicotinic acid mononucleotide adenylyltransferase|Predicted HD superfamily hydrolase involved in NAD metabolism
Msmi741142|CDS|CDS	1.6	0.5	10.6	H	COG1587|COG2959	Uroporphyrinogen-III synthase|Uncharacterized enzyme of heme biosynthesis
Clep0665|CDS|CDS	8.0	2.5	10.6	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
Msmi750831|CDS|CDS	3.2	1.0	10.5	H	COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases
Bhan0543|CDS|CDS	6.3	2.0	10.5	H	COG0192	S-adenosylmethionine synthetase
TS28Rum09689|CDS|CDS	0.5	16.8	0.1	H	COG0181	Porphobilinogen deaminase
TS28Fae20138|CDS|CDS	1.0	34.5	0.1	H	COG1893	Ketopantoate reductase
TS28Met1166|CDS|CDS	0.2	7.2	0.1	H	COG0142	Geranylgeranyl pyrophosphate synthase
TS28Fae07535|CDS|CDS	0.3	12.0	0.1	H	COG2896	Molybdenum cofactor biosynthesis enzyme
TS28Clo01758|CDS|CDS	3.0	110.0	0.1	H	COG1893	Ketopantoate reductase
TS28Rum14043|CDS|CDS	0.5	19.5	0.1	H	COG0302	GTP cyclohydrolase I
TS28Rum13361|CDS|CDS	1.0	39.5	0.1	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
TS28Rum09690|CDS|CDS	0.5	21.0	0.1	H	COG0007|COG1648|COG1587	Uroporphyrinogen-III methylase|Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)|Uroporphyrinogen-III synthase
Robe3132|CDS|CDS	0.5	23.0	0.1	H	COG0535|COG2896|COG1964	Predicted Fe-S oxidoreductases|Molybdenum cofactor biosynthesis enzyme|Predicted Fe-S oxidoreductases
TS28Met1701|CDS|CDS	0.3	15.7	0.1	H	COG1427|COG1060	Predicted periplasmic solute-binding protein|Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes
TS29Bac08714|CDS|CDS	0.2	8.0	0.1	H	COG1060|COG0502	Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes|Biotin synthase and related enzymes
TS28Eub6225|CDS|CDS	1.0	53.0	0.1	H	COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase
TS28Eub6949|CDS|CDS	1.0	55.5	0.1	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
TS28Fae18752|CDS|CDS	0.5	28.0	0.1	H	COG0535|COG4001|COG2896|COG1964	Predicted Fe-S oxidoreductases|Predicted metal-binding protein|Molybdenum cofactor biosynthesis enzyme|Predicted Fe-S oxidoreductases
TS28Met0696|CDS|CDS	0.2	11.2	0.1	H	COG0113	Delta-aminolevulinic acid dehydratase
TS28Met1435|CDS|CDS	0.3	15.3	0.1	H	COG0388|COG0171	Predicted amidohydrolase|NAD synthase
TS28Clo01629|CDS|CDS	4.0	245.0	0.1	H	COG0388|COG0171	Predicted amidohydrolase|NAD synthase
TS28Eub6150|CDS|CDS	1.0	66.0	0.1	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases

TS28Fae16564|CDS|CDS	1.0	77.0	0.0	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
TS28Met1020|CDS|CDS	0.2	18.8	0.0	H	COG2038	NaMN:DMB phosphoribosyltransferase
TS28Clo00752|CDS|CDS	1.0	122.0	0.0	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
Dlon1667|CDS|CDS	0.3	51.8	0.0	H	COG0192	S-adenosylmethionine synthetase
Cnex3101|CDS|CDS	0.3	55.2	0.0	H	COG0192	S-adenosylmethionine synthetase
TS28Eub7936|CDS|CDS	0.5	87.0	0.0	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
TS29Dor2247|CDS|CDS	0.3	65.7	0.0	H	COG0192	S-adenosylmethionine synthetase
TS28Clo01329|CDS|CDS	1.0	243.0	0.0	H	COG2978	Putative p-aminobenzoyl-glutamate transporter
Msmi750933|CDS|CDS	3.3	0.3	43.0	H|C	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
CspM6212214|CDS|CDS	5.0	1.0	16.5	H|C	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
Msmi740508|CDS|CDS	7.8	2.3	11.1	H|C	COG1251|COG2158|COG1492|COG2243|COG2073|COG2241|COG2082|COG1010	NAD(P)H-nitrite reductase|Uncharacterized protein containing a Zn-finger-like domain|Cobyric acid synthase|Precorrin-2 methylase|Cobalamin biosynthesis protein CbiG|Precorrin-6B methylase 1|Precorrin isomerase|Precorrin-3B methylase
Csym3626|CDS|CDS	10.0	1.0	33.1	H|G|I	COG0021|COG1154|COG3958	Transketolase|Deoxyxylulose-5-phosphate synthase|Transketolase, C-terminal subunit
Acol2917|CDS|CDS	5.0	1.0	16.5	H|G|I	COG0021|COG1154|COG3958	Transketolase|Deoxyxylulose-5-phosphate synthase|Transketolase, C-terminal subunit
ShigspD91088|CDS|CDS	3.5	1.0	11.6	H|I	COG1767|COG3697	Triphosphoribosyl-dephospho-CoA synthetase|Phosphoribosyl-dephospho-CoA transferase (holo-ACP synthetase)
CspSS21548|CDS|CDS	0.5	22.0	0.1	H|I	COG1154	Deoxyxylulose-5-phosphate synthase
Bpse0421|CDS|CDS	0.3	22.5	0.0	H|I	COG1154	Deoxyxylulose-5-phosphate synthase
Msmi751101|CDS|CDS	9.1	0.7	45.2	H|M|G	COG0794|COG0269|COG0684|COG1795	Predicted sugar phosphate isomerase involved in capsule formation|3-hexulose-6-phosphate synthase and related proteins|Demethylmenaquinone methyltransferase|Uncharacterized conserved protein
Msmi741130|CDS|CDS	2.3	0.3	29.8	H|O	COG1992|COG0611|COG0309	Uncharacterized conserved protein|Thiamine monophosphate kinase|Hydrogenase maturation factor
Msmi750547|CDS|CDS	2.3	0.3	29.8	H|O	COG1992|COG0611|COG0309	Uncharacterized conserved protein|Thiamine monophosphate kinase|Hydrogenase maturation factor
CspM6212613|CDS|CDS	18.0	1.0	59.5	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
Eeli1143|CDS|CDS	13.0	1.0	43.0	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
TS28Fae08352|CDS|CDS	22.0	2.0	36.4	I	COG2057|COG1788	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit|Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit
TS28Fae08350|CDS|CDS	11.0	1.0	36.4	I	COG2057	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit
Ehal0979|CDS|CDS	11.0	1.0	36.4	I	COG0020	Undecaprenyl pyrophosphate synthase
Msmi750824|CDS|CDS	5.3	0.5	34.7	I	COG1267	Phosphatidylglycerophosphatase A and related proteins
TS28Fae05115|CDS|CDS	17.0	2.0	28.1	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
Bdor2836|CDS|CDS	7.8	1.0	25.9	I	COG0688	Phosphatidylserine decarboxylase
Msmi750485|CDS|CDS	12.1	1.6	25.3	I	COG3425	3-hydroxy-3-methylglutaryl CoA synthase
Pmer0008|CDS|CDS	14.0	2.0	23.1	I	COG0439|COG4770	Biotin carboxylase|Acetyl/propionyl-CoA carboxylase, alpha subunit
Msmi741194|CDS|CDS	10.2	1.7	20.3	I	COG0183	Acetyl-CoA acetyltransferase
TS29Rum20889|CDS|CDS	6.0	1.0	19.8	I	COG0671	Membrane-associated phospholipid phosphatase
Csym2599|CDS|CDS	6.0	1.0	19.8	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
TS28Bac1575|CDS|CDS	27.0	5.0	17.9	I	COG2185|COG1884	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)|Methylmalonyl-CoA mutase, N-terminal domain/subunit
BactD21157|CDS|CDS	5.4	1.0	17.9	I	COG0688	Phosphatidylserine decarboxylase
Msmi741193|CDS|CDS	10.1	1.9	17.4	I	COG3425	3-hydroxy-3-methylglutaryl CoA synthase
Dlon0128|CDS|CDS	5.0	1.0	16.5	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Csym3917|CDS|CDS	5.0	1.0	16.5	I	COG0331	(acyl-carrier-protein) S-malonyltransferase
TS28Clo03439|CDS|CDS	10.0	2.0	16.5	I	COG0183	Acetyl-CoA acetyltransferase
Svar2369|CDS|CDS	5.0	1.0	16.5	I	COG0183	Acetyl-CoA acetyltransferase
Msmi741436|CDS|CDS	1.7	0.3	16.5	I	COG0170	Dolichol kinase
Msmi750283|CDS|CDS	1.7	0.3	16.5	I	COG0170	Dolichol kinase
Msmi750855|CDS|CDS	4.3	1.0	14.3	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
Rgna0317|CDS|CDS	4.0	1.0	13.2	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Aput1559|CDS|CDS	2.0	0.5	13.2	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
RintL10190|CDS|CDS	4.0	1.0	13.2	I	COG1597	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase
Bdor0002|CDS|CDS	14.2	4.0	11.7	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
Msmi741029|CDS|CDS	9.7	2.8	11.6	I	COG0439	Biotin carboxylase
TS28Fae18421|CDS|CDS	14.0	4.0	11.6	I	COG2030	Acyl dehydratase
ShigspD90991|CDS|CDS	3.5	1.0	11.6	I	COG0657	Esterase/lipase
TS28Fae22399|CDS|CDS	5.0	1.5	11.0	I	COG1211	4-diphosphocytidyl-2-methyl-D-erithritol synthase
Bxyl1247|CDS|CDS	3.3	1.0	11.0	I	COG0439|COG4770	Biotin carboxylase|Acetyl/propionyl-CoA carboxylase, alpha subunit
BactD11354|CDS|CDS	3.3	1.0	11.0	I	COG0439|COG4770	Biotin carboxylase|Acetyl/propionyl-CoA carboxylase, alpha subunit
Bthe7335680|CDS|CDS	1.7	0.5	11.0	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
TS28Fae20825|CDS|CDS	3.0	104.0	0.1	I	COG3581|COG3580|COG1924	Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria|Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)
TS28Fae20697|CDS|CDS	0.7	24.5	0.1	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
TS28Bif3034|CDS|CDS	0.3	12.7	0.1	I	COG0558	Phosphatidylglycerophosphate synthase
TS28Eub0147|CDS|CDS	0.5	20.0	0.1	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
TS28Eub6445|CDS|CDS	1.0	42.0	0.1	I	COG1024|COG1250	Enoyl-CoA hydratase/carnithine racemase|3-hydroxyacyl-CoA dehydrogenase
TS28Fae08601|CDS|CDS	0.3	14.0	0.1	I	COG0020	Undecaprenyl pyrophosphate synthase
TS28Clo01678|CDS|CDS	2.0	85.0	0.1	I	COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase
CspM6210569|CDS|CDS	1.6	70.9	0.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes

TS28Fae11977|CDS|CDS	1.0	44.5	0.1	I	COG0657	Esterase/lipase
RintL10791|CDS|CDS	1.0	44.7	0.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
Bova3226|CDS|CDS	0.1	6.5	0.1	I	COG1260	Myo-inositol-1-phosphate synthase
Ccom1280|CDS|CDS	0.5	21.9	0.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
Dlon2017|CDS|CDS	1.3	64.2	0.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS28Bif0934|CDS|CDS	1.0	52.3	0.1	I	COG4982|COG4981	3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
TS28Rum13913|CDS|CDS	0.5	28.5	0.1	I	COG3884	Acyl-ACP thioesterase
TS28Clo00515|CDS|CDS	2.0	116.0	0.1	I	COG1597	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase
TS28Bac8505|CDS|CDS	0.5	29.0	0.1	I	COG0743	1-deoxy-D-xylulose 5-phosphate reductoisomerase
TS28Bac0460|CDS|CDS	0.3	19.5	0.1	I	COG4221|COG1211	Short-chain alcohol dehydrogenase of unknown specificity|4-diphosphocytidyl-2-methyl-D-erithritol synthase
TS28Met0636|CDS|CDS	0.3	14.8	0.1	I	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
Dlon2016|CDS|CDS	1.4	88.9	0.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS28Eub6406|CDS|CDS	1.0	64.0	0.1	I	COG0821	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis
Buni1120|CDS|CDS	0.2	14.5	0.0	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
TS28Eub1501|CDS|CDS	0.5	56.0	0.0	I	COG2267	Lysophospholipase
Eeli2701|CDS|CDS	0.4	69.0	0.0	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
Rlac0733|CDS|CDS	0.1	24.3	0.0	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS28Eub5632|CDS|CDS	0.5	110.0	0.0	I	COG3581|COG3580|COG1924	Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria|Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)
TS29Rum10008|CDS|CDS	7.0	2.0	11.6	I|H	COG1154	Deoxyxylulose-5-phosphate synthase
TS29Bif1588|CDS|CDS	0.3	13.0	0.1	I|H	COG1154	Deoxyxylulose-5-phosphate synthase
TS28Eub4799|CDS|CDS	1.0	52.5	0.1	I|H	COG1154	Deoxyxylulose-5-phosphate synthase
TS28Eub8664|CDS|CDS	1.0	88.5	0.0	I|H	COG1154	Deoxyxylulose-5-phosphate synthase
TS29Rum06857|CDS|CDS	385.0	1.0	1,273.2	I|Q	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase
Msmi741306|CDS|CDS	10.7	0.3	105.8	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Msmi750377|CDS|CDS	10.7	0.3	105.8	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS29Dor0403|CDS|CDS	36.5	3.0	40.2	I|Q	COG1028|COG4221	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)|Short-chain alcohol dehydrogenase of unknown specificity
TS29Bac09588|CDS|CDS	4.0	0.3	39.7	I|Q	COG1022|COG0318	Long-chain acyl-CoA synthetases (AMP-forming)|Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II
BactD11793|CDS|CDS	4.0	0.3	39.7	I|Q	COG0318|COG1022	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II|Long-chain acyl-CoA synthetases (AMP-forming)
TS28Par0338|CDS|CDS	5.0	0.5	33.1	I|Q	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase
Bxyl2434|CDS|CDS	3.0	0.3	29.7	I|Q	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase
Ehal1157|CDS|CDS	3.0	0.5	19.8	I|Q	COG1028|COG4221|COG0300	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)|Short-chain alcohol dehydrogenase of unknown specificity|Short-chain dehydrogenases of various substrate specificities
Bste0087|CDS|CDS	24.0	4.0	19.8	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Bste1896|CDS|CDS	6.0	1.0	19.8	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Dfor3140|CDS|CDS	40.5	7.0	19.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Bova0854|CDS|CDS	4.5	1.0	14.9	I|Q	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase
Ehal0198|CDS|CDS	14.0	3.5	13.2	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Bdor0045|CDS|CDS	7.7	2.0	12.7	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS29Bac04519|CDS|CDS	1.7	0.5	11.0	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
BactD12255|CDS|CDS	1.7	0.5	11.0	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
BactD13825|CDS|CDS	4.3	1.3	10.7	I|Q	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase
TS29Rum21155|CDS|CDS	1.0	34.0	0.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS29Bif2375|CDS|CDS	1.1	44.1	0.1	I|Q	COG0304|COG0331|COG3321|COG4982|COG4981	3-oxoacyl-(acyl-carrier-protein) synthase|(acyl-carrier-protein) S-malonyltransferase|Polyketide synthase modules and related proteins|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
TS29Bif1282|CDS|CDS	2.1	87.0	0.1	I|Q	COG0304|COG0331|COG4982|COG4981	3-oxoacyl-(acyl-carrier-protein) synthase|(acyl-carrier-protein) S-malonyltransferase|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
TS28Eub3875|CDS|CDS	1.0	45.3	0.1	I|Q	COG0331|COG3321	(acyl-carrier-protein) S-malonyltransferase|Polyketide synthase modules and related proteins
TS28Clo00510|CDS|CDS	2.0	96.0	0.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS28Bif3900|CDS|CDS	2.1	254.5	0.0	I|Q	COG0304|COG0331|COG4982|COG4981	3-oxoacyl-(acyl-carrier-protein) synthase|(acyl-carrier-protein) S-malonyltransferase|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
Bpse1183|CDS|CDS	0.1	17.5	0.0	I|Q	COG0331|COG0304|COG4982|COG4981	(acyl-carrier-protein) S-malonyltransferase|3-oxoacyl-(acyl-carrier-protein) synthase|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
TS28Bif0933|CDS|CDS	0.1	53.6	0.0	I|Q	COG0304|COG0331|COG3321|COG4982|COG4981	3-oxoacyl-(acyl-carrier-protein) synthase|(acyl-carrier-protein) S-malonyltransferase|Polyketide synthase modules and related proteins|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1

Bdor4334|CDS|CDS	59.2	1.0	195.7	J	COG0091	Ribosomal protein L22
TS28Bac6836|CDS|CDS	13.4	0.3	133.3	J	COG0092	Ribosomal protein S3
Bdor4349|CDS|CDS	18.7	0.5	123.4	J	COG0080	Ribosomal protein L11
Bdor0498|CDS|CDS	36.0	1.0	119.0	J	COG0360	Ribosomal protein S6
Bxyl1683|CDS|CDS	14.8	0.5	97.6	J	COG0089	Ribosomal protein L23
BactD14452|CDS|CDS	14.8	0.5	97.6	J	COG0089	Ribosomal protein L23
Msmi740406|CDS|CDS	14.5	0.5	95.9	J	COG2139	Ribosomal protein L21E
TS29Bac09449|CDS|CDS	8.3	0.3	82.5	J	COG0198	Ribosomal protein L24
BactD14460|CDS|CDS	8.3	0.3	82.5	J	COG0198	Ribosomal protein L24
Bxyl1674|CDS|CDS	8.3	0.3	82.5	J	COG0198	Ribosomal protein L24
Pmer3253|CDS|CDS	12.0	0.5	79.4	J	COG0211	Ribosomal protein L27
TS29Met0859|CDS|CDS	4.7	0.2	76.9	J	COG0087	Ribosomal protein L3
Bste2297|CDS|CDS	22.8	1.0	75.2	J	COG0089	Ribosomal protein L23
Ccom1709|CDS|CDS	45.5	2.0	75.2	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Msmi751330|CDS|CDS	20.3	1.0	67.2	J	COG2167	Ribosomal protein L39E
TS28Met1554|CDS|CDS	20.3	1.0	67.2	J	COG2167	Ribosomal protein L39E
Bple0391|CDS|CDS	20.0	1.0	66.1	J	COG0333	Ribosomal protein L32
Hfil1190|CDS|CDS	10.0	0.5	66.1	J	COG0050	GTPases - translation elongation factors
Bdor4332|CDS|CDS	64.6	3.5	61.1	J	COG0197	Ribosomal protein L16/L10E
Bdor4318|CDS|CDS	9.0	0.5	59.5	J	COG0099	Ribosomal protein S13
Bdor4325|CDS|CDS	17.0	1.0	56.2	J	COG0096	Ribosomal protein S8
Bcap3102|CDS|CDS	17.0	1.0	56.2	J	COG0080	Ribosomal protein L11
Bdor4342|CDS|CDS	16.2	1.0	53.5	J	COG0048	Ribosomal protein S12
PRABACTJOHN3622|CDS|CDS	8.0	0.5	52.9	J	COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases
Msmi740409|CDS|CDS	10.6	0.7	52.5	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
TS29Bac10602|CDS|CDS	7.7	0.5	50.7	J	COG0360	Ribosomal protein S6
BactD12035|CDS|CDS	7.7	0.5	50.7	J	COG0360	Ribosomal protein S6
Dfor0679|CDS|CDS	15.0	1.0	49.6	J	COG1544	Ribosome-associated protein Y (PSrp-1)
Bdor4328|CDS|CDS	42.7	3.0	47.0	J	COG0198	Ribosomal protein L24
TS28Fae00079|CDS|CDS	40.0	3.0	44.1	J	COG1544	Ribosome-associated protein Y (PSrp-1)
Pmer3079|CDS|CDS	13.3	1.0	44.1	J	COG0198	Ribosomal protein L24
Bhan0175|CDS|CDS	13.2	1.0	43.5	J	COG0050	GTPases - translation elongation factors
PRABACTJOHN2259|CDS|CDS	13.0	1.0	43.0	J	COG0185	Ribosomal protein S19
Bryfor1738|CDS|CDS	13.0	1.0	43.0	J	COG0080	Ribosomal protein L11
Msmi740893|CDS|CDS	21.0	1.7	41.6	J	COG5256	Translation elongation factor EF-1alpha (GTPase)
TS28Col0566|CDS|CDS	25.0	2.0	41.3	J	COG0211	Ribosomal protein L27
Bste2309|CDS|CDS	12.0	1.0	39.8	J	COG0081	Ribosomal protein L1
BactD13588|CDS|CDS	6.0	0.5	39.7	J	COG0621	2-methylthioadenine synthetase
Bdor0499|CDS|CDS	11.3	1.0	37.5	J	COG0238	Ribosomal protein S18
TS29Met0472|CDS|CDS	6.0	0.5	37.2	J	COG0081	Ribosomal protein L1
TS28Fae05977|CDS|CDS	11.0	1.0	36.4	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
Bdor4347|CDS|CDS	32.8	3.0	36.1	J	COG0244	Ribosomal protein L10
TS28Fae13722|CDS|CDS	5.3	0.5	35.3	J	COG0097	Ribosomal protein L6P/L9E
TS28Ali2084|CDS|CDS	94.0	9.0	34.5	J	COG0198	Ribosomal protein L24
Msmi750793|CDS|CDS	17.0	1.7	33.7	J	COG5256	Translation elongation factor EF-1alpha (GTPase)
Casp0953|CDS|CDS	5.0	0.5	33.1	J	COG0094	Ribosomal protein L5
Pmer3073|CDS|CDS	9.8	1.0	32.5	J	COG0089	Ribosomal protein L23
BactD14454|CDS|CDS	9.8	1.0	32.5	J	COG0185	Ribosomal protein S19
ShigspD90005|CDS|CDS	3.3	0.3	32.2	J	COG0050	GTPases - translation elongation factors
Bdor4333|CDS|CDS	66.2	6.8	32.0	J	COG0092	Ribosomal protein S3
TS29Bac11453|CDS|CDS	14.0	1.5	30.9	J	COG0050	GTPases - translation elongation factors
Cbol5942|CDS|CDS	9.0	1.0	29.8	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS29Rum12035|CDS|CDS	27.0	3.0	29.8	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS28Rum07032|CDS|CDS	9.0	1.0	29.8	J	COG0480	Translation elongation factors (GTPases)
TS29Col1050|CDS|CDS	9.0	1.0	29.8	J	COG0441	Threonyl-tRNA synthetase
TS29Fae10022|CDS|CDS	4.5	0.5	29.8	J	COG0290	Translation initiation factor 3 (IF-3)
RintL10535|CDS|CDS	9.0	1.0	29.8	J	COG0255	Ribosomal protein L29
Dfor0762|CDS|CDS	9.0	1.0	29.8	J	COG0251|COG1357	Putative translation initiation inhibitor, yjgF family|Uncharacterized low-complexity proteins
Acol2340|CDS|CDS	9.0	1.0	29.8	J	COG0093	Ribosomal protein L14
RintL10530|CDS|CDS	9.0	1.0	29.8	J	COG0089	Ribosomal protein L23
TS29Col0074|CDS|CDS	8.5	1.0	28.2	J	COG0050	GTPases - translation elongation factors
Svar1484|CDS|CDS	8.5	1.0	28.1	J	COG0087	Ribosomal protein L3
Bste1207|CDS|CDS	8.5	1.0	27.9	J	COG0227	Ribosomal protein L28
ShigspD91105|CDS|CDS	8.3	1.0	27.6	J	COG0495	Leucyl-tRNA synthetase
TS28Ali2087|CDS|CDS	75.0	9.0	27.6	J	COG0089	Ribosomal protein L23
Pmer1931|CDS|CDS	49.8	6.0	27.5	J	COG0008|COG0064	Glutamyl- and glutaminyl-tRNA synthetases|Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
Aput1563|CDS|CDS	107.5	13.0	27.3	J	COG0052	Ribosomal protein S2
TS28Eub1333|CDS|CDS	8.0	1.0	26.5	J	COG0267	Ribosomal protein L33
Bcap3099|CDS|CDS	8.0	1.0	26.5	J	COG0267	Ribosomal protein L33
Acol2349|CDS|CDS	8.0	1.0	26.5	J	COG0088	Ribosomal protein L4
Cste0994|CDS|CDS	7.6	1.0	25.1	J	COG0050	GTPases - translation elongation factors
TS29Rum19669|CDS|CDS	15.0	2.0	24.8	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
Bdor4315|CDS|CDS	7.5	1.0	24.8	J	COG0203	Ribosomal protein L17
BactD14438|CDS|CDS	2.5	0.3	24.7	J	COG0050	GTPases - translation elongation factors
Bxyl1699|CDS|CDS	2.5	0.3	24.7	J	COG0050	GTPases - translation elongation factors
TS29Bac03348|CDS|CDS	2.5	0.3	24.7	J	COG0050	GTPases - translation elongation factors
BactD14457|CDS|CDS	5.0	0.7	24.6	J	COG0197	Ribosomal protein L16/L10E
Bxyl1678|CDS|CDS	5.0	0.7	24.6	J	COG0197	Ribosomal protein L16/L10E
TS29Bac09453|CDS|CDS	5.0	0.7	24.6	J	COG0197	Ribosomal protein L16/L10E
Bste2295|CDS|CDS	14.8	2.0	24.5	J	COG0185	Ribosomal protein S19
Hfil1189|CDS|CDS	7.3	1.0	24.3	J	COG0480	Translation elongation factors (GTPases)
Robe1737|CDS|CDS	7.3	1.0	24.3	J	COG0255	Ribosomal protein L29
Bfin1190|CDS|CDS	2.4	0.3	23.9	J	COG0539	Ribosomal protein S1
CspSS20706|CDS|CDS	14.0	2.0	23.1	J	COG1534	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein
Casp3349|CDS|CDS	7.0	1.0	23.1	J	COG1190	Lysyl-tRNA synthetase (class II)
Pmer3139|CDS|CDS	3.5	0.5	23.1	J	COG0617|COG0618	tRNA nucleotidyltransferase/poly(A) polymerase|Exopolyphosphatase-related proteins

Ccom0845|CDS|CDS	7.0	1.0	23.1	J	COG0480	Translation elongation factors (GTPases)
Acol0660|CDS|CDS	7.0	1.0	23.1	J	COG0335	Ribosomal protein L19
TS29Rum00793|CDS|CDS	7.0	1.0	23.1	J	COG0251|COG1357	Putative translation initiation inhibitor, yjgF family|Uncharacterized low-complexity proteins
Rtor1396|CDS|CDS	14.0	2.0	23.1	J	COG0228	Ribosomal protein S16
Robe1841|CDS|CDS	2.3	0.3	23.1	J	COG0184	Ribosomal protein S15P/S13E
TS29Rum10660|CDS|CDS	2.3	0.3	23.1	J	COG0184	Ribosomal protein S15P/S13E
Msmi750618|CDS|CDS	1.8	0.3	23.1	J	COG0130	Pseudouridine synthase
TS28Fae11044|CDS|CDS	7.0	1.0	23.1	J	COG0048	Ribosomal protein S12
Acol0410|CDS|CDS	7.0	1.0	23.1	J	COG0012	Predicted GTPase, probable translation factor
TS29Rum15321|CDS|CDS	6.8	1.0	22.6	J	COG2868	Predicted ribosomal protein
BactD12583|CDS|CDS	5.3	0.8	22.5	J	COG0423	Glycyl-tRNA synthetase (class II)
Bste2951|CDS|CDS	17.0	2.5	22.5	J	COG0324	tRNA delta(2)-isopentenylpyrophosphate transferase
TS29Bac02529|CDS|CDS	6.8	1.0	22.5	J	COG0238	Ribosomal protein S18
Msmi751413|CDS|CDS	3.0	0.5	22.0	J	COG0081	Ribosomal protein L1
Bryfor3831|CDS|CDS	5.5	0.8	21.8	J	COG0050	GTPases - translation elongation factors
TS29Rum17981|CDS|CDS	13.0	2.0	21.5	J	COG0244	Ribosomal protein L10
TS29Clo0293|CDS|CDS	13.0	2.0	21.5	J	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
Pmer0609|CDS|CDS	6.5	1.0	21.5	J	COG0216	Protein chain release factor A
Robe1728|CDS|CDS	6.5	1.0	21.5	J	COG0051	Ribosomal protein S10
Cste1464|CDS|CDS	19.0	3.0	20.9	J	COG0525	Valyl-tRNA synthetase
Bdor4329|CDS|CDS	12.5	2.0	20.7	J	COG0093	Ribosomal protein L14
TS29Bac09458|CDS|CDS	3.1	0.5	20.6	J	COG0090	Ribosomal protein L2
TS29Rum13729|CDS|CDS	6.2	1.0	20.4	J	COG0098	Ribosomal protein S5
Msmi750610|CDS|CDS	3.0	0.5	20.1	J	COG0522	Ribosomal protein S4 and related proteins
Bste2299|CDS|CDS	18.2	3.0	20.0	J	COG0087	Ribosomal protein L3
Msmi740284|CDS|CDS	5.0	0.8	19.8	J	COG1537|COG1503	Predicted RNA-binding proteins|Peptide chain release factor 1 (eRF1)
TS28Rum03141|CDS|CDS	2.0	0.3	19.8	J	COG0525	Valyl-tRNA synthetase
Msmi741116|CDS|CDS	9.0	1.5	19.8	J	COG0016	Phenylalanyl-tRNA synthetase alpha subunit
Bste2069|CDS|CDS	12.0	2.0	19.8	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29Fae00886|CDS|CDS	6.0	1.0	19.8	J	COG0482	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain
TS28Rum09388|CDS|CDS	6.0	1.0	19.8	J	COG0230	Ribosomal protein L34
Cspo2314|CDS|CDS	6.0	1.0	19.8	J	COG0228	Ribosomal protein S16
Acol2320|CDS|CDS	6.0	1.0	19.8	J	COG0203	Ribosomal protein L17
Bcap2263|CDS|CDS	6.0	1.0	19.8	J	COG0186	Ribosomal protein S17
TS29Met0854|CDS|CDS	1.2	0.2	19.8	J	COG0092	Ribosomal protein S3
Msmi750643|CDS|CDS	1.5	0.3	19.8	J	COG0091	Ribosomal protein L22
FpraM2121572|CDS|CDS	3.0	0.5	19.8	J	COG0018	Arginyl-tRNA synthetase
TS29Fae08149|CDS|CDS	3.0	0.5	19.8	J	COG0018	Arginyl-tRNA synthetase
BactD14441|CDS|CDS	3.0	0.5	19.8	J	COG0081	Ribosomal protein L1
Bxyl1695|CDS|CDS	3.0	0.5	19.8	J	COG0081	Ribosomal protein L1
Bdor4338|CDS|CDS	38.0	6.5	19.3	J	COG0088	Ribosomal protein L4
TS28Fae22827|CDS|CDS	5.8	1.0	19.3	J	COG0098	Ribosomal protein S5
TS28Met0720|CDS|CDS	14.5	2.5	19.2	J	COG2139	Ribosomal protein L21E
Msmi751271|CDS|CDS	14.5	2.5	19.2	J	COG2139	Ribosomal protein L21E
Bste2294|CDS|CDS	17.2	3.0	18.9	J	COG0091	Ribosomal protein L22
Bdor4351|CDS|CDS	40.1	7.0	18.9	J	COG0050	GTPases - translation elongation factors
TS29Met0155|CDS|CDS	5.7	1.0	18.8	J	COG1534|COG2023	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein|RNase P subunit RPR2
RintL10533|CDS|CDS	22.7	4.0	18.8	J	COG0091	Ribosomal protein L22
Bdor4341|CDS|CDS	17.0	3.0	18.7	J	COG0049	Ribosomal protein S7
TS28Ali0073|CDS|CDS	72.0	13.0	18.3	J	COG0291	Ribosomal protein L35
Bdor4336|CDS|CDS	38.5	7.0	18.2	J	COG0090	Ribosomal protein L2
BactD11765|CDS|CDS	1.8	0.3	18.2	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
Msmi740277|CDS|CDS	2.8	0.5	18.2	J	COG1549	Queuine tRNA-ribosyltransferases, contain PUA domain
TS28RumUnc0514|CDS|CDS	22.0	4.0	18.2	J	COG1544	Ribosome-associated protein Y (PSrp-1)
Eeli2048|CDS|CDS	11.0	2.0	18.2	J	COG0292	Ribosomal protein L20
TS28Col1433|CDS|CDS	5.5	1.0	18.2	J	COG0257	Ribosomal protein L36
TS29Bac12092|CDS|CDS	2.6	0.5	17.1	J	COG0052	Ribosomal protein S2
TS28Ali0299|CDS|CDS	164.0	32.0	16.9	J	COG0480	Translation elongation factors (GTPases)
CspM6212581|CDS|CDS	20.3	4.0	16.8	J	COG0050	GTPases - translation elongation factors
RintL11448|CDS|CDS	5.0	1.0	16.5	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS29Rum16455|CDS|CDS	5.0	1.0	16.5	J	COG1490	D-Tyr-tRNAtyr deacylase
Cste1248|CDS|CDS	5.0	1.0	16.5	J	COG1206	NAD(FAD)-utilizing enzyme possibly involved in translation
Cnex2441|CDS|CDS	5.0	1.0	16.5	J	COG0828	Ribosomal protein S21
TS29LacUnc019|CDS|CDS	5.0	1.0	16.5	J	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
TS29Rum01821|CDS|CDS	1.7	0.3	16.5	J	COG0144	tRNA and rRNA cytosine-C5-methylases
Csci2161|CDS|CDS	5.0	1.0	16.5	J	COG0094	Ribosomal protein L5
Cspo0074|CDS|CDS	10.0	2.0	16.5	J	COG0094	Ribosomal protein L5
TS29Bac09450|CDS|CDS	10.0	2.0	16.5	J	COG0093	Ribosomal protein L14
Bryfor4429|CDS|CDS	5.0	1.0	16.5	J	COG0092	Ribosomal protein S3
Casp0965|CDS|CDS	5.0	1.0	16.5	J	COG0087	Ribosomal protein L3
Cbol4252|CDS|CDS	5.0	1.0	16.5	J	COG0052	Ribosomal protein S2
Chir2104|CDS|CDS	5.0	1.0	16.5	J	COG0050	GTPases - translation elongation factors
Bryfor0132|CDS|CDS	5.0	1.0	16.5	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Begg2625|CDS|CDS	5.0	1.0	16.5	J	COG0091	Ribosomal protein L22
Bova0755|CDS|CDS	2.5	0.5	16.5	J	COG0050	GTPases - translation elongation factors
TS29Bac08987|CDS|CDS	2.5	0.5	16.4	J	COG0172	Seryl-tRNA synthetase
Bxyl3163|CDS|CDS	2.5	0.5	16.4	J	COG0172	Seryl-tRNA synthetase
Msmi750990|CDS|CDS	5.7	1.2	16.0	J	COG0064	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
Begg2623|CDS|CDS	24.0	5.0	15.9	J	COG0197	Ribosomal protein L16/L10E
Msmi751252|CDS|CDS	3.6	0.8	15.8	J	COG1736	Diphthamide synthase subunit DPH2
Bste2716|CDS|CDS	62.0	13.0	15.8	J	COG0480	Translation elongation factors (GTPases)
Msmi751432|CDS|CDS	3.2	0.7	15.7	J	COG2888	Predicted Zn-ribbon RNA-binding protein with a function in translation

TS28Met1650|CDS|CDS	3.2	0.7	15.7	J	COG2888	Predicted Zn-ribbon RNA-binding protein with a function in translation
Msmi740247|CDS|CDS	3.2	0.7	15.7	J	COG2888	Predicted Zn-ribbon RNA-binding protein with a function in translation
Pmer0391|CDS|CDS	9.5	2.0	15.7	J	COG0290	Translation initiation factor 3 (IF-3)
Bdor0226|CDS|CDS	23.6	5.0	15.6	J	COG0102	Ribosomal protein L13
Bste0410|CDS|CDS	23.5	5.0	15.5	J	COG0228	Ribosomal protein S16
Msmi750689|CDS|CDS	7.0	1.5	15.4	J	COG1798	Diphthamide biosynthesis methyltransferase
Bdor4319|CDS|CDS	16.7	3.7	15.0	J	COG0024	Methionine aminopeptidase
Msmi750171|CDS|CDS	1.5	0.3	14.9	J	COG2125	Ribosomal protein S6E (S10)
Msmi741546|CDS|CDS	1.5	0.3	14.9	J	COG2125	Ribosomal protein S6E (S10)
Msmi750306|CDS|CDS	1.5	0.3	14.9	J	COG1514	2'-5' RNA ligase
RintL12917|CDS|CDS	9.0	2.0	14.9	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
Msmi740571|CDS|CDS	3.0	0.7	14.9	J	COG0441	Threonyl-tRNA synthetase
TS29Col1654|CDS|CDS	9.0	2.0	14.9	J	COG0256	Ribosomal protein L18
TS29Bac05406|CDS|CDS	3.0	0.7	14.9	J	COG0173	Aspartyl-tRNA synthetase
Bxyl1668|CDS|CDS	4.5	1.0	14.9	J	COG0098	Ribosomal protein S5
BactD14465|CDS|CDS	4.5	1.0	14.9	J	COG0098	Ribosomal protein S5
TS28Ali1617|CDS|CDS	40.0	9.0	14.7	J	COG0290	Translation initiation factor 3 (IF-3)
TS28Ali2091|CDS|CDS	62.0	14.0	14.6	J	COG0049	Ribosomal protein S7
Msmi740553|CDS|CDS	2.7	0.6	14.6	J	COG0018	Arginyl-tRNA synthetase
Bste2272|CDS|CDS	11.0	2.5	14.6	J	COG0203	Ribosomal protein L17
TS28Fae20651|CDS|CDS	8.8	2.0	14.5	J	COG0049	Ribosomal protein S7
TS29Rum18959|CDS|CDS	13.0	3.0	14.3	J	COG0480	Translation elongation factors (GTPases)
BactD14440|CDS|CDS	5.8	1.3	14.3	J	COG0080	Ribosomal protein L11
Bxyl1696|CDS|CDS	5.8	1.3	14.3	J	COG0080	Ribosomal protein L11
Msmi750206|CDS|CDS	2.2	0.5	14.2	J	COG0721	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit
TS28Met0377|CDS|CDS	2.2	0.5	14.2	J	COG0721	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit
Msmi741506|CDS|CDS	2.2	0.5	14.2	J	COG0721	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit
TS28Fae22828|CDS|CDS	8.5	2.0	14.1	J	COG0256	Ribosomal protein L18
Pmer1102|CDS|CDS	8.5	2.0	14.1	J	COG0244	Ribosomal protein L10
Pmer1294|CDS|CDS	87.0	20.5	14.0	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
Bdor4348|CDS|CDS	20.9	5.0	13.8	J	COG0081	Ribosomal protein L1
Aput0546|CDS|CDS	54.0	13.0	13.7	J	COG0090	Ribosomal protein L2
Rtor0546|CDS|CDS	8.2	2.0	13.6	J	COG0050	GTPases - translation elongation factors
TS29Bac04438|CDS|CDS	2.3	0.6	13.2	J	COG0013	Alanyl-tRNA synthetase
Casp3434|CDS|CDS	4.0	1.0	13.2	J	COG4108	Peptide chain release factor RF-3
Pmer3258|CDS|CDS	12.0	3.0	13.2	J	COG2264	Ribosomal protein L11 methylase
Eeli1078|CDS|CDS	12.0	3.0	13.2	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS29Bif2532|CDS|CDS	1.0	0.3	13.2	J	COG1544	Ribosome-associated protein Y (PSrp-1)
Even0467|CDS|CDS	8.0	2.0	13.2	J	COG1186	Protein chain release factor B
CspL21674|CDS|CDS	8.0	2.0	13.2	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
Robe1192|CDS|CDS	2.0	0.5	13.2	J	COG0621	2-methylthioadenine synthetase
Svar1457|CDS|CDS	4.0	1.0	13.2	J	COG0522	Ribosomal protein S4 and related proteins
TS28Fae19635|CDS|CDS	8.0	2.0	13.2	J	COG0267	Ribosomal protein L33
Pmer3228|CDS|CDS	4.0	1.0	13.2	J	COG0254	Ribosomal protein L31
Cbol5373|CDS|CDS	4.0	1.0	13.2	J	COG0233	Ribosome recycling factor
Bdor1113|CDS|CDS	8.0	2.0	13.2	J	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
Eeli1561|CDS|CDS	8.0	2.0	13.2	J	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
TS29Bac11681|CDS|CDS	4.0	1.0	13.2	J	COG0203	Ribosomal protein L17
Bova4074|CDS|CDS	2.0	0.5	13.2	J	COG0193	Peptidyl-tRNA hydrolase
BactD24017|CDS|CDS	2.0	0.5	13.2	J	COG0193	Peptidyl-tRNA hydrolase
Rumhyd2310|CDS|CDS	4.0	1.0	13.2	J	COG0173	Aspartyl-tRNA synthetase
Dfor1285|CDS|CDS	4.0	1.0	13.2	J	COG0094	Ribosomal protein L5
Casp0959|CDS|CDS	10.0	2.5	13.2	J	COG0092	Ribosomal protein S3
PRABACTJOHN2262|CDS|CDS	4.0	1.0	13.2	J	COG0088	Ribosomal protein L4
Ehal0879|CDS|CDS	4.0	1.0	13.2	J	COG0081	Ribosomal protein L1
Acac2532|CDS|CDS	4.0	1.0	13.2	J	COG0064	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
Rgna2644|CDS|CDS	2.0	0.5	13.2	J	COG0042	tRNA-dihydrouridine synthase
TS29Bac10366|CDS|CDS	2.0	0.5	13.2	J	COG0024	Methionine aminopeptidase
CspM6213067|CDS|CDS	6.0	1.5	13.2	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Msmi751268|CDS|CDS	10.6	2.7	13.1	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
BactD11536|CDS|CDS	3.9	1.0	12.9	J	COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases
TS28Col1447|CDS|CDS	39.0	10.0	12.9	J	COG0198	Ribosomal protein L24
CspSS23028|CDS|CDS	15.5	4.0	12.8	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS29Bac07466|CDS|CDS	6.5	1.7	12.8	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS28Col1171|CDS|CDS	27.0	7.0	12.8	J	COG0049	Ribosomal protein S7
Msmi740134|CDS|CDS	2.9	0.8	12.7	J	COG0423	Glycyl-tRNA synthetase (class II)
TS28Ali1618|CDS|CDS	159.0	42.0	12.5	J	COG0441	Threonyl-tRNA synthetase
TS29Bac02937|CDS|CDS	1.3	0.3	12.4	J	COG0180	Tryptophanyl-tRNA synthetase
TS29Bac10265|CDS|CDS	2.5	0.7	12.4	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
Pmer1139|CDS|CDS	11.2	3.0	12.3	J	COG0480	Translation elongation factors (GTPases)
Bdor0693|CDS|CDS	22.0	6.0	12.1	J	COG0290	Translation initiation factor 3 (IF-3)
TS28Rum10022|CDS|CDS	11.0	3.0	12.1	J	COG0228	Ribosomal protein S16
Csci2146|CDS|CDS	3.7	1.0	12.1	J	COG0100	Ribosomal protein S11
Begg0034|CDS|CDS	7.3	2.0	12.1	J	COG0052	Ribosomal protein S2
TS28Clo09186|CDS|CDS	22.0	6.0	12.1	J	COG0050	GTPases - translation elongation factors
TS28Fae02145|CDS|CDS	40.0	11.0	12.0	J	COG0324	tRNA delta(2)-isopentenylpyrophosphate transferase
Msmi750560|CDS|CDS	9.0	2.5	11.9	J	COG0016	Phenylalanyl-tRNA synthetase alpha subunit
TS29Bac05585|CDS|CDS	3.6	1.0	11.8	J	COG0267	Ribosomal protein L33
Msmi750050|CDS|CDS	3.3	0.9	11.7	J	COG1632	Ribosomal protein L15E
Bste2298|CDS|CDS	17.5	5.0	11.6	J	COG0088	Ribosomal protein L4
Bdor1364|CDS|CDS	3.5	1.0	11.6	J	COG3743|COG0261	Uncharacterized conserved protein|Ribosomal protein L21
Msmi740761|CDS|CDS	1.8	0.5	11.6	J	COG1867	N2,N2-dimethylguanosine tRNA methyltransferase
Msmi740991|CDS|CDS	7.0	2.0	11.6	J	COG1798	Diphthamide biosynthesis methyltransferase
TS28Dor0970|CDS|CDS	7.0	2.0	11.6	J	COG1534	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein

TS28Fae06298|CDS|CDS	14.0	4.0	11.6	J	COG0441	Threonyl-tRNA synthetase
Casp6313|CDS|CDS	7.0	2.0	11.6	J	COG0222	Ribosomal protein L7/L12
Rtor2165|CDS|CDS	7.0	2.0	11.6	J	COG0184	Ribosomal protein S15P/S13E
Cnex0801|CDS|CDS	7.0	2.0	11.6	J	COG0098	Ribosomal protein S5
Bhan0424|CDS|CDS	7.0	2.0	11.6	J	COG0096	Ribosomal protein S8
Cste1403|CDS|CDS	3.5	1.0	11.6	J	COG0060	Isoleucyl-tRNA synthetase
Bste0953|CDS|CDS	3.5	1.0	11.6	J	COG0024	Methionine aminopeptidase
Bdor2412|CDS|CDS	17.0	5.0	11.2	J	COG0621	2-methylthioadenine synthetase
TS28Bac6839|CDS|CDS	23.7	7.0	11.2	J	COG0186	Ribosomal protein S17
Cnex0780|CDS|CDS	4.5	1.3	11.2	J	COG0480	Translation elongation factors (GTPases)
TS28Fae12903|CDS|CDS	13.5	4.0	11.2	J	COG0050	GTPases - translation elongation factors
Msmi751329|CDS|CDS	4.2	1.3	11.1	J	COG2117	Predicted subunit of tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain
BactD20036|CDS|CDS	1.7	0.5	11.0	J	COG0081	Ribosomal protein L1
TS28Fae21704|CDS|CDS	5.0	1.5	11.0	J	COG1490	D-Tyr-tRNAtyr deacylase
Dfor1540|CDS|CDS	10.0	3.0	11.0	J	COG0227	Ribosomal protein L28
Acol2347|CDS|CDS	10.0	3.0	11.0	J	COG0090	Ribosomal protein L2
PRABACTJOHN3551|CDS|CDS	10.0	3.0	11.0	J	COG0050	GTPases - translation elongation factors
Bste2293|CDS|CDS	13.2	4.0	10.9	J	COG0092	Ribosomal protein S3
Bdor0461|CDS|CDS	11.5	3.5	10.9	J	COG0009	Putative translation factor (SUA5)
TS28Ali0403|CDS|CDS	49.0	15.0	10.8	J	COG0222	Ribosomal protein L7/L12
Dlon2187|CDS|CDS	13.0	4.0	10.7	J	COG2868	Predicted ribosomal protein
Rbro1252|CDS|CDS	6.5	2.0	10.7	J	COG0495	Leucyl-tRNA synthetase
TS29Fae01100|CDS|CDS	3.3	1.0	10.7	J	COG0215	Cysteinyl-tRNA synthetase
Pmer1043|CDS|CDS	13.0	4.0	10.7	J	COG0024	Methionine aminopeptidase
Svar0370|CDS|CDS	9.8	3.0	10.7	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
Bdor0222|CDS|CDS	26.0	8.0	10.7	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
TS29Dor2153|CDS|CDS	9.7	3.0	10.7	J	COG0091	Ribosomal protein L22
Acol1128|CDS|CDS	9.7	3.0	10.7	J	COG0050	GTPases - translation elongation factors
Bdor0692|CDS|CDS	25.7	8.0	10.6	J	COG0441	Threonyl-tRNA synthetase
TS29Rum21010|CDS|CDS	12.8	4.0	10.6	J	COG0087	Ribosomal protein L3
Svar0550|CDS|CDS	20.7	6.5	10.5	J	COG0050	GTPases - translation elongation factors
Begg1340|CDS|CDS	3.2	1.0	10.5	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)
Bdor1425|CDS|CDS	6.3	2.0	10.5	J	COG0324	tRNA delta(2)-isopentenylpyrophosphate transferase
TS28Fae15518|CDS|CDS	19.0	6.0	10.5	J	COG0292	Ribosomal protein L20
TS28Par2565|CDS|CDS	9.5	3.0	10.5	J	COG0290	Translation initiation factor 3 (IF-3)
Msmi750796|CDS|CDS	3.2	1.0	10.5	J	COG0048	Ribosomal protein S12
Acac2828|CDS|CDS	9.3	3.0	10.3	J	COG0050	GTPases - translation elongation factors
Bcap2652|CDS|CDS	33.9	11.0	10.2	J	COG0050	GTPases - translation elongation factors
TS28Fae10272|CDS|CDS	17.3	5.7	10.1	J	COG0238	Ribosomal protein S18
TS28Eub6198|CDS|CDS	3.8	127.0	0.1	J	COG0495	Leucyl-tRNA synthetase
TS28Bif4388|CDS|CDS	0.3	8.3	0.1	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
TS29Bif0456|CDS|CDS	0.3	8.3	0.1	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
TS28Eub8888|CDS|CDS	1.0	33.5	0.1	J	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
TS29Bif2967|CDS|CDS	0.5	16.8	0.1	J	COG0013	Alanyl-tRNA synthetase
TS29Bif1236|CDS|CDS	0.3	11.2	0.1	J	COG0215	Cysteinyl-tRNA synthetase
TS28Clo01330|CDS|CDS	5.0	168.0	0.1	J	COG0012	Predicted GTPase, probable translation factor
TS28Fae15574|CDS|CDS	2.0	67.3	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Eub8322|CDS|CDS	1.0	34.5	0.1	J	COG0100	Ribosomal protein S11
TS29Bif3639|CDS|CDS	0.3	11.5	0.1	J	COG0018	Arginyl-tRNA synthetase
TS28Clo00521|CDS|CDS	6.0	208.0	0.1	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
TS28Rum02927|CDS|CDS	0.5	17.5	0.1	J	COG0495	Leucyl-tRNA synthetase
TS28RumUnc1650|CDS|CDS	2.0	70.0	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Eub5095|CDS|CDS	2.0	70.0	0.1	J	COG0008|COG0064	Glutamyl- and glutaminyl-tRNA synthetases|Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
TS28Eub8628|CDS|CDS	3.0	106.0	0.1	J	COG0173	Aspartyl-tRNA synthetase
TS28Clo00811|CDS|CDS	3.0	106.0	0.1	J	COG0052	Ribosomal protein S2
Bpse0181|CDS|CDS	0.1	4.0	0.1	J	COG0089	Ribosomal protein L23
TS29Bif1363|CDS|CDS	0.1	4.0	0.1	J	COG0089	Ribosomal protein L23
TS28Bif3992|CDS|CDS	0.1	4.0	0.1	J	COG0089	Ribosomal protein L23
TS28Clo01294|CDS|CDS	6.0	217.0	0.1	J	COG0143	Methionyl-tRNA synthetase
TS28Fae18279|CDS|CDS	2.0	72.5	0.1	J	COG0621	2-methylthioadenine synthetase
Robe2299|CDS|CDS	0.5	18.5	0.1	J	COG1236|COG1782	Predicted exonuclease of the beta-lactamase fold involved in RNA processing|Predicted metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain
TS28Met0468|CDS|CDS	1.5	56.2	0.1	J	COG0060	Isoleucyl-tRNA synthetase
TS28Fae01901|CDS|CDS	0.5	19.0	0.1	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29Rum17008|CDS|CDS	2.0	78.0	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Eub8311|CDS|CDS	0.5	19.5	0.1	J	COG0256	Ribosomal protein L18
TS28Bac7651|CDS|CDS	0.5	19.5	0.1	J	COG0180	Tryptophanyl-tRNA synthetase
Dfor0369|CDS|CDS	1.0	39.8	0.1	J	COG1190	Lysyl-tRNA synthetase (class II)
TS29Fae02030|CDS|CDS	0.5	20.0	0.1	J	COG0143	Methionyl-tRNA synthetase
TS28Fae14972|CDS|CDS	0.2	8.0	0.1	J	COG0052	Ribosomal protein S2
TS28Eub4460|CDS|CDS	1.0	40.0	0.1	J	COG0012	Predicted GTPase, probable translation factor
TS28Fae20208|CDS|CDS	1.2	47.0	0.1	J	COG0264	Translation elongation factor Ts
TS28Col0359|CDS|CDS	1.0	40.8	0.1	J	COG0162	Tyrosyl-tRNA synthetase
Bpse1096|CDS|CDS	0.3	13.8	0.1	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
TS29Bif1200|CDS|CDS	0.3	13.8	0.1	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
TS28Rum05971|CDS|CDS	1.0	42.0	0.1	J	COG0525	Valyl-tRNA synthetase
TS28Eub8765|CDS|CDS	2.0	84.0	0.1	J	COG0008|COG0064	Glutamyl- and glutaminyl-tRNA synthetases|Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
TS28Met1508|CDS|CDS	0.3	11.0	0.1	J	COG1746	tRNA nucleotidyltransferase (CCA-adding enzyme)
RintL10531|CDS|CDS	0.3	11.0	0.1	J	COG0090	Ribosomal protein L2
TS28Clo00476|CDS|CDS	7.0	310.0	0.1	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
TS29Fae06399|CDS|CDS	0.4	19.0	0.1	J	COG0441	Threonyl-tRNA synthetase
TS28Fae10189|CDS|CDS	1.0	44.5	0.1	J	COG4108	Peptide chain release factor RF-3
TS29Rum16762|CDS|CDS	0.5	22.5	0.1	J	COG0566	rRNA methylases
TS28Clo00686|CDS|CDS	4.0	180.0	0.1	J	COG0124	Histidyl-tRNA synthetase

TS28Eub8321|CDS|CDS	0.7	31.5	0.1	J	COG0099	Ribosomal protein S13
TS28Fae14040|CDS|CDS	0.3	15.0	0.1	J	COG0621	2-methylthioadenine synthetase
TS28Fae01826|CDS|CDS	1.2	52.5	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Eub8298|CDS|CDS	1.0	45.5	0.1	J	COG0087	Ribosomal protein L3
Clep2095|CDS|CDS	0.5	23.0	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Fae18978|CDS|CDS	0.5	23.0	0.1	J	COG0042	tRNA-dihydrouridine synthase
TS28Rum14152|CDS|CDS	0.5	23.5	0.1	J	COG0566	rRNA methylases
TS28Fae18276|CDS|CDS	1.0	48.0	0.1	J	COG2890|COG3872	Methylase of polypeptide chain release factors|Predicted metal-dependent enzyme
TS28Eub8308|CDS|CDS	0.5	24.0	0.1	J	COG0094	Ribosomal protein L5
TS28Clo01032|CDS|CDS	5.0	245.0	0.1	J	COG0173	Aspartyl-tRNA synthetase
TS28Clo00842|CDS|CDS	3.0	148.0	0.1	J	COG0809	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)
TS28Eub7262|CDS|CDS	1.5	74.5	0.1	J	COG0042	tRNA-dihydrouridine synthase
Dlon0199|CDS|CDS	0.2	10.0	0.1	J	COG0099	Ribosomal protein S13
TS28Clo01445|CDS|CDS	2.0	100.0	0.1	J	COG0024	Methionine aminopeptidase
TS29Rum13769|CDS|CDS	2.0	102.0	0.1	J	COG0525	Valyl-tRNA synthetase
TS28Met0433|CDS|CDS	0.3	17.2	0.1	J	COG1498	Protein implicated in ribosomal biogenesis, Nop56p homolog
TS28Col0590|CDS|CDS	1.0	52.0	0.1	J	COG0495	Leucyl-tRNA synthetase
TS28Fae11125|CDS|CDS	0.4	23.0	0.1	J	COG0441	Threonyl-tRNA synthetase
TS28Eub7783|CDS|CDS	1.5	80.5	0.1	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
Robe2865|CDS|CDS	0.5	27.0	0.1	J	COG4108	Peptide chain release factor RF-3
TS28Bac6270|CDS|CDS	0.5	27.0	0.1	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
TS28Clo00307|CDS|CDS	0.5	27.8	0.1	J	COG0018	Arginyl-tRNA synthetase
TS28Eub5337|CDS|CDS	0.5	28.5	0.1	J	COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases
TS28Clo01505|CDS|CDS	3.0	173.0	0.1	J	COG0162	Tyrosyl-tRNA synthetase
RintL13310|CDS|CDS	1.6	97.5	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Bif0821|CDS|CDS	0.2	12.1	0.1	J	COG0200	Ribosomal protein L15
TS28Bif1069|CDS|CDS	0.7	41.3	0.1	J	COG0060	Isoleucyl-tRNA synthetase
TS29Bif2797|CDS|CDS	0.2	10.5	0.1	J	COG0441	Threonyl-tRNA synthetase
TS28Eub8644|CDS|CDS	0.5	31.5	0.1	J	COG0018	Arginyl-tRNA synthetase
TS28Clo01346|CDS|CDS	2.0	130.0	0.1	J	COG0216	Protein chain release factor A
TS28Clo01430|CDS|CDS	1.0	65.0	0.1	J	COG0197	Ribosomal protein L16/L10E
TS28Clo01494|CDS|CDS	6.0	394.0	0.1	J	COG0495	Leucyl-tRNA synthetase
TS28Clo01639|CDS|CDS	1.0	66.0	0.1	J	COG0858	Ribosome-binding factor A
TS28Col1547|CDS|CDS	0.3	22.0	0.1	J	COG0060	Isoleucyl-tRNA synthetase
TS28Fae14467|CDS|CDS	1.7	111.3	0.0	J	COG0441	Threonyl-tRNA synthetase
TS28Fae18605|CDS|CDS	0.5	33.5	0.0	J	COG0617	tRNA nucleotidyltransferase/poly(A) polymerase
TS28Fae17730|CDS|CDS	1.0	69.0	0.0	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
TS28Fae18864|CDS|CDS	0.6	41.5	0.0	J	COG0143	Methionyl-tRNA synthetase
Svar2455|CDS|CDS	3.1	213.6	0.0	J	COG0480	Translation elongation factors (GTPases)
Ccom2219|CDS|CDS	3.1	213.6	0.0	J	COG0480	Translation elongation factors (GTPases)
Cmet2527|CDS|CDS	3.1	213.6	0.0	J	COG0480	Translation elongation factors (GTPases)
CspM6211935|CDS|CDS	3.1	213.6	0.0	J	COG0480	Translation elongation factors (GTPases)
TS28Eub7794|CDS|CDS	0.3	23.7	0.0	J	COG0101	Pseudouridylate synthase
TS28Rum15742|CDS|CDS	1.0	72.3	0.0	J	COG0013	Alanyl-tRNA synthetase
TS28Clo00812|CDS|CDS	1.0	73.0	0.0	J	COG0292	Ribosomal protein L20
TS28Clo00518|CDS|CDS	6.0	438.0	0.0	J	COG0060	Isoleucyl-tRNA synthetase
TS28Fae18180|CDS|CDS	0.8	56.0	0.0	J	COG0215	Cysteinyl-tRNA synthetase
TS28Eub7522|CDS|CDS	0.4	27.5	0.0	J	COG0049	Ribosomal protein S7
TS28Eub8301|CDS|CDS	0.7	50.5	0.0	J	COG0090	Ribosomal protein L2
TS28Bif2061|CDS|CDS	0.3	25.5	0.0	J	COG0018	Arginyl-tRNA synthetase
TS28Clo01458|CDS|CDS	1.0	81.0	0.0	J	COG0103	Ribosomal protein S9
TS29Bif1289|CDS|CDS	0.6	49.8	0.0	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
TS29Fae00448|CDS|CDS	0.2	17.0	0.0	J	COG0052	Ribosomal protein S2
TS28Fae00276|CDS|CDS	0.4	37.0	0.0	J	COG0441	Threonyl-tRNA synthetase
TS28Col0051|CDS|CDS	0.3	32.5	0.0	J	COG0172	Seryl-tRNA synthetase
Robe1736|CDS|CDS	0.2	21.0	0.0	J	COG0197	Ribosomal protein L16/L10E
TS28Clo01287|CDS|CDS	1.0	108.0	0.0	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
TS28Fae12522|CDS|CDS	1.0	110.0	0.0	J	COG4108	Peptide chain release factor RF-3
TS28Bif3798|CDS|CDS	0.3	37.3	0.0	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
TS29Rum21117|CDS|CDS	1.0	112.5	0.0	J	COG0143	Methionyl-tRNA synthetase
TS28Eub6374|CDS|CDS	0.5	60.0	0.0	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
TS28Eub6414|CDS|CDS	0.5	62.0	0.0	J	COG0264	Translation elongation factor Ts
TS28Fae20304|CDS|CDS	0.5	63.5	0.0	J	COG0144	tRNA and rRNA cytosine-C5-methylases
TS28Fae05536|CDS|CDS	0.1	16.0	0.0	J	COG0197	Ribosomal protein L16/L10E
TS28Bif3842|CDS|CDS	0.3	44.7	0.0	J	COG0215	Cysteinyl-tRNA synthetase
Rtor0519|CDS|CDS	0.1	17.0	0.0	J	COG0197	Ribosomal protein L16/L10E
CspM6210039|CDS|CDS	1.6	224.5	0.0	J	COG0480	Translation elongation factors (GTPases)
TS28Fae20473|CDS|CDS	0.6	81.0	0.0	J	COG0480	Translation elongation factors (GTPases)
TS28Eub4235|CDS|CDS	0.5	72.0	0.0	J	COG0621	2-methylthioadenine synthetase
TS29Rum19841|CDS|CDS	0.1	18.5	0.0	J	COG0264	Translation elongation factor Ts
TS28Fae17629|CDS|CDS	0.5	80.5	0.0	J	COG0442	Prolyl-tRNA synthetase
TS28Eub3887|CDS|CDS	0.5	86.0	0.0	J	COG0018	Arginyl-tRNA synthetase
TS28Fae16609|CDS|CDS	0.5	94.5	0.0	J	COG1190	Lysyl-tRNA synthetase (class II)
TS28Rum00720|CDS|CDS	0.1	28.5	0.0	J	COG0264	Translation elongation factor Ts
TS28Eub8794|CDS|CDS	0.5	156.8	0.0	J	COG0060	Isoleucyl-tRNA synthetase
Buni3675|CDS|CDS	0.0	18.5	0.0	J	COG0539	Ribosomal protein S1
Msmi740151|CDS|CDS	8.3	2.2	12.6	J|C	COG1032|COG0060	Fe-S oxidoreductase|Isoleucyl-tRNA synthetase
Bste0247|CDS|CDS	5.5	1.0	18.2	J|E	COG0252	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D
RintL13630|CDS|CDS	4.0	1.0	13.2	J|H	COG0564|COG2320|COG0237	Pseudouridylate synthases, 23S RNA-specific|Uncharacterized conserved protein|Dephospho-CoA kinase
TS28Eub1354|CDS|CDS	0.5	31.0	0.1	J|H	COG0564|COG2320|COG0237	Pseudouridylate synthases, 23S RNA-specific|Uncharacterized conserved protein|Dephospho-CoA kinase
Bdor0233|CDS|CDS	21.5	4.0	17.8	J|I	COG0336|COG1211|COG0245	tRNA-(guanine-N1)-methyltransferase|4-diphosphocytidyl-2-methyl-D-erithritol synthase|2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase

Msmi750862|CDS|CDS	1.5	0.3	14.9	J|K	COG0042|COG4008	tRNA-dihydrouridine synthase|Predicted metal-binding transcription factor
Pmer2803|CDS|CDS	8.0	2.0	13.2	J|K|F	COG0590|COG3070|COG0596	Cytosine/adenosine deaminases|Regulator of competence-specific genes|Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
Bste0101|CDS|CDS	54.0	5.0	35.7	J|K|L	COG0513	Superfamily II DNA and RNA helicases
Bdor1906|CDS|CDS	74.0	11.0	22.2	J|K|L	COG0513	Superfamily II DNA and RNA helicases
Bdor4353|CDS|CDS	20.0	3.0	22.0	J|L	COG4974|COG1544	Site-specific recombinase XerD|Ribosome-associated protein Y (PSrp-1)
Msmi751349|CDS|CDS	3.5	1.0	11.6	J|L	COG0494|COG1670|COG1194	NTP pyrophosphohydrolases including oxidative damage repair enzymes|Acetyltransferases, including N-acetylases of ribosomal proteins|A/G-specific DNA glycosylase
Casp2902|CDS|CDS	9.0	1.0	29.8	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
Cbol1182|CDS|CDS	10.0	2.0	16.5	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
Csci1308|CDS|CDS	2.3	0.5	15.4	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
TS29Bac05982|CDS|CDS	335.8	1.0	1,110.4	K	COG1609	Transcriptional regulators
Bxyl1779|CDS|CDS	335.8	1.0	1,110.4	K	COG1609	Transcriptional regulators
TS29Bac01524|CDS|CDS	88.0	2.0	145.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bdor2086|CDS|CDS	25.8	1.0	85.4	K	COG0782	Transcription elongation factor
TS29Bac05143|CDS|CDS	12.9	0.5	85.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bxyl0677|CDS|CDS	12.9	0.5	85.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Msmi750333|CDS|CDS	16.7	0.7	82.7	K	COG1396	Predicted transcriptional regulators
TS29Bac07839|CDS|CDS	23.3	1.0	77.2	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Robe1131|CDS|CDS	10.5	0.5	69.4	K	COG1609	Transcriptional regulators
Bdor2161|CDS|CDS	18.2	1.0	60.1	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Clo09855|CDS|CDS	129.5	8.0	53.5	K	COG2186	Transcriptional regulators
CspSS20241|CDS|CDS	7.5	0.5	49.6	K	COG1316	Transcriptional regulator
Bcap0565|CDS|CDS	15.0	1.0	49.6	K	COG1278	Cold shock proteins
Msmi751667|CDS|CDS	3.8	0.3	49.6	K	COG0864	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain and a metal-binding domain
TS29Fae09412|CDS|CDS	22.0	1.5	48.5	K	COG1309	Transcriptional regulator
Msmi741382|CDS|CDS	16.7	1.2	47.2	K	COG1396	Predicted transcriptional regulators
TS29Bac02294|CDS|CDS	4.7	0.3	46.3	K	COG2183	Transcriptional accessory protein
TS29Bac10393|CDS|CDS	14.0	1.0	46.3	K	COG1396	Predicted transcriptional regulators
Pmer2306|CDS|CDS	13.5	1.0	44.6	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bxyl2502|CDS|CDS	6.6	0.5	43.9	K	COG0195	Transcription elongation factor
Dfor2714|CDS|CDS	26.0	2.0	43.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS29Rum04536|CDS|CDS	6.5	0.5	43.0	K	COG1278	Cold shock proteins
TS28Ali2350|CDS|CDS	85.0	7.0	40.2	K	COG1278	Cold shock proteins
Bdor4350|CDS|CDS	23.5	2.0	38.9	K	COG0250	Transcription antiterminator
Bxyl1906|CDS|CDS	5.7	0.5	37.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
BactD14212|CDS|CDS	5.7	0.5	37.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bxyl1519|CDS|CDS	3.8	0.3	37.2	K	COG0782	Transcription elongation factor
BactD11187|CDS|CDS	3.8	0.3	37.2	K	COG0782	Transcription elongation factor
Dfor0047|CDS|CDS	11.0	1.0	36.4	K	COG1309	Transcriptional regulator
TS28Rum03626|CDS|CDS	11.0	1.0	36.4	K	COG1278	Cold shock proteins
DpigATC0064|CDS|CDS	5.5	0.5	36.4	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
Bste1692|CDS|CDS	31.0	3.0	34.2	K	COG0782	Transcription elongation factor
TS28Bac5364|CDS|CDS	36.0	3.5	34.0	K	COG0557	Exoribonuclease R
Msmi751676|CDS|CDS	2.5	0.3	33.1	K	COG1813	Predicted transcription factor, homolog of eukaryotic MBF1
Msmi740181|CDS|CDS	2.5	0.3	33.1	K	COG1813	Predicted transcription factor, homolog of eukaryotic MBF1
TS29Clo4552|CDS|CDS	10.0	1.0	33.1	K	COG1475	Predicted transcriptional regulators
TS29Fae10006|CDS|CDS	4.5	0.5	29.8	K	COG1316	Transcriptional regulator
Cnex0068|CDS|CDS	9.0	1.0	29.8	K	COG1158	Transcription termination factor
Svar1456|CDS|CDS	8.7	1.0	28.7	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS29Fae08744|CDS|CDS	8.5	1.0	28.1	K	COG1316	Transcriptional regulator
Ccom0288|CDS|CDS	8.2	1.0	27.0	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
Eeli1311|CDS|CDS	8.0	1.0	26.5	K	COG2740	Predicted nucleic-acid-binding protein implicated in transcription termination
Cnex2020|CDS|CDS	8.0	1.0	26.5	K	COG1309	Transcriptional regulator
TS29Bac03509|CDS|CDS	9.8	1.3	24.2	K	COG0782	Transcription elongation factor
Ehal0174|CDS|CDS	14.5	2.0	24.0	K	COG2002	Regulators of stationary/sporulation gene expression
Begg3122|CDS|CDS	14.5	2.0	24.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
ShigspD90635|CDS|CDS	7.2	1.0	23.7	K	COG2183	Transcriptional accessory protein
TS29Fae01223|CDS|CDS	3.5	0.5	23.1	K	COG1609	Transcriptional regulators
Bcap0224|CDS|CDS	14.0	2.0	23.1	K	COG1508	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
TS28Fae01560|CDS|CDS	7.0	1.0	23.1	K	COG0250	Transcription antiterminator
Aput0026|CDS|CDS	7.0	1.0	23.1	K	COG0195	Transcription elongation factor
Bdor3259|CDS|CDS	13.7	2.0	22.6	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Pmer0927|CDS|CDS	13.0	2.0	21.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bste2068|CDS|CDS	50.7	8.0	21.0	K	COG0195	Transcription elongation factor
Bdor1383|CDS|CDS	36.5	6.0	20.1	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bdor4316|CDS|CDS	24.3	4.0	20.1	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
BactD12306|CDS|CDS	3.0	0.5	19.8	K	COG2207	AraC-type DNA-binding domain-containing proteins
Bxyl4009|CDS|CDS	3.0	0.5	19.8	K	COG2207	AraC-type DNA-binding domain-containing proteins
Eeli0895|CDS|CDS	12.0	2.0	19.8	K	COG0789	Predicted transcriptional regulators

Msmi751607|CDS|CDS	7.4	1.3	19.4	K	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiation factor TFIIB
Msmi740826|CDS|CDS	5.8	1.0	19.0	K	COG4008	Predicted metal-binding transcription factor
Msmi750859|CDS|CDS	5.8	1.0	19.0	K	COG4008	Predicted metal-binding transcription factor
TS28Met0214|CDS|CDS	5.8	1.0	19.0	K	COG4008	Predicted metal-binding transcription factor
TS28Par1035|CDS|CDS	23.0	4.0	19.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS29Bac05314|CDS|CDS	24.7	4.3	18.8	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
TS28Ali2059|CDS|CDS	51.0	9.0	18.7	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS29Bac08379|CDS|CDS	5.7	1.0	18.7	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
ShigspD90021|CDS|CDS	16.0	2.8	18.7	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
Bdor3071|CDS|CDS	11.0	2.0	18.2	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
TS28Fae17761|CDS|CDS	5.5	1.0	18.2	K	COG2740	Predicted nucleic-acid-binding protein implicated in transcription termination
TS28Fae12290|CDS|CDS	5.5	1.0	18.2	K	COG1191	DNA-directed RNA polymerase specialized sigma subunit
TS28Ali1895|CDS|CDS	27.0	5.0	17.9	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
BactD22269|CDS|CDS	2.6	0.5	17.5	K	COG0195	Transcription elongation factor
TS28Bac6888|CDS|CDS	10.5	2.0	17.4	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS29Fae01904|CDS|CDS	2.5	0.5	16.5	K	COG1609	Transcriptional regulators
PRABACTJOHN2766|CDS|CDS	5.0	1.0	16.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bste1843|CDS|CDS	5.0	1.0	16.5	K	COG1522	Transcriptional regulators
Msmi741137|CDS|CDS	2.5	0.5	16.5	K	COG1497	Predicted transcriptional regulator
Rgna0821|CDS|CDS	5.0	1.0	16.5	K	COG1475	Predicted transcriptional regulators
Robe3022|CDS|CDS	3.3	0.7	16.5	K	COG1396	Predicted transcriptional regulators
TS29Rum09285|CDS|CDS	3.3	0.7	16.5	K	COG1396	Predicted transcriptional regulators
TS28Rum03046|CDS|CDS	3.3	0.7	16.5	K	COG1396	Predicted transcriptional regulators
Rlac0479|CDS|CDS	10.0	2.0	16.5	K	COG1309	Transcriptional regulator
Bdor3909|CDS|CDS	10.0	2.0	16.5	K	COG0454	Histone acetyltransferase HPA2 and related acetyltransferases
Acol2321|CDS|CDS	5.0	1.0	16.5	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS28Fae15750|CDS|CDS	54.0	11.0	16.2	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Ali0056|CDS|CDS	116.0	24.0	16.0	K	COG0195	Transcription elongation factor
Bdor1564|CDS|CDS	19.0	4.0	15.7	K	COG0571	dsRNA-specific ribonuclease
Robe0357|CDS|CDS	1.5	0.3	14.9	K	COG0557	Exoribonuclease R
Pmer3286|CDS|CDS	13.3	3.0	14.7	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bdor3869|CDS|CDS	28.0	6.3	14.6	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
Bste1880|CDS|CDS	42.0	9.5	14.6	K	COG0557	Exoribonuclease R
Rtor1812|CDS|CDS	6.5	1.5	14.3	K	COG1278	Cold shock proteins
Eeli2015|CDS|CDS	17.0	4.0	14.1	K	COG1609	Transcriptional regulators
Bste2311|CDS|CDS	16.9	4.0	14.0	K	COG0250	Transcription antiterminator
TS28Bac0277|CDS|CDS	24.7	5.8	14.0	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
Msmi750801|CDS|CDS	1.4	0.3	13.9	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Col0260|CDS|CDS	21.0	5.0	13.9	K	COG1329	Transcriptional regulators, similar to M. xanthus CarD
Bryfor4357|CDS|CDS	8.3	2.0	13.6	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
Cbol4254|CDS|CDS	4.0	1.0	13.2	K	COG4465	Pleiotropic transcriptional repressor
Bcap1353|CDS|CDS	8.0	2.0	13.2	K	COG2002	Regulators of stationary/sporulation gene expression
Bdor0465|CDS|CDS	16.0	4.0	13.2	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Pmer2898|CDS|CDS	4.0	1.0	13.2	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Rum07864|CDS|CDS	8.0	2.0	13.2	K	COG1475	Predicted transcriptional regulators
TS28Met1495|CDS|CDS	16.7	4.2	13.2	K	COG1396	Predicted transcriptional regulators
TS28Rum05858|CDS|CDS	2.0	0.5	13.2	K	COG1327	Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone domains
Bdor1990|CDS|CDS	45.8	11.5	13.2	K	COG0195	Transcription elongation factor
Bdor1066|CDS|CDS	21.5	5.5	12.9	K	COG1396	Predicted transcriptional regulators
TS29Bac07467|CDS|CDS	9.6	2.5	12.7	K	COG0195	Transcription elongation factor
TS29Bac00273|CDS|CDS	7.5	2.0	12.4	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Csym0386|CDS|CDS	13.0	3.5	12.3	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS28RumUnc1063|CDS|CDS	11.0	3.0	12.1	K	COG2002	Regulators of stationary/sporulation gene expression
TS29Bac11640|CDS|CDS	7.3	2.0	12.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bsp1160241|CDS|CDS	24.7	6.8	11.9	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
Rtor0295|CDS|CDS	9.0	2.5	11.9	K	COG0250	Transcription antiterminator
TS28Rum08196|CDS|CDS	9.0	2.5	11.9	K	COG0250	Transcription antiterminator
Cnex0769|CDS|CDS	9.0	2.5	11.9	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS29Bac00071|CDS|CDS	6.5	1.8	11.7	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Pmer1341|CDS|CDS	14.0	4.0	11.6	K	COG2186	Transcriptional regulators
TS29Rum03472|CDS|CDS	7.0	2.0	11.6	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS29Bac02103|CDS|CDS	3.5	1.0	11.6	K	COG1521	Putative transcriptional regulator, homolog of Bvg accessory factor
TS29Rum01474|CDS|CDS	7.0	2.0	11.6	K	COG0454	Histone acetyltransferase HPA2 and related acetyltransferases
PRABACTJOHN3549|CDS|CDS	3.5	1.0	11.6	K	COG0250	Transcription antiterminator

TS28Fae01245|CDS|CDS	31.3	9.0	11.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Fae16097|CDS|CDS	34.0	10.0	11.2	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Ali0401|CDS|CDS	47.0	14.0	11.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Fae18996|CDS|CDS	23.3	7.0	11.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bdor2598|CDS|CDS	23.5	7.5	10.4	K	COG2207	AraC-type DNA-binding domain-containing proteins
Msmi740269|CDS|CDS	4.2	1.3	10.3	K	COG0250	Transcription antiterminator
Msmi751411|CDS|CDS	4.2	1.3	10.3	K	COG0250	Transcription antiterminator
TS28Met1812|CDS|CDS	4.2	1.3	10.3	K	COG0250	Transcription antiterminator
TS28Clo01324|CDS|CDS	5.0	180.0	0.1	K	COG1475	Predicted transcriptional regulators
Csci3170|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
Rgna3452|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
Dlon0492|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
Bhan1176|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
Robe2629|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
Edol0287|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
Clep2040|CDS|CDS	0.1	3.3	0.1	K	COG1475	Predicted transcriptional regulators
TS28Rum14530|CDS|CDS	1.3	49.7	0.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Clo01665|CDS|CDS	1.0	38.0	0.1	K	COG0640	Predicted transcriptional regulators
Cnex1994|CDS|CDS	0.1	3.5	0.1	K	COG1475	Predicted transcriptional regulators
Acac2279|CDS|CDS	0.1	3.5	0.1	K	COG1475	Predicted transcriptional regulators
Buni3361|CDS|CDS	0.2	6.5	0.1	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
Bdor2070|CDS|CDS	0.3	13.0	0.1	K	COG1508	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
TS28Rum14083|CDS|CDS	3.0	117.7	0.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Eub4980|CDS|CDS	1.0	39.3	0.1	K	COG0846	NAD-dependent protein deacetylases, SIR2 family
TS28Clo04900|CDS|CDS	0.5	20.0	0.1	K	COG1508	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
TS29Rum11457|CDS|CDS	1.0	42.0	0.1	K	COG2909	ATP-dependent transcriptional regulator
CspSS21223|CDS|CDS	1.0	43.0	0.1	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
Buni3486|CDS|CDS	0.2	7.3	0.1	K	COG1158	Transcription termination factor
TS28Bac0626|CDS|CDS	0.2	7.3	0.1	K	COG1158	Transcription termination factor
TS28Eub0737|CDS|CDS	1.5	67.5	0.1	K	COG1475	Predicted transcriptional regulators
TS28Clo01364|CDS|CDS	1.0	45.0	0.1	K	COG1278	Cold shock proteins
TS28Fae20871|CDS|CDS	1.9	90.0	0.1	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS28Eub0252|CDS|CDS	1.0	48.0	0.1	K	COG2932	Predicted transcriptional regulator
TS28Rum00876|CDS|CDS	1.5	77.8	0.1	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
Svar0544|CDS|CDS	0.5	26.0	0.1	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS28Clo01682|CDS|CDS	4.0	213.0	0.1	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
TS29Fae00048|CDS|CDS	0.5	27.5	0.1	K	COG1475	Predicted transcriptional regulators
TS28Fae18142|CDS|CDS	0.5	27.5	0.1	K	COG1475	Predicted transcriptional regulators
TS28Bif0033|CDS|CDS	0.5	28.5	0.1	K	COG1609	Transcriptional regulators
TS29Fae02482|CDS|CDS	0.3	20.0	0.1	K	COG0571	dsRNA-specific ribonuclease
TS29Eub1018|CDS|CDS	0.5	32.0	0.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
Dlon1164|CDS|CDS	1.0	65.0	0.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Fae21885|CDS|CDS	0.5	33.0	0.1	K	COG1475	Predicted transcriptional regulators
TS28Clo01311|CDS|CDS	1.0	68.0	0.0	K	COG4903	Genetic competence transcription factor
TS29Rum00333|CDS|CDS	0.5	37.5	0.0	K	COG2186	Transcriptional regulators
TS28Fae20342|CDS|CDS	1.0	75.0	0.0	K	COG0557	Exoribonuclease R
TS28Clo01295|CDS|CDS	1.0	90.0	0.0	K	COG2002	Regulators of stationary/sporulation gene expression
TS28Bac5730|CDS|CDS	0.3	31.0	0.0	K	COG1508	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
TS28Clo00678|CDS|CDS	2.0	200.0	0.0	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
TS28Clo01326|CDS|CDS	1.0	103.0	0.0	K	COG1475	Predicted transcriptional regulators
TS28Fae01168|CDS|CDS	0.3	36.0	0.0	K	COG0571	dsRNA-specific ribonuclease
TS28Clo01450|CDS|CDS	1.0	137.0	0.0	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS28Clo01633|CDS|CDS	1.0	166.0	0.0	K	COG1396	Predicted transcriptional regulators
TS29Fae06507|CDS|CDS	0.5	111.5	0.0	K	COG1475	Predicted transcriptional regulators
Rbro0292|CDS|CDS	0.5	116.5	0.0	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Clo01205|CDS|CDS	3.0	116.0	0.1	K|B	COG1242|COG1243	Predicted Fe-S oxidoreductase|Histone acetyltransferase
Dlon1710|CDS|CDS	2,092.5	2.0	3,459.9	K|G	COG1940	Transcriptional regulator/sugar kinase
Robe3270|CDS|CDS	11.0	0.5	72.8	K|G	COG1349	Transcriptional regulators of sugar metabolism
Bdor0620|CDS|CDS	64.0	5.0	42.3	K|G	COG1940	Transcriptional regulator/sugar kinase
Bdor0319|CDS|CDS	32.0	3.0	35.3	K|G	COG1940	Transcriptional regulator/sugar kinase
Acol3388|CDS|CDS	10.0	1.0	33.1	K|G	COG1940	Transcriptional regulator/sugar kinase
Pmer1132|CDS|CDS	31.3	5.0	20.7	K|G	COG1940	Transcriptional regulator/sugar kinase
PRABACTJOHN3582|CDS|CDS	3.8	1.0	12.4	K|G	COG1940	Transcriptional regulator/sugar kinase
BactD20285|CDS|CDS	6.5	2.0	10.7	K|G	COG1940	Transcriptional regulator/sugar kinase
Bova1142|CDS|CDS	6.5	2.0	10.7	K|G	COG1940	Transcriptional regulator/sugar kinase
Msmi741028|CDS|CDS	9.8	1.0	32.2	K|H	COG0340|COG1654	Biotin-(acetyl-CoA carboxylase) ligase|Biotin operon repressor
Msmi750652|CDS|CDS	10.3	2.0	16.9	K|H	COG0340|COG1654	Biotin-(acetyl-CoA carboxylase) ligase|Biotin operon repressor
TS29Rum11753|CDS|CDS	1.0	39.0	0.1	K|H	COG0340|COG1654	Biotin-(acetyl-CoA carboxylase) ligase|Biotin operon repressor
TS28Fae16525|CDS|CDS	1.0	42.0	0.1	K|H	COG0340|COG1654	Biotin-(acetyl-CoA carboxylase) ligase|Biotin operon repressor
TS28Fae14495|CDS|CDS	1.0	105.0	0.0	K|J|L	COG0513	Superfamily II DNA and RNA helicases
TS28Eub7645|CDS|CDS	0.5	104.0	0.0	K|J|L	COG0513	Superfamily II DNA and RNA helicases
TS29Fae03658|CDS|CDS	3.5	0.3	34.7	K|L	COG1200	RecG-like helicase
ShigspD91497|CDS|CDS	10.0	1.0	33.1	K|L	COG0553	Superfamily II DNA/RNA helicases, SNF2 family
Ccom0364|CDS|CDS	7.0	1.0	23.1	K|L	COG4646	DNA methylase
Rbro0308|CDS|CDS	2.0	0.3	19.8	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
BactD14152|CDS|CDS	7.0	1.5	15.4	K|L	COG0553|COG4279	Superfamily II DNA/RNA helicases, SNF2 family|Uncharacterized conserved protein
TS28Fae20392|CDS|CDS	4.5	151.0	0.1	K|L	COG0587|COG0847|COG2176|COG1199	DNA polymerase III, alpha subunit|DNA polymerase III, epsilon subunit and related 3'-5' exonucleases|DNA polymerase III, alpha subunit (gram-positive type)|Rad3-related DNA helicases
TS28Fae14347|CDS|CDS	2.2	73.0	0.1	K|L	COG4646	DNA methylase
Buni0472|CDS|CDS	0.5	17.5	0.1	K|L	COG4646	DNA methylase

Ccom0363|CDS|CDS	2.5	94.8	0.1	K|L	COG4646	DNA methylase
FpraM2120225|CDS|CDS	4.7	180.3	0.1	K|L	COG4646	DNA methylase
TS29Rum19618|CDS|CDS	0.5	19.5	0.1	K|L	COG4646	DNA methylase
TS28Fae13120|CDS|CDS	1.0	39.0	0.1	K|L	COG1200	RecG-like helicase
Bste0889|CDS|CDS	0.5	21.7	0.1	K|L	COG4646	DNA methylase
TS28Fae22501|CDS|CDS	1.3	54.5	0.1	K|L	COG4646	DNA methylase
TS28Fae18375|CDS|CDS	1.7	70.5	0.1	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
Bfra31120117|CDS|CDS	0.5	24.0	0.1	K|L	COG4646	DNA methylase
TS29Dor2220|CDS|CDS	3.5	162.0	0.1	K|L	COG2176|COG1199	DNA polymerase III, alpha subunit (gram-positive type)|Rad3-related DNA helicases
Rtor1774|CDS|CDS	0.5	24.5	0.1	K|L	COG0847|COG2176|COG0587|COG1199	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases|DNA polymerase III, alpha subunit (gram-positive type)|DNA polymerase III, alpha subunit|Rad3-related DNA helicases
TS28Fae22425|CDS|CDS	3.0	151.5	0.1	K|L	COG4646	DNA methylase
TS28Clo00926|CDS|CDS	13.0	671.0	0.1	K|L	COG0847|COG2176|COG1199	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases|DNA polymerase III, alpha subunit (gram-positive type)|Rad3-related DNA helicases
TS29RumUnc1438|CDS|CDS	6.0	313.0	0.1	K|L	COG4646|COG0249	DNA methylase|Mismatch repair ATPase (MutS family)
TS28Rum15982|CDS|CDS	1.5	79.5	0.1	K|L	COG0587|COG0847|COG2176|COG1199	DNA polymerase III, alpha subunit|DNA polymerase III, epsilon subunit and related 3'-5' exonucleases|DNA polymerase III, alpha subunit (gram-positive type)|Rad3-related DNA helicases
TS28LacUnc460|CDS|CDS	1.0	53.5	0.1	K|L	COG4646	DNA methylase
TS29Fae06227|CDS|CDS	2.3	142.5	0.1	K|L	COG4646	DNA methylase
Bsp1160234|CDS|CDS	0.5	35.0	0.1	K|L	COG4646	DNA methylase
TS29Fae04253|CDS|CDS	1.0	70.0	0.0	K|L	COG4646	DNA methylase
TS28Fae10662|CDS|CDS	0.5	36.5	0.0	K|L	COG4646	DNA methylase
CspM6211234|CDS|CDS	0.5	36.5	0.0	K|L	COG4646	DNA methylase
TS28Eub8475|CDS|CDS	2.0	162.3	0.0	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
TS29Rum11602|CDS|CDS	1.0	85.0	0.0	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
TS28Eub6362|CDS|CDS	2.0	192.5	0.0	K|L	COG4646	DNA methylase
TS29Fae06228|CDS|CDS	2.0	227.0	0.0	K|L	COG4646	DNA methylase
TS28Clo10619|CDS|CDS	1.0	163.5	0.0	K|L	COG4646	DNA methylase
TS28Dor2259|CDS|CDS	5.0	1,022.5	0.0	K|L	COG4646	DNA methylase
TS28Fae14355|CDS|CDS	0.5	114.5	0.0	K|L	COG0553	Superfamily II DNA/RNA helicases, SNF2 family
TS28Clo01001|CDS|CDS	1.0	278.0	0.0	K|L	COG1200	RecG-like helicase
TS29Rum05409|CDS|CDS	3.8	0.5	25.4	K|L|T	COG0515|COG2815	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria
TS29Rum16622|CDS|CDS	2.0	83.0	0.1	K|L|T	COG0515|COG2815|COG5616	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Predicted integral membrane protein
TS28Fae13881|CDS|CDS	0.5	25.5	0.1	K|L|T	COG0515|COG2815|COG0631|COG3899|COG5635	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Serine/threonine protein phosphatase|Predicted ATPase|Predicted NTPase (NACHT family)
TS28Bac4871|CDS|CDS	0.3	15.5	0.1	K|L|V	COG4096|COG3886|COG1061	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Predicted HKD family nuclease|DNA or RNA helicases of superfamily II
TS29Bac09646|CDS|CDS	0.3	19.0	0.1	K|L|V	COG4096|COG3886|COG1061|COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Predicted HKD family nuclease|DNA or RNA helicases of superfamily II|Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
Cspi1824|CDS|CDS	10.0	1.0	33.1	K|M|G	COG4464|COG1316	Capsular polysaccharide biosynthesis protein|Transcriptional regulator
Msmi750253|CDS|CDS	6.0	0.3	79.4	K|O	COG0378	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase
Msmi741460|CDS|CDS	8.3	1.3	22.0	K|O	COG0378	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase
Pmer3592|CDS|CDS	4.5	1.0	14.9	K|O	COG0378	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase
Msmi750482|CDS|CDS	1.3	0.3	12.4	K|Q	COG0500|COG0789	SAM-dependent methyltransferases|Predicted transcriptional regulators
TS29Bac03068|CDS|CDS	54.0	2.0	89.3	K|T	COG3279	Response regulator of the LytR/AlgR family
TS28Rum11325|CDS|CDS	117.0	7.0	55.3	K|T	COG0745|COG0784|COG3706|COG3707	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|FOG: CheY-like receiver|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulator with putative antiterminator output domain
TS29Eub1244|CDS|CDS	3.7	0.3	36.4	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Fae10112|CDS|CDS	21.0	2.0	34.7	K|T	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
TS29Rum01745|CDS|CDS	8.0	1.0	26.5	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Rum04145|CDS|CDS	3.7	0.5	24.3	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS29Met0650|CDS|CDS	5.3	0.9	18.9	K|T	COG0517|COG0589|COG1994|COG2524|COG3448	FOG: CBS domain|Universal stress protein UspA and related nucleotide-binding proteins|Zn-dependent proteases|Predicted transcriptional regulator, contains C-terminal CBS domains|CBS-domain-containing membrane protein
TS28Clo05696|CDS|CDS	33.0	7.0	15.6	K|T	COG1974	SOS-response transcriptional repressors (RecA-mediated autopeptidases)
TS29Bac03994|CDS|CDS	3.1	0.8	13.7	K|T	COG0642|COG5002|COG2202|COG2770|COG0784|COG3614|COG2203|COG3437|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Osmosensitive K+ channel histidine kinase

TS29Fae08798|CDS|CDS	1.3	0.3	13.2	K|T	COG2770|COG4252|COG3437|COG2206	FOG: HAMP domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|HD-GYP domain
TS29Rum16440|CDS|CDS	4.0	1.0	13.2	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Bac08350|CDS|CDS	8.3	2.3	11.8	K|T	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
TS29Fae07089|CDS|CDS	5.0	1.5	11.0	K|T	COG2770|COG3437|COG4936|COG2206	FOG: HAMP domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted sensor domain|HD-GYP domain
TS28Eub6152|CDS|CDS	3.0	104.0	0.1	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS29Rum16904|CDS|CDS	2.0	70.0	0.1	K|T	COG0642|COG0745|COG4753|COG2207|COG2204|COG0784|COG3279|COG4936|COG3706|COG2197|COG2208|COG3707	Signal transduction histidine kinase|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|FOG: CheY-like receiver|Response regulator of the LytR/AlgR family|Predicted sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Serine phosphatase RsbU, regulator of sigma subunit|Response regulator with putative antiterminator output domain
TS29Rum17065|CDS|CDS	1.0	37.5	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS28Clo01606|CDS|CDS	3.0	115.0	0.1	K|T	COG0789|COG0631	Predicted transcriptional regulators|Serine/threonine protein phosphatase
TS28Fae16821|CDS|CDS	3.0	116.0	0.1	K|T	COG0642|COG2202|COG3452|COG0784|COG3614|COG2198|COG2203|COG3300|COG3437|COG5278|COG5001	Signal transduction histidine kinase|FOG: PAS/PAC domain|Predicted periplasmic ligand-binding sensor domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|FOG: HPt domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain
TS28Dor2810|CDS|CDS	0.3	10.0	0.1	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Rum16217|CDS|CDS	1.0	41.0	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS28Rum13359|CDS|CDS	1.0	42.0	0.1	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS28Col0835|CDS|CDS	1.0	46.0	0.1	K|T	COG2770|COG4252|COG3437|COG2206	FOG: HAMP domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|HD-GYP domain
TS28Rum02266|CDS|CDS	3.0	139.0	0.1	K|T	COG0642|COG3437|COG4251	Signal transduction histidine kinase|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)
TS28Fae21178|CDS|CDS	1.0	46.5	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS28Eub8874|CDS|CDS	0.5	23.5	0.1	K|T	COG3279	Response regulator of the LytR/AlgR family
TS29Fae06932|CDS|CDS	0.5	25.5	0.1	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS29Rum17051|CDS|CDS	1.0	54.0	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS28Fae21013|CDS|CDS	0.5	37.0	0.0	K|T	COG2208	Serine phosphatase RsbU, regulator of sigma subunit
TS28Fae10546|CDS|CDS	0.5	39.0	0.0	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS28Eub5717|CDS|CDS	0.5	50.0	0.0	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Rum16556|CDS|CDS	0.3	33.0	0.0	K|T	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
TS28Fae17711|CDS|CDS	0.5	112.5	0.0	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS28Fae00886|CDS|CDS	250.0	6.0	137.8	L	COG3747	Phage terminase, small subunit
Bdor1507|CDS|CDS	40.0	1.0	132.3	L	COG0776	Bacterial nucleoid DNA-binding protein
Bcac3586|CDS|CDS	7.7	0.2	127.0	L	COG3666	Transposase and inactivated derivatives
Bcac1263|CDS|CDS	7.7	0.2	127.0	L	COG3666	Transposase and inactivated derivatives
TS29Rum15354|CDS|CDS	15.0	0.5	99.2	L	COG3077	DNA-damage-inducible protein J
TS29Bac08102|CDS|CDS	23.0	1.0	76.1	L	COG0776	Bacterial nucleoid DNA-binding protein
ShigspD91957|CDS|CDS	7.5	0.5	49.6	L	COG1330	Exonuclease V gamma subunit
TS29Bac09000|CDS|CDS	14.0	1.0	46.3	L	COG0497	ATPase involved in DNA repair
Msmi741450|CDS|CDS	6.7	0.5	44.1	L	COG0535|COG0084	Predicted Fe-S oxidoreductases|Mg-dependent DNase
TS28Rum15890|CDS|CDS	6.5	0.5	43.0	L	COG0629	Single-stranded DNA-binding protein
TS29Fae04135|CDS|CDS	12.5	1.0	41.3	L	COG0776	Bacterial nucleoid DNA-binding protein
Bdor4354|CDS|CDS	45.5	4.0	37.6	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
Csci0290|CDS|CDS	5.5	0.5	36.4	L	COG0338	Site-specific DNA methylase
Bcat0630|CDS|CDS	2.8	0.3	36.4	L	COG0178	Excinuclease ATPase subunit
TS29Fae09571|CDS|CDS	27.0	2.5	35.7	L	COG3077	DNA-damage-inducible protein J
Svar2615|CDS|CDS	10.3	1.0	34.2	L	COG0863	DNA modification methylase
Bste3093|CDS|CDS	15.2	1.5	33.4	L	COG0608|COG4199	Single-stranded DNA-specific exonuclease|Uncharacterized protein conserved in bacteria
BactD20693|CDS|CDS	5.0	0.5	33.1	L	COG0419	ATPase involved in DNA repair

<table>
<tr><td>CspM6210208|CDS|CDS</td><td>10.0</td><td>1.0</td><td>33.1</td><td>L</td><td>COG0187</td><td>Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit</td></tr>
<tr><td>Msmi750357|CDS|CDS</td><td>3.3</td><td>0.3</td><td>32.2</td><td>L</td><td>COG0582</td><td>Integrase</td></tr>
<tr><td>Pmer0709|CDS|CDS</td><td>4.8</td><td>0.5</td><td>32.0</td><td>L</td><td>COG0629</td><td>Single-stranded DNA-binding protein</td></tr>
<tr><td>ShigspD92095|CDS|CDS</td><td>4.8</td><td>0.5</td><td>32.0</td><td>L</td><td>COG0497</td><td>ATPase involved in DNA repair</td></tr>
<tr><td>TS29Bac11459|CDS|CDS</td><td>19.0</td><td>2.0</td><td>31.4</td><td>L</td><td>COG3677</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>BVU2684|CDS|integrase</td><td>4.7</td><td>0.5</td><td>30.9</td><td>L</td><td>COG4974|COG0582</td><td>Site-specific recombinase XerD|Integrase</td></tr>
<tr><td>Msmi740832|CDS|CDS</td><td>2.3</td><td>0.3</td><td>30.9</td><td>L</td><td>COG0648</td><td>Endonuclease IV</td></tr>
<tr><td>Bcap0408|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>L</td><td>COG0420</td><td>DNA repair exonuclease</td></tr>
<tr><td>Bcap2043|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>L</td><td>COG0389</td><td>Nucleotidyltransferase/DNA polymerase involved in DNA repair</td></tr>
<tr><td>ShigspD90567|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>L</td><td>COG0266</td><td>Formamidopyrimidine-DNA glycosylase</td></tr>
<tr><td>BactD20034|CDS|CDS</td><td>17.2</td><td>2.0</td><td>28.5</td><td>L</td><td>COG4974|COG0582|COG4973</td><td>Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC</td></tr>
<tr><td>TS29Bac07655|CDS|CDS</td><td>8.3</td><td>1.0</td><td>27.6</td><td>L</td><td>COG1092|COG0116</td><td>Predicted SAM-dependent methyltransferases|Predicted N6-adenine-specific DNA methylase</td></tr>
<tr><td>Ehal0472|CDS|CDS</td><td>4.0</td><td>0.5</td><td>26.5</td><td>L</td><td>COG2812|COG0470</td><td>DNA polymerase III, gamma/tau subunits|ATPase involved in DNA replication</td></tr>
<tr><td>Bdor1374|CDS|CDS</td><td>8.0</td><td>1.0</td><td>26.5</td><td>L</td><td>COG0749</td><td>DNA polymerase I - 3'-5' exonuclease and polymerase domains</td></tr>
<tr><td>Cbol2875|CDS|CDS</td><td>8.0</td><td>1.0</td><td>26.5</td><td>L</td><td>COG0497</td><td>ATPase involved in DNA repair</td></tr>
<tr><td>TS29Bac09004|CDS|CDS</td><td>15.3</td><td>2.0</td><td>25.3</td><td>L</td><td>COG0592</td><td>DNA polymerase sliding clamp subunit (PCNA homolog)</td></tr>
<tr><td>Pmer0706|CDS|CDS</td><td>7.5</td><td>1.0</td><td>24.8</td><td>L</td><td>COG0776</td><td>Bacterial nucleoid DNA-binding protein</td></tr>
<tr><td>Bdor2037|CDS|CDS</td><td>104.0</td><td>14.0</td><td>24.6</td><td>L</td><td>COG0187</td><td>Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit</td></tr>
<tr><td>Bste1695|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste1631|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste2396|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste2529|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste2197|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste0976|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste1975|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste3032|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste2904|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Bste2982|CDS|CDS</td><td>0.6</td><td>0.1</td><td>23.9</td><td>L</td><td>COG3666</td><td>Transposase and inactivated derivatives</td></tr>
<tr><td>Msmi751226|CDS|CDS</td><td>7.2</td><td>1.0</td><td>23.8</td><td>L</td><td>COG1599</td><td>Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins</td></tr>
<tr><td>Msmi740029|CDS|CDS</td><td>1.8</td><td>0.3</td><td>23.1</td><td>L</td><td>COG1372|COG1241</td><td>Intein/homing endonuclease|Predicted ATPase involved in replication control, Cdc46/Mcm family</td></tr>
<tr><td>TS28Fae01135|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>L</td><td>COG0708</td><td>Exonuclease III</td></tr>
<tr><td>TS29Fae02977|CDS|CDS</td><td>3.5</td><td>0.5</td><td>23.1</td><td>L</td><td>COG0497</td><td>ATPase involved in DNA repair</td></tr>
<tr><td>Pmer1109|CDS|CDS</td><td>54.0</td><td>8.0</td><td>22.3</td><td>L</td><td>COG4974|COG0582|COG4973</td><td>Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC</td></tr>
<tr><td>BactD12360|CDS|CDS</td><td>2.3</td><td>0.3</td><td>22.3</td><td>L</td><td>COG2812|COG0470</td><td>DNA polymerase III, gamma/tau subunits|ATPase involved in DNA replication</td></tr>
<tr><td>Msmi741433|CDS|CDS</td><td>5.5</td><td>0.8</td><td>21.8</td><td>L</td><td>COG1467</td><td>Eukaryotic-type DNA primase, catalytic (small) subunit</td></tr>
<tr><td>Msmi741346|CDS|CDS</td><td>3.3</td><td>0.5</td><td>21.5</td><td>L</td><td>COG0582</td><td>Integrase</td></tr>
<tr><td>TS29Fae07402|CDS|CDS</td><td>127.0</td><td>20.0</td><td>21.0</td><td>L</td><td>COG0350</td><td>Methylated DNA-protein cysteine methyltransferase</td></tr>
<tr><td>Bova3473|CDS|CDS</td><td>6.3</td><td>1.0</td><td>20.7</td><td>L</td><td>COG0494</td><td>NTP pyrophosphohydrolases including oxidative damage repair enzymes</td></tr>
<tr><td>TS29Bac00690|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>L</td><td>COG4974|COG0582|COG4973</td><td>Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC</td></tr>
<tr><td>TS29Fae04944|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>L</td><td>COG3077</td><td>DNA-damage-inducible protein J</td></tr>
<tr><td>TS29Rum06027|CDS|CDS</td><td>3.0</td><td>0.5</td><td>19.8</td><td>L</td><td>COG1570</td><td>Exonuclease VII, large subunit</td></tr>
<tr><td>TS28CorUnc132|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>L</td><td>COG1484</td><td>DNA replication protein</td></tr>
<tr><td>Acol3943|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>L</td><td>COG0629</td><td>Single-stranded DNA-binding protein</td></tr>
<tr><td>TS29Rum12668|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>L</td><td>COG0358</td><td>DNA primase (bacterial type)</td></tr>
<tr><td>TS28Rum14396|CDS|CDS</td><td>20.0</td><td>3.5</td><td>18.9</td><td>L</td><td>COG3077</td><td>DNA-damage-inducible protein J</td></tr>
<tr><td>TS29Fae05592|CDS|CDS</td><td>5.5</td><td>1.0</td><td>18.2</td><td>L</td><td>COG0608|COG4199</td><td>Single-stranded DNA-specific exonuclease|Uncharacterized protein conserved in bacteria</td></tr>
<tr><td>BactD11046|CDS|CDS</td><td>2.8</td><td>0.5</td><td>18.2</td><td>L</td><td>COG0494</td><td>NTP pyrophosphohydrolases including oxidative damage repair enzymes</td></tr>
<tr><td>Bxyl0125|CDS|CDS</td><td>5.3</td><td>1.0</td><td>17.5</td><td>L</td><td>COG0178</td><td>Excinuclease ATPase subunit</td></tr>
<tr><td>TS29Bac04603|CDS|CDS</td><td>5.3</td><td>1.0</td><td>17.5</td><td>L</td><td>COG0178</td><td>Excinuclease ATPase subunit</td></tr>
<tr><td>Cnex0605|CDS|CDS</td><td>13.0</td><td>2.5</td><td>17.2</td><td>L</td><td>COG1961</td><td>Site-specific recombinases, DNA invertase Pin homologs</td></tr>
<tr><td>Bste1189|CDS|CDS</td><td>51.2</td><td>10.0</td><td>16.9</td><td>L</td><td>COG0188</td><td>Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit</td></tr>
<tr><td>TS29Met0388|CDS|CDS</td><td>6.8</td><td>1.4</td><td>16.7</td><td>L</td><td>COG0592</td><td>DNA polymerase sliding clamp subunit (PCNA homolog)</td></tr>
<tr><td>Bhan1923|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG4974|COG0582|COG4973</td><td>Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC</td></tr>
<tr><td>Bcel3796|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG4974|COG0582</td><td>Site-specific recombinase XerD|Integrase</td></tr>
<tr><td>TS29Bac11452|CDS|CDS</td><td>10.0</td><td>2.0</td><td>16.5</td><td>L</td><td>COG4974</td><td>Site-specific recombinase XerD</td></tr>
<tr><td>CspM6211329|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG3935</td><td>Putative primosome component and related proteins</td></tr>
<tr><td>RintL11139|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG0827</td><td>Adenine-specific DNA methylase</td></tr>
<tr><td>Bdor0651|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG0776</td><td>Bacterial nucleoid DNA-binding protein</td></tr>
<tr><td>Csym1464|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG0749</td><td>DNA polymerase I - 3'-5' exonuclease and polymerase domains</td></tr>
<tr><td>Dfor1535|CDS|CDS</td><td>10.0</td><td>2.0</td><td>16.5</td><td>L</td><td>COG0742</td><td>N6-adenine-specific methylase</td></tr>
<tr><td>Aput2051|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>L</td><td>COG0497</td><td>ATPase involved in DNA repair</td></tr>
<tr><td>TS29Bac09565|CDS|CDS</td><td>30.0</td><td>6.0</td><td>16.5</td><td>L</td><td>COG0322</td><td>Nuclease subunit of the excinuclease complex</td></tr>
<tr><td>ShigspD91897|CDS|CDS</td><td>4.8</td><td>1.0</td><td>16.0</td><td>L</td><td>COG0608|COG4199</td><td>Single-stranded DNA-specific exonuclease|Uncharacterized protein conserved in bacteria</td></tr>
<tr><td>Msmi740449|CDS|CDS</td><td>7.2</td><td>1.5</td><td>15.8</td><td>L</td><td>COG1599</td><td>Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins</td></tr>
<tr><td>Bste2315|CDS|CDS</td><td>23.0</td><td>5.0</td><td>15.2</td><td>L</td><td>COG4974|COG0582|COG4973</td><td>Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC</td></tr>
<tr><td>Msmi740106|CDS|CDS</td><td>1.5</td><td>0.3</td><td>14.9</td><td>L</td><td>COG4974|COG0582|COG4973</td><td>Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC</td></tr>
<tr><td>Bple2418|CDS|CDS</td><td>1.1</td><td>0.3</td><td>14.9</td><td>L</td><td>COG4974|COG0582</td><td>Site-specific recombinase XerD|Integrase</td></tr>
<tr><td>Pmer0904|CDS|CDS</td><td>1.1</td><td>0.3</td><td>14.9</td><td>L</td><td>COG4974|COG0582</td><td>Site-specific recombinase XerD|Integrase</td></tr>
<tr><td>TS28Fae02206|CDS|CDS</td><td>13.0</td><td>3.0</td><td>14.3</td><td>L</td><td>COG1573</td><td>Uracil-DNA glycosylase</td></tr>
<tr><td>TS28Dor1424|CDS|CDS</td><td>6.5</td><td>1.5</td><td>14.3</td><td>L</td><td>COG0776</td><td>Bacterial nucleoid DNA-binding protein</td></tr>
<tr><td>Dfor2783|CDS|CDS</td><td>6.5</td><td>1.5</td><td>14.3</td><td>L</td><td>COG0776</td><td>Bacterial nucleoid DNA-binding protein</td></tr>
<tr><td>Csym3370|CDS|CDS</td><td>4.3</td><td>1.0</td><td>14.3</td><td>L</td><td>COG0323</td><td>DNA mismatch repair enzyme (predicted ATPase)</td></tr>
</table>

TS28Fae22057|CDS|CDS	28.0	6.5	14.2	L	COG3077	DNA-damage-inducible protein J
Msmi751024|CDS|CDS	6.8	1.6	14.1	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
TS29Fae08192|CDS|CDS	10.5	2.5	13.9	L	COG3857	ATP-dependent nuclease, subunit B
Cnex3309|CDS|CDS	14.3	3.4	13.8	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
Pmer1472|CDS|CDS	10.3	2.5	13.7	L	COG1466	DNA polymerase III, delta subunit
Msmi741117|CDS|CDS	5.5	1.3	13.6	L	COG0708	Exonuclease III
TS29RumUnc1301|CDS|CDS	119.0	29.0	13.6	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Bste2314|CDS|CDS	4.0	1.0	13.2	L	COG4974	Site-specific recombinase XerD
TS29Fae03430|CDS|CDS	4.0	1.0	13.2	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
BactD21156|CDS|CDS	4.0	1.0	13.2	L	COG0587	DNA polymerase III, alpha subunit
TS29Bac00084|CDS|CDS	2.0	0.5	13.2	L	COG0468	RecA/RadA recombinase
Rgna1549|CDS|CDS	4.0	1.0	13.2	L	COG0419	ATPase involved in DNA repair
Even0310|CDS|CDS	8.0	2.0	13.2	L	COG0249|COG1193	Mismatch repair ATPase (MutS family)|Mismatch repair ATPase (MutS family)
TS29Bac11051|CDS|CDS	4.0	1.0	13.2	L	COG0210	Superfamily I DNA and RNA helicases
Cnex3307|CDS|CDS	9.0	2.3	12.8	L	COG1484	DNA replication protein
Buni0626|CDS|CDS	18.5	5.0	12.2	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
Pmer3066|CDS|CDS	5.5	1.5	12.1	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
Cbol1027|CDS|CDS	3.5	1.0	11.6	L	COG2256	ATPase related to the helicase subunit of the Holliday junction resolvase
TS28Met1205|CDS|CDS	3.5	1.0	11.6	L	COG0258	5'-3' exonuclease (including N-terminal domain of PolI)
TS29Bac01498|CDS|CDS	3.5	1.0	11.6	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Bova0516|CDS|CDS	3.4	1.0	11.3	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS29Fae07925|CDS|CDS	17.0	5.0	11.2	L	COG1484	DNA replication protein
Eeli0593|CDS|CDS	10.0	3.0	11.0	L	COG2256|COG2110	ATPase related to the helicase subunit of the Holliday junction resolvase|Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1
Pmer2081|CDS|CDS	5.0	1.5	11.0	L	COG0608|COG4199	Single-stranded DNA-specific exonuclease|Uncharacterized protein conserved in bacteria
TS29Bac00518|CDS|CDS	3.3	1.0	11.0	L	COG0582	Integrase
Bdor2747|CDS|CDS	6.7	2.0	11.0	L	COG0338	Site-specific DNA methylase
BT4011|CDS|DNA-methyltransferase	6.7	2.0	11.0	L	COG0338	Site-specific DNA methylase
Bple1073|CDS|CDS	7.7	2.3	10.9	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
RintL10085|CDS|CDS	6.7	2.0	10.9	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Bcap2227|CDS|CDS	1.0	0.3	10.7	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Par1582|CDS|CDS	4.8	1.5	10.7	L	COG0629	Single-stranded DNA-binding protein
Buni1462|CDS|CDS	16.0	5.0	10.6	L	COG3436	Transposase and inactivated derivatives
Bdor3575|CDS|CDS	16.0	5.0	10.6	L	COG1573	Uracil-DNA glycosylase
TS28Fae17704|CDS|CDS	38.0	12.0	10.5	L	COG0776	Bacterial nucleoid DNA-binding protein
BactD10040|CDS|CDS	1.5	0.5	10.2	L	COG0514	Superfamily II DNA helicase
CspL20344|CDS|CDS	0.1	3.3	0.1	L	COG0582	Integrase
TS28Bac6344|CDS|CDS	2.0	67.0	0.1	L	COG4644	Transposase and inactivated derivatives, TnpA family
TS28Fae20444|CDS|CDS	5.8	196.5	0.1	L	COG3547	Transposase and inactivated derivatives
TS29Rum16629|CDS|CDS	1.0	34.0	0.1	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase
TS28Bac6624|CDS|CDS	1.0	34.0	0.1	L	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes
TS28Fae08113|CDS|CDS	1.0	34.0	0.1	L	COG0419	ATPase involved in DNA repair
Dlon2223|CDS|CDS	0.5	17.0	0.1	L	COG0249	Mismatch repair ATPase (MutS family)
Eeli1963|CDS|CDS	0.5	17.0	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS28Fae13116|CDS|CDS	1.0	34.0	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
Cmet2531|CDS|CDS	2.0	68.9	0.1	L	COG1484	DNA replication protein
CspM6211929|CDS|CDS	2.0	68.9	0.1	L	COG1484	DNA replication protein
Bsp1160226|CDS|CDS	0.7	23.0	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
CspSS22971|CDS|CDS	1.2	41.4	0.1	L	COG2946	Putative phage replication protein RstA
TS28Fae12128|CDS|CDS	1.0	35.0	0.1	L	COG1961|COG3293	Site-specific recombinases, DNA invertase Pin homologs|Transposase and inactivated derivatives
TS28Clo10670|CDS|CDS	1.0	35.0	0.1	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
Ccom0063|CDS|CDS	1.0	35.3	0.1	L	COG0582	Integrase
Ehal0926|CDS|CDS	1.0	35.3	0.1	L	COG0582	Integrase
TS28Bac0268|CDS|CDS	1.0	35.5	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Bac8358|CDS|CDS	1.0	36.0	0.1	L	COG3649	Uncharacterized protein predicted to be involved in DNA repair
Cbol3944|CDS|CDS	1.0	36.0	0.1	L	COG3344	Retron-type reverse transcriptase
TS28Bac8091|CDS|CDS	0.5	18.0	0.1	L	COG1195	Recombinational DNA repair ATPase (RecF pathway)
Robe2389|CDS|CDS	1.5	54.0	0.1	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
FpraM2121286|CDS|CDS	0.3	12.0	0.1	L	COG0593	ATPase involved in DNA replication initiation
TS28Fae20705|CDS|CDS	1.5	55.0	0.1	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase
TS28Rum15361|CDS|CDS	2.0	73.5	0.1	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS28Fae22092|CDS|CDS	3.0	110.5	0.1	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
Bcap3404|CDS|CDS	2.0	74.0	0.1	L	COG3328	Transposase and inactivated derivatives
TS28Fae20510|CDS|CDS	0.5	19.0	0.1	L	COG0776	Bacterial nucleoid DNA-binding protein
TS28Dor0412|CDS|CDS	0.5	19.0	0.1	L	COG0249	Mismatch repair ATPase (MutS family)
Rlac1490|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Rlac1736|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Rlac1778|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Rlac0850|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Rlac1138|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Rlac1122|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Rlac0941|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
TS28Eub3958|CDS|CDS	0.9	33.7	0.1	L	COG3335	Transposase and inactivated derivatives
Bxyl3533|CDS|CDS	2.5	97.5	0.1	L	COG3666	Transposase and inactivated derivatives

TS28Rum13352|CDS|CDS	1.0	39.0	0.1	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase
Cbol3956|CDS|CDS	1.1	42.8	0.1	L	COG0358	DNA primase (bacterial type)
TS28Clo02235|CDS|CDS	0.5	19.8	0.1	L	COG0675	Transposase and inactivated derivatives
TS28Dor3030|CDS|CDS	0.8	29.9	0.1	L	COG3344	Retron-type reverse transcriptase
TS28Bac8191|CDS|CDS	2.7	109.2	0.1	L	COG1484	DNA replication protein
TS28Clo02127|CDS|CDS	1.0	40.0	0.1	L	COG0675	Transposase and inactivated derivatives
TS28Fae15426|CDS|CDS	1.0	40.0	0.1	L	COG0593	ATPase involved in DNA replication initiation
TS28Clo00872|CDS|CDS	5.0	201.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Fae22378|CDS|CDS	1.5	61.0	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS29RumUnc0317|CDS|CDS	0.7	27.2	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
FpraM2121397|CDS|CDS	10.5	432.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Clo00639|CDS|CDS	3.0	124.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Eub8222|CDS|CDS	1.5	62.0	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS28Clo01309|CDS|CDS	6.0	249.0	0.1	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
TS28Fae20092|CDS|CDS	2.0	83.5	0.1	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
TS29Dor1974|CDS|CDS	0.8	31.4	0.1	L	COG3344	Retron-type reverse transcriptase
TS28Eub6661|CDS|CDS	1.0	42.0	0.1	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
TS29Rum17160|CDS|CDS	1.0	42.5	0.1	L	COG0305	Replicative DNA helicase
TS28Clo00742|CDS|CDS	8.0	343.0	0.1	L	COG0249	Mismatch repair ATPase (MutS family)
TS28Fae22543|CDS|CDS	1.0	43.0	0.1	L	COG3857	ATP-dependent nuclease, subunit B
Dlon1636|CDS|CDS	1.3	58.7	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
FpraM2120693|CDS|CDS	1.3	55.5	0.1	L	COG2189	Adenine specific DNA methylase Mod
TS28Eub5322|CDS|CDS	2.0	88.8	0.1	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS28Col0008|CDS|CDS	1.0	45.0	0.1	L	COG3593	Predicted ATP-dependent endonuclease of the OLD family
TS28Eub8102|CDS|CDS	1.0	45.0	0.1	L	COG2801|COG2963	Transposase and inactivated derivatives|Transposase and inactivated derivatives
TS28Met0340|CDS|CDS	0.3	15.0	0.1	L	COG0116|COG1041	Predicted N6-adenine-specific DNA methylase|Predicted DNA modification methylase
TS28Clo01484|CDS|CDS	4.0	181.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Msmi740925|CDS|CDS	0.3	11.3	0.1	L	COG0551|COG0210|COG1599	Zn-finger domain associated with topoisomerase type I|Superfamily I DNA and RNA helicases|Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins
TS29Rum19567|CDS|CDS	1.0	45.8	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Bif3472|CDS|CDS	1.0	45.8	0.1	L	COG1643	HrpA-like helicases
TS28Dor2622|CDS|CDS	1.3	61.2	0.1	L	COG0582	Integrase
TS28Clo00768|CDS|CDS	2.0	92.0	0.1	L	COG1381	Recombinational DNA repair protein (RecF pathway)
TS28Fae08139|CDS|CDS	1.0	46.0	0.1	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
FpraM2122493|CDS|CDS	0.4	20.7	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Eub8038|CDS|CDS	2.0	93.5	0.1	L	COG0210	Superfamily I DNA and RNA helicases
TS28Clo01016|CDS|CDS	8.0	378.0	0.1	L	COG3886	Predicted HKD family nuclease
Ehal0368|CDS|CDS	2.7	127.5	0.1	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
TS29Fae02067|CDS|CDS	0.5	24.0	0.1	L	COG0497	ATPase involved in DNA repair
Bcap2730|CDS|CDS	1.0	48.5	0.1	L	COG0178	Excinuclease ATPase subunit
TS28Eub4034|CDS|CDS	1.0	49.0	0.1	L	COG3857	ATP-dependent nuclease, subunit B
TS28Eub1506|CDS|CDS	3.0	147.0	0.1	L	COG0556	Helicase subunit of the DNA excision repair complex
TS28Fae19299|CDS|CDS	1.3	61.5	0.1	L	COG2189	Adenine specific DNA methylase Mod
TS29Rum19926|CDS|CDS	1.0	49.5	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS28Rum12508|CDS|CDS	1.5	75.0	0.1	L	COG0587	DNA polymerase III, alpha subunit
TS28Clo00694|CDS|CDS	2.0	100.0	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Fae20680|CDS|CDS	0.5	25.0	0.1	L	COG0210	Superfamily I DNA and RNA helicases
TS28Eub4620|CDS|CDS	1.5	75.5	0.1	L	COG0249	Mismatch repair ATPase (MutS family)
TS29Rum13789|CDS|CDS	1.0	50.5	0.1	L	COG2826	Transposase and inactivated derivatives, IS30 family
Robe3832|CDS|CDS	1.3	65.2	0.1	L	COG2946	Putative phage replication protein RstA
RintL11218|CDS|CDS	1.0	51.0	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS28Bac6549|CDS|CDS	0.3	17.3	0.1	L	COG0305	Replicative DNA helicase
PRABACTJOHN0078|CDS|CDS	1.0	53.0	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS28Clo09295|CDS|CDS	1.0	53.0	0.1	L	COG3857	ATP-dependent nuclease, subunit B
TS28Col0535|CDS|CDS	2.0	106.0	0.1	L	COG3547	Transposase and inactivated derivatives
TS28Clo00674|CDS|CDS	2.0	106.0	0.1	L	COG0266	Formamidopyrimidine-DNA glycosylase
TS28Eub0269|CDS|CDS	0.5	27.0	0.1	L	COG1484	DNA replication protein
TS28Bac0448|CDS|CDS	0.3	18.0	0.1	L	COG0420	DNA repair exonuclease
Bdor0430|CDS|CDS	0.3	18.0	0.1	L	COG0178	Excinuclease ATPase subunit
Ccom2074|CDS|CDS	1.1	59.7	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
RintL10505|CDS|CDS	1.3	68.7	0.1	L	COG0582	Integrase
TS28Clo01306|CDS|CDS	4.0	218.0	0.1	L	COG2812	DNA polymerase III, gamma/tau subunits
Bcap2375|CDS|CDS	0.5	27.5	0.1	L	COG3935	Putative primosome component and related proteins
TS28Eub7196|CDS|CDS	1.0	55.5	0.1	L	COG1573	Uracil-DNA glycosylase
TS28Fae21539|CDS|CDS	1.0	55.8	0.1	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
TS28Clo01332|CDS|CDS	1.0	56.0	0.1	L	COG0629	Single-stranded DNA-binding protein
Bdor0019|CDS|CDS	0.3	19.0	0.1	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
TS28Eub7283|CDS|CDS	1.0	57.0	0.1	L	COG0270	Site-specific DNA methylase
Ccom0035|CDS|CDS	1.0	58.0	0.1	L	COG3547	Transposase and inactivated derivatives
TS29Rum17166|CDS|CDS	0.5	29.0	0.1	L	COG0629	Single-stranded DNA-binding protein
TS28Fae13421|CDS|CDS	0.5	29.0	0.1	L	COG0514	Superfamily II DNA helicase
TS28Fae15421|CDS|CDS	0.5	30.0	0.1	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
TS28Clo01308|CDS|CDS	6.0	367.0	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS28Clo00644|CDS|CDS	4.0	245.0	0.1	L	COG0550|COG0551|COG1754	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|Uncharacterized C-terminal domain of topoisomerase IA
CspSS20175|CDS|CDS	0.1	6.2	0.1	L	COG0582	Integrase

CspM6212150|CDS|CDS	0.1	6.2	0.1	L	COG0582	Integrase
RintL13994|CDS|CDS	1.3	79.5	0.1	L	COG2946	Putative phage replication protein RstA
TS29Rum20070|CDS|CDS	1.0	62.0	0.1	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
Rgna2448|CDS|CDS	1.3	79.2	0.1	L	COG0582	Integrase
TS28Eub8662|CDS|CDS	1.0	63.0	0.1	L	COG1570	Exonuclease VII, large subunit
TS29Fae09550|CDS|CDS	1.5	95.5	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Ccom2343|CDS|CDS	1.0	66.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Dor3157|CDS|CDS	0.5	34.0	0.0	L	COG0178	Excinuclease ATPase subunit
Rlac0724|CDS|CDS	1.3	86.7	0.0	L	COG0582	Integrase
Ebif0586|CDS|CDS	1.3	85.7	0.0	L	COG3344	Retron-type reverse transcriptase
TS29Rum16055|CDS|CDS	1.0	70.0	0.0	L	COG0419	ATPase involved in DNA repair
Hfil2883|CDS|CDS	1.0	73.5	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Eub0075|CDS|CDS	0.7	49.2	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Clo00652|CDS|CDS	3.0	223.0	0.0	L	COG0322	Nuclease subunit of the excinuclease complex
TS28Clo01312|CDS|CDS	2.0	151.0	0.0	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
TS29Rum21113|CDS|CDS	0.5	38.0	0.0	L	COG0535|COG0084	Predicted Fe-S oxidoreductases|Mg-dependent DNase
TS28Eub7056|CDS|CDS	1.0	77.0	0.0	L	COG2826	Transposase and inactivated derivatives, IS30 family
Dfor3100|CDS|CDS	1.8	135.5	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Rum10639|CDS|CDS	0.3	25.8	0.0	L	COG0272	NAD-dependent DNA ligase (contains BRCT domain type II)
TS29Rum11531|CDS|CDS	0.5	39.0	0.0	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
TS28Fae22424|CDS|CDS	1.7	132.0	0.0	L	COG3344	Retron-type reverse transcriptase
TS28Eub7005|CDS|CDS	1.5	119.0	0.0	L	COG0322	Nuclease subunit of the excinuclease complex
CspSS21757|CDS|CDS	1.2	96.2	0.0	L	COG2946	Putative phage replication protein RstA
TS28Clo00673|CDS|CDS	4.0	326.0	0.0	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS28Clo01577|CDS|CDS	3.0	249.0	0.0	L	COG0210	Superfamily I DNA and RNA helicases
TS28Fae22387|CDS|CDS	1.0	84.0	0.0	L	COG3886|COG4889	Predicted HKD family nuclease|Predicted helicase
TS28RumUnc1796|CDS|CDS	1.0	85.5	0.0	L	COG3547	Transposase and inactivated derivatives
TS28Rum15611|CDS|CDS	0.5	43.0	0.0	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Ehal2601|CDS|CDS	4.0	349.0	0.0	L	COG2801|COG2963	Transposase and inactivated derivatives|Transposase and inactivated derivatives
TS28Clo00695|CDS|CDS	2.0	175.0	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Fae15419|CDS|CDS	0.3	23.0	0.0	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
CspL22444|CDS|CDS	1.3	119.5	0.0	L	COG0582	Integrase
TS29Fae10383|CDS|CDS	0.5	47.5	0.0	L	COG3935	Putative primosome component and related proteins
Cnex1410|CDS|CDS	0.3	32.5	0.0	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS28Bac7421|CDS|CDS	0.5	48.8	0.0	L	COG0582	Integrase
Bhan2466|CDS|CDS	0.3	26.2	0.0	L	COG3344	Retron-type reverse transcriptase
Rgna0713|CDS|CDS	0.3	26.2	0.0	L	COG3344	Retron-type reverse transcriptase
Cnex0946|CDS|CDS	0.3	31.2	0.0	L	COG2946	Putative phage replication protein RstA
Bryfor2985|CDS|CDS	0.5	57.5	0.0	L	COG2801|COG3344	Transposase and inactivated derivatives|Retron-type reverse transcriptase
TS28Eub4573|CDS|CDS	0.7	81.0	0.0	L	COG0210|COG1074	Superfamily I DNA and RNA helicases|ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)
TS28Clo00711|CDS|CDS	1.0	122.0	0.0	L	COG1039	Ribonuclease HIII
CspSS21813|CDS|CDS	2.0	249.8	0.0	L	COG2946	Putative phage replication protein RstA
TS28Fae09681|CDS|CDS	0.2	25.0	0.0	L	COG0468	RecA/RadA recombinase
TS28Eub5249|CDS|CDS	0.3	43.3	0.0	L	COG0468	RecA/RadA recombinase
Rgna2452|CDS|CDS	0.8	117.5	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Rum11761|CDS|CDS	1.0	145.0	0.0	L	COG0587	DNA polymerase III, alpha subunit
Rlac0721|CDS|CDS	0.8	121.4	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
CspL22448|CDS|CDS	0.8	121.7	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Rum02257|CDS|CDS	1.0	147.5	0.0	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Ccom0774|CDS|CDS	1.0	149.5	0.0	L	COG3547	Transposase and inactivated derivatives
TS28Clo01600|CDS|CDS	2.0	308.0	0.0	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase
TS28Eub5722|CDS|CDS	1.0	162.0	0.0	L	COG1112	Superfamily I DNA and RNA helicases and helicase subunits
RintL10347|CDS|CDS	0.1	16.4	0.0	L	COG0582	Integrase
Hfil2877|CDS|CDS	0.5	91.3	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Clo01555|CDS|CDS	1.0	210.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Cbol3901|CDS|CDS	0.5	110.5	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS28Rum15759|CDS|CDS	0.3	128.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum14797|CDS|CDS	2.0	0.3	19.8	L|B	COG0550|COG0551|COG5531|COG1754	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling|Uncharacterized C-terminal domain of topoisomerase IA
TS28Par0305|CDS|CDS	8.0	1.5	17.6	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29RumUnc1287|CDS|CDS	1.0	33.3	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Fae13913|CDS|CDS	0.5	19.0	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Csci0096|CDS|CDS	0.2	8.5	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Bint0768|CDS|CDS	0.5	20.3	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling

Even0438|CDS|CDS	3.0	123.5	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Fae15514|CDS|CDS	1.0	50.0	0.1	L|B	COG0550|COG0551|COG5531|COG1754	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling|Uncharacterized C-terminal domain of topoisomerase IA
Bsp1160232|CDS|CDS	0.3	17.0	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Bthe3732593|CDS|CDS	0.5	30.1	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Eub6491|CDS|CDS	1.0	76.0	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Clo10822|CDS|CDS	0.2	16.0	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Rum20503|CDS|CDS	0.5	55.0	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
FpraM2121396|CDS|CDS	0.5	67.5	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Rum16465|CDS|CDS	1.0	147.0	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Rum19622|CDS|CDS	0.9	190.6	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Csci3151|CDS|CDS	0.2	45.2	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Cbol3089|CDS|CDS	0.2	60.2	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Bac8435|CDS|CDS	1.0	55.0	0.1	L|D|Z	COG0419|COG5022|COG1196	ATPase involved in DNA repair|Myosin heavy chain|Chromosome segregation ATPases
Csci1586|CDS|CDS	14.0	1.0	46.3	L|F	COG1372|COG1328|COG0209	Intein/homing endonuclease|Oxygen-sensitive ribonucleoside-triphosphate reductase|Ribonucleotide reductase, alpha subunit
Bryfor3487|CDS|CDS	6.0	1.0	19.8	L|F	COG1372|COG1328	Intein/homing endonuclease|Oxygen-sensitive ribonucleoside-triphosphate reductase
Acol1170|CDS|CDS	5.0	1.0	16.5	L|F	COG1372|COG0209	Intein/homing endonuclease|Ribonucleotide reductase, alpha subunit
Msmi740807|CDS|CDS	5.3	1.3	14.1	L|G	COG1372|COG0574	Intein/homing endonuclease|Phosphoenolpyruvate synthase/pyruvate phosphate dikinase
Begg0139|CDS|CDS	7.0	2.0	11.6	L|I	COG0494|COG1443	NTP pyrophosphohydrolases including oxidative damage repair enzymes|Isopentenyldiphosphate isomerase
Msmi740319|CDS|CDS	2.5	0.3	33.1	L|O	COG1474	Cdc6-related protein, AAA superfamily ATPase
Msmi751365|CDS|CDS	3.2	0.8	14.0	L|O	COG1474	Cdc6-related protein, AAA superfamily ATPase
Robe2649|CDS|CDS	1.6	54.5	0.1	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
FpraM2120213|CDS|CDS	1.1	36.0	0.1	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
FpraM2122491|CDS|CDS	0.4	15.7	0.1	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
TS28Fae16408|CDS|CDS	0.5	29.0	0.1	L|U	COG0758	Predicted Rossmann fold nucleotide-binding protein involved in DNA uptake
CspM6211944|CDS|CDS	2.8	200.2	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
TS28Fae00187|CDS|CDS	0.3	31.0	0.0	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
Rtor1326|CDS|CDS	0.7	103.9	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
Acol2738|CDS|CDS	3.0	530.6	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
Robe2672|CDS|CDS	0.7	124.4	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
Msmi741122|CDS|CDS	3.7	1.0	12.1	L|V	COG3666|COG1131	Transposase and inactivated derivatives|ABC-type multidrug transport system, ATPase component
TS28Rum07177|CDS|CDS	131.5	2.0	217.4	M	COG3764	Sortase (surface protein transpeptidase)
Msmi750501|CDS|CDS	11.3	0.3	149.9	M	COG3475	LPS biosynthesis protein
Msmi741174|CDS|CDS	11.3	0.3	149.9	M	COG3475	LPS biosynthesis protein
Casp3572|CDS|CDS	45.0	1.0	148.8	M	COG1686	D-alanyl-D-alanine carboxypeptidase
Rtor1960|CDS|CDS	131.5	3.0	145.0	M	COG3764	Sortase (surface protein transpeptidase)
Dfor2251|CDS|CDS	40.0	2.0	66.1	M	COG0438	Glycosyltransferase
Msmi741275|CDS|CDS	24.3	1.5	53.5	M	COG1087	UDP-glucose 4-epimerase
Pmer2386|CDS|CDS	13.0	1.0	43.0	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
Msmi741230|CDS|CDS	14.3	1.2	40.6	M	COG1210	UDP-glucose pyrophosphorylase
TS29Bac04981|CDS|CDS	3.0	0.3	39.7	M	COG1089	GDP-D-mannose dehydratase
TS29Fae08403|CDS|CDS	11.5	1.0	38.0	M	COG0791	Cell wall-associated hydrolases (invasion-associated proteins)
Dfor2764|CDS|CDS	11.0	1.0	36.4	M	COG2088	Uncharacterized protein, involved in the regulation of septum location
Bste0130|CDS|CDS	5.5	0.5	36.4	M	COG0845	Membrane-fusion protein
Bfra31123865|CDS|CDS	5.4	0.5	35.5	M	COG3209	Rhs family protein
TS29Fae08028|CDS|CDS	5.0	0.5	33.1	M	COG3757	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
Bxyl4005|CDS|CDS	5.0	0.5	33.1	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Svar0805|CDS|CDS	10.0	1.0	33.1	M	COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis
TS29Fae01172|CDS|CDS	9.5	1.0	31.4	M	COG5434	Endopolygalacturonase

Bdor0862|CDS|CDS	24.5	2.7	30.4	M	COG1087	UDP-glucose 4-epimerase
Msmi750406|CDS|CDS	24.3	2.8	28.3	M	COG1087	UDP-glucose 4-epimerase
TS29Fae05583|CDS|CDS	8.5	1.0	28.1	M	COG0750	Predicted membrane-associated Zn-dependent proteases 1
Bste2165|CDS|CDS	8.5	1.0	28.1	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
Ehal1689|CDS|CDS	4.0	0.5	26.5	M	COG3409|COG1376	Putative peptidoglycan-binding domain-containing protein|Uncharacterized protein conserved in bacteria
BactD21100|CDS|CDS	8.0	1.0	26.5	M	COG1560	Lauroyl/myristoyl acyltransferase
TS28Clo00100|CDS|CDS	4.0	0.5	26.5	M	COG1209	dTDP-glucose pyrophosphorylase
TS29Fae06305|CDS|CDS	4.0	0.5	26.5	M	COG1207	N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)
CspL21787|CDS|CDS	4.0	0.5	26.5	M	COG1087	UDP-glucose 4-epimerase
Pmer0411|CDS|CDS	31.0	4.0	25.6	M	COG2148	Sugar transferases involved in lipopolysaccharide synthesis
Bthe3733491|CDS|CDS	3.8	0.5	25.4	M	COG3209	Rhs family protein
Bxyl0277|CDS|CDS	2.3	0.3	23.1	M	COG1088	dTDP-D-glucose 4,6-dehydratase
BactD11851|CDS|CDS	2.3	0.3	23.1	M	COG1088	dTDP-D-glucose 4,6-dehydratase
BactD23416|CDS|CDS	3.5	0.5	23.1	M	COG0845	Membrane-fusion protein
RintL13032|CDS|CDS	7.0	1.0	23.1	M	COG0739	Membrane proteins related to metalloendopeptidases
TS29Bac06222|CDS|CDS	3.3	0.5	22.0	M	COG5434	Endopolygalacturonase
Bste1969|CDS|CDS	20.0	3.0	22.0	M	COG0682	Prolipoprotein diacylglyceryltransferase
TS28Bac6573|CDS|CDS	9.5	1.5	20.9	M	COG4775	Outer membrane protein/protective antigen OMA87
TS29Bac01090|CDS|CDS	3.2	0.5	20.9	M	COG1388|COG0741	FOG: LysM repeat|Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)
Bxyl3330|CDS|CDS	3.2	0.5	20.9	M	COG0741|COG1388	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|FOG: LysM repeat
TS29Fae06882|CDS|CDS	6.2	1.0	20.4	M	COG0677|COG0381	UDP-N-acetyl-D-mannosaminuronate dehydrogenase|UDP-N-acetylglucosamine 2-epimerase
TS29Bac04166|CDS|CDS	2.0	0.3	19.8	M	COG1004	Predicted UDP-glucose 6-dehydrogenase
Robe0430|CDS|CDS	3.0	0.5	19.8	M	COG1686	D-alanyl-D-alanine carboxypeptidase
Bste1372|CDS|CDS	6.0	1.0	19.8	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS29Bac08440|CDS|CDS	6.0	1.0	19.8	M	COG1089	GDP-D-mannose dehydratase
Dfor1067|CDS|CDS	6.0	1.0	19.8	M	COG0812	UDP-N-acetylmuramate dehydrogenase
TS28Met0797|CDS|CDS	3.0	0.5	19.8	M	COG0463|COG2246	Glycosyltransferases involved in cell wall biogenesis|Predicted membrane protein
Bste3034|CDS|CDS	35.0	6.0	19.3	M	COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
Pmer0881|CDS|CDS	34.0	6.0	18.7	M	COG3206	Uncharacterized protein involved in exopolysaccharide biosynthesis
TS28Rum03384|CDS|CDS	22.0	4.0	18.2	M	COG2088	Uncharacterized protein, involved in the regulation of septum location
Bste1331|CDS|CDS	5.5	1.0	18.2	M	COG0845	Membrane-fusion protein
Bova1358|CDS|CDS	5.5	1.0	18.2	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
Even0846|CDS|CDS	11.0	2.0	18.2	M	COG0769	UDP-N-acetylmuramyl tripeptide synthase
BactD20877|CDS|CDS	5.4	1.0	17.9	M	COG1088	dTDP-D-glucose 4,6-dehydratase
TS28Bac6398|CDS|CDS	80.7	15.0	17.8	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
BactD12310|CDS|CDS	13.0	2.5	17.2	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Hfil1145|CDS|CDS	5.0	1.0	16.5	M	COG1686	D-alanyl-D-alanine carboxypeptidase
CspM6213055|CDS|CDS	5.0	1.0	16.5	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
Bova3023|CDS|CDS	5.0	1.0	16.5	M	COG0438|COG1922	Glycosyltransferase|Teichoic acid biosynthesis proteins
BactD12214|CDS|CDS	3.2	0.7	15.7	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
Pmer0412|CDS|CDS	47.0	10.0	15.5	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Msmi741183|CDS|CDS	12.5	2.7	15.5	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS29Bac01956|CDS|CDS	4.7	1.0	15.4	M	COG0845	Membrane-fusion protein
TS29Bac11615|CDS|CDS	14.0	3.0	15.4	M	COG0438	Glycosyltransferase
TS28Fae16710|CDS|CDS	16.0	3.5	15.1	M	COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes
BactD14207|CDS|CDS	1.5	0.3	14.9	M	COG2173	D-alanyl-D-alanine dipeptidase
Dfor2990|CDS|CDS	9.0	2.0	14.9	M	COG0791|COG3883	Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria
TS28Fae06121|CDS|CDS	9.0	2.0	14.9	M	COG0750	Predicted membrane-associated Zn-dependent proteases 1
TS29Fae08321|CDS|CDS	4.5	1.0	14.9	M	COG0463|COG1887	Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC
TS29Fae03036|CDS|CDS	4.5	1.0	14.9	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
Bxyl1472|CDS|CDS	4.3	1.0	14.3	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Rtor2548|CDS|CDS	8.5	2.0	14.1	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Bxyl2439|CDS|CDS	4.2	1.0	13.8	M	COG0859	ADP-heptose:LPS heptosyltransferase
TS28Bac5602|CDS|CDS	2.0	0.5	13.2	M	COG0463|COG2246	Glycosyltransferases involved in cell wall biogenesis|Predicted membrane protein
TS29Bac05719|CDS|CDS	4.0	1.0	13.2	M	COG4775|COG1752	Outer membrane protein/protective antigen OMA87|Predicted esterase of the alpha-beta hydrolase superfamily
Rbro1588|CDS|CDS	2.0	0.5	13.2	M	COG1686	D-alanyl-D-alanine carboxypeptidase
Bste3161|CDS|CDS	2.0	0.5	13.2	M	COG1519|COG0220	3-deoxy-D-manno-octulosonic-acid transferase|Predicted S-adenosylmethionine-dependent methyltransferase

Bova3828|CDS|CDS	1.0	0.3	13.2	M	COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
Even1780|CDS|CDS	4.0	1.0	13.2	M	COG0860	N-acetylmuramoyl-L-alanine amidase
Bcap0372|CDS|CDS	8.0	2.0	13.2	M	COG0791|COG3883|COG0739|COG2951|COG5412	Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria|Membrane proteins related to metalloendopeptidases|Membrane-bound lytic murein transglycosylase B|Phage-related protein
TS29Fae00292|CDS|CDS	2.0	0.5	13.2	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
Msmi740437|CDS|CDS	1.0	0.3	13.2	M	COG0750	Predicted membrane-associated Zn-dependent proteases 1
Pmer2341|CDS|CDS	8.0	2.0	13.2	M	COG0677	UDP-N-acetyl-D-mannosaminuronate dehydrogenase
Chir1900|CDS|CDS	4.0	1.0	13.2	M	COG0481	Membrane GTPase LepA
Csym0305|CDS|CDS	4.0	1.0	13.2	M	COG0481	Membrane GTPase LepA
TS29Rum06209|CDS|CDS	1.3	0.3	13.2	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Msmi740919|CDS|CDS	3.9	1.0	12.8	M	COG0449|COG2222	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains|Predicted phosphosugar isomerases
Bdor3264|CDS|CDS	38.3	10.0	12.7	M	COG0845	Membrane-fusion protein
Msmi751223|CDS|CDS	3.8	1.0	12.7	M	COG0463|COG1216	Glycosyltransferases involved in cell wall biogenesis|Predicted glycosyltransferases
Msmi750494|CDS|CDS	12.5	3.3	12.4	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS29Bac11368|CDS|CDS	11.0	3.0	12.1	M	COG3049	Penicillin V acylase and related amidases
Dfor0849|CDS|CDS	11.0	3.0	12.1	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
b2477|CDS|lipoprotein	3.5	1.0	11.6	M	COG3317	Uncharacterized lipoprotein
Ceut0547|CDS|CDS	7.0	2.0	11.6	M	COG1898|COG1091	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes|dTDP-4-dehydrorhamnose reductase
Bova3477|CDS|CDS	1.8	0.5	11.6	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS28Fae06929|CDS|CDS	14.0	4.0	11.6	M	COG1087	UDP-glucose 4-epimerase
ShigspD90082|CDS|CDS	3.5	1.0	11.6	M	COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
TS29Ali042|CDS|CDS	3.5	1.0	11.6	M	COG1044	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
TS29Fae07471|CDS|CDS	7.0	2.0	11.6	M	COG0741|COG3757	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
TS29Fae00294|CDS|CDS	3.5	1.0	11.6	M	COG0739|COG3883|COG0791	Membrane proteins related to metalloendopeptidases|Uncharacterized protein conserved in bacteria|Cell wall-associated hydrolases (invasion-associated proteins)
Csym1006|CDS|CDS	7.0	2.0	11.6	M	COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis
TS29Rum08114|CDS|CDS	3.5	1.0	11.6	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Fae12901|CDS|CDS	7.0	2.0	11.6	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Msmi750455|CDS|CDS	14.3	4.2	11.4	M	COG1210	UDP-glucose pyrophosphorylase
TS28Ali0613|CDS|CDS	89.0	26.0	11.3	M	COG1663	Tetraacyldisaccharide-1-P 4'-kinase
Bdor1170|CDS|CDS	25.5	7.5	11.2	M	COG0791|COG0739|COG5412	Cell wall-associated hydrolases (invasion-associated proteins)|Membrane proteins related to metalloendopeptidases|Phage-related protein
TS28Fae06281|CDS|CDS	10.0	3.0	11.0	M	COG4750	CTP:phosphocholine cytidylyltransferase involved in choline phosphorylation for cell surface LPS epitopes
Bdor1096|CDS|CDS	10.0	3.0	11.0	M	COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes
Pmer2778|CDS|CDS	22.5	7.0	10.6	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Fae05625|CDS|CDS	16.0	5.0	10.6	M	COG1876	D-alanyl-D-alanine carboxypeptidase
Pmer3242|CDS|CDS	16.0	5.0	10.6	M	COG1596	Periplasmic protein involved in polysaccharide export
BactD21848|CDS|CDS	1.6	0.5	10.6	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
Pmer2340|CDS|CDS	12.5	4.0	10.3	M	COG3774	Mannosyltransferase OCH1 and related enzymes
TS28Fae19977|CDS|CDS	2.0	67.0	0.1	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
TS28Clo01153|CDS|CDS	4.0	135.0	0.1	M	COG0438|COG1887	Glycosyltransferase|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC
Cbol3084|CDS|CDS	0.9	31.5	0.1	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
Robe0376|CDS|CDS	0.5	17.0	0.1	M	COG0773	UDP-N-acetylmuramate-alanine ligase
TS28Eub7015|CDS|CDS	5.5	188.5	0.1	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS28Fae12961|CDS|CDS	1.0	35.0	0.1	M	COG0562	UDP-galactopyranose mutase
TS28Met1402|CDS|CDS	0.5	17.7	0.1	M	COG0769	UDP-N-acetylmuramyl tripeptide synthase
TS28Fae12487|CDS|CDS	2.0	72.5	0.1	M	COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily
TS28Met1075|CDS|CDS	0.3	9.2	0.1	M	COG0562	UDP-galactopyranose mutase
TS28Eub7639|CDS|CDS	1.0	37.0	0.1	M	COG3940|COG5520	Predicted beta-xylosidase|O-Glycosyl hydrolase
Robe1058|CDS|CDS	0.3	12.3	0.1	M	COG5498	Predicted glycosyl hydrolase
Ehal1311|CDS|CDS	2.0	75.0	0.1	M	COG3049	Penicillin V acylase and related amidases
TS28Clo01670|CDS|CDS	4.0	151.0	0.1	M	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
TS28Bac2721|CDS|CDS	0.5	19.0	0.1	M	COG1089	GDP-D-mannose dehydratase
TS28Bac0435|CDS|CDS	1.0	38.0	0.1	M	COG0438	Glycosyltransferase
TS28Rum14609|CDS|CDS	1.2	45.0	0.1	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
TS28Fae21505|CDS|CDS	2.3	91.0	0.1	M	COG1087	UDP-glucose 4-epimerase
TS28Fae02412|CDS|CDS	0.5	19.5	0.1	M	COG1209	dTDP-glucose pyrophosphorylase
Cbol3950|CDS|CDS	0.7	26.5	0.1	M	COG0741|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Cell wall-associated hydrolases (invasion-associated proteins)
TS28Rum00130|CDS|CDS	1.0	40.0	0.1	M	COG0771|COG0769	UDP-N-acetylmuramoylalanine-D-glutamate ligase|UDP-N-acetylmuramyl tripeptide synthase
TS28Dor2263|CDS|CDS	16.0	656.0	0.1	M	COG4932	Predicted outer membrane protein

TS28Rum00317|CDS|CDS	0.3	13.8	0.1	M	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
TS28Fae20211|CDS|CDS	2.0	84.5	0.1	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS28Eub7159|CDS|CDS	3.0	129.0	0.1	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Fae18484|CDS|CDS	0.5	21.5	0.1	M	COG0707	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
TS29Rum18703|CDS|CDS	2.0	87.0	0.1	M	COG4932	Predicted outer membrane protein
TS28Fae22393|CDS|CDS	0.5	22.0	0.1	M	COG0438	Glycosyltransferase
TS29RumUnc0410|CDS|CDS	0.5	22.0	0.1	M	COG0438	Glycosyltransferase
TS28Clo00523|CDS|CDS	8.0	363.0	0.1	M	COG4932|COG4886|COG1357	Predicted outer membrane protein|Leucine-rich repeat (LRR) protein|Uncharacterized low-complexity proteins
TS29Rum11714|CDS|CDS	1.5	69.0	0.1	M	COG0741|COG3757	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
Even0431|CDS|CDS	4.0	185.3	0.1	M	COG4932|COG4509	Predicted outer membrane protein|Uncharacterized protein conserved in bacteria
TS29Rum13768|CDS|CDS	1.0	47.0	0.1	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS28Fae06646|CDS|CDS	0.3	16.0	0.1	M	COG0481	Membrane GTPase LepA
TS28Clo01156|CDS|CDS	2.0	96.0	0.1	M	COG1876	D-alanyl-D-alanine carboxypeptidase
TS28Eub4469|CDS|CDS	1.3	68.0	0.1	M	COG0739|COG3883|COG5283|COG0791	Membrane proteins related to metalloendopeptidases|Uncharacterized protein conserved in bacteria|Phage-related tail protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS28Eub7161|CDS|CDS	1.0	52.0	0.1	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Ebif0599|CDS|CDS	2.0	105.7	0.1	M	COG4932	Predicted outer membrane protein
TS28Eub3993|CDS|CDS	1.0	53.0	0.1	M	COG0438|COG1543	Glycosyltransferase|Uncharacterized conserved protein
TS28Rum11599|CDS|CDS	0.7	35.7	0.1	M	COG4932	Predicted outer membrane protein
Cnex0942|CDS|CDS	0.7	36.8	0.1	M	COG4932	Predicted outer membrane protein
TS28Clo01565|CDS|CDS	2.0	111.0	0.1	M	COG3049	Penicillin V acylase and related amidases
TS28Bac7137|CDS|CDS	0.5	28.0	0.1	M	COG0438|COG0859	Glycosyltransferase|ADP-heptose:LPS heptosyltransferase
TS28Clo00945|CDS|CDS	2.0	112.0	0.1	M	COG0438	Glycosyltransferase
TS29Dor2226|CDS|CDS	10.0	564.1	0.1	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
Ehal2405|CDS|CDS	0.3	14.5	0.1	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS28Fae18452|CDS|CDS	0.3	19.5	0.1	M	COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes
TS28Dor2628|CDS|CDS	10.0	593.1	0.1	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
TS29Eub1923|CDS|CDS	0.5	31.0	0.1	M	COG4932	Predicted outer membrane protein
TS29RumUnc1441|CDS|CDS	2.0	124.0	0.1	M	COG4932	Predicted outer membrane protein
CspM6210958|CDS|CDS	2.5	157.5	0.1	M	COG4932	Predicted outer membrane protein
TS28Eub7158|CDS|CDS	1.5	94.5	0.1	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
EUBREC1319|CDS|phospho-N-acetylmuramoyl-pentapeptide-transferase	1.0	64.0	0.1	M	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
Robe2641|CDS|CDS	0.7	44.5	0.0	M	COG4932	Predicted outer membrane protein
TS28Clo00532|CDS|CDS	4.0	274.0	0.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Fae19368|CDS|CDS	0.3	22.8	0.0	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
CspSS23032|CDS|CDS	1.0	69.2	0.0	M	COG4932	Predicted outer membrane protein
TS28Eub6911|CDS|CDS	0.5	35.5	0.0	M	COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)
TS28Eub6232|CDS|CDS	0.5	36.0	0.0	M	COG1087	UDP-glucose 4-epimerase
TS28Clo00579|CDS|CDS	4.0	290.0	0.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS29Bif3129|CDS|CDS	1.0	73.0	0.0	M	COG4932	Predicted outer membrane protein
TS28Fae18231|CDS|CDS	1.0	75.0	0.0	M	COG1696	Predicted membrane protein involved in D-alanine export
TS28Fae07317|CDS|CDS	0.5	37.0	0.0	M	COG0481	Membrane GTPase LepA
TS28Fae01838|CDS|CDS	0.5	39.0	0.0	M	COG2148|COG0707	Sugar transferases involved in lipopolysaccharide synthesis|UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
TS28Clo01323|CDS|CDS	1.0	78.5	0.0	M	COG0357	Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division
TS28Fae03718|CDS|CDS	0.1	12.0	0.0	M	COG0481	Membrane GTPase LepA
TS28Bac3778|CDS|CDS	0.5	43.0	0.0	M	COG5434	Endopolygalacturonase
CspSS20003|CDS|CDS	1.0	89.1	0.0	M	COG4932	Predicted outer membrane protein
TS28Eub6387|CDS|CDS	0.5	45.0	0.0	M	COG1792	Cell shape-determining protein
TS28Eub0524|CDS|CDS	1.0	91.5	0.0	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
TS28Eub5438|CDS|CDS	1.0	93.2	0.0	M	COG1887	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC
TS28Eub5610|CDS|CDS	1.0	96.0	0.0	M	COG0438|COG2148|COG0707	Glycosyltransferase|Sugar transferases involved in lipopolysaccharide synthesis|UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
Ccom1803|CDS|CDS	0.7	67.3	0.0	M	COG4932	Predicted outer membrane protein
TS28Clo01587|CDS|CDS	3.0	317.0	0.0	M	COG4932|COG4886|COG3291|COG1357	Predicted outer membrane protein|Leucine-rich repeat (LRR) protein|FOG: PKD repeat|Uncharacterized low-complexity proteins
TS28Clo00819|CDS|CDS	1.0	107.0	0.0	M	COG0796	Glutamate racemase
Robe0860|CDS|CDS	2.0	218.7	0.0	M	COG4932	Predicted outer membrane protein
TS28Eub4771|CDS|CDS	0.3	38.0	0.0	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
TS28Eub7945|CDS|CDS	0.7	77.3	0.0	M	COG0845	Membrane-fusion protein
TS28Rum13650|CDS|CDS	0.5	59.5	0.0	M	COG1696	Predicted membrane protein involved in D-alanine export
TS29Rum11739|CDS|CDS	2.0	261.8	0.0	M	COG4932	Predicted outer membrane protein
TS28Clo01531|CDS|CDS	3.0	400.5	0.0	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS28Fae13752|CDS|CDS	1.0	151.0	0.0	M	COG4932	Predicted outer membrane protein
TS28Clo01350|CDS|CDS	1.0	159.0	0.0	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
TS28Eub6386|CDS|CDS	1.0	162.0	0.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Eub8415|CDS|CDS	0.5	89.0	0.0	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
Ehal0341|CDS|CDS	0.2	37.6	0.0	M	COG4932	Predicted outer membrane protein
TS28Rum16195|CDS|CDS	0.5	109.0	0.0	M	COG5434	Endopolygalacturonase

Robe3825|CDS|CDS	0.7	149.0	0.0	M	COG4932	Predicted outer membrane protein
CspSS21752|CDS|CDS	0.7	158.1	0.0	M	COG4932	Predicted outer membrane protein
TS28Eub7419|CDS|CDS	0.2	109.0	0.0	M	COG4932	Predicted outer membrane protein
Ccom0358|CDS|CDS	0.2	134.3	0.0	M	COG4932	Predicted outer membrane protein
TS28Eub7705|CDS|CDS	0.2	218.5	0.0	M	COG4932	Predicted outer membrane protein
TS28RumUnc0947|CDS|CDS	40.0	5.0	26.5	M|D	COG0489|COG3944	ATPases involved in chromosome partitioning|Capsular polysaccharide biosynthesis protein
TS28Fae06722|CDS|CDS	10.0	3.0	11.0	M|D	COG0489|COG3944	ATPases involved in chromosome partitioning|Capsular polysaccharide biosynthesis protein
BactD13176|CDS|CDS	10.0	3.0	11.0	M|D	COG0489|COG3206|COG3944|COG2148	ATPases involved in chromosome partitioning|Uncharacterized protein involved in exopolysaccharide biosynthesis|Capsular polysaccharide biosynthesis protein|Sugar transferases involved in lipopolysaccharide synthesis
TS28Clo00838|CDS|CDS	1.0	84.0	0.0	M|D	COG0489|COG3944	ATPases involved in chromosome partitioning|Capsular polysaccharide biosynthesis protein
Bdor2088|CDS|CDS	179.5	15.0	39.6	M|G	COG2942|COG0836	N-acyl-D-glucosamine 2-epimerase|Mannose-1-phosphate guanylyltransferase
Msmi751206|CDS|CDS	4.5	0.5	29.8	M|G	COG0463|COG3594|COG1887|COG1442|COG4641	Glycosyltransferases involved in cell wall biogenesis|Fucose 4-O-acetylase and related acetyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases|Uncharacterized protein conserved in bacteria
Msmi750020|CDS|CDS	2.5	0.3	24.8	M|G	COG0451|COG1087	Nucleoside-diphosphate-sugar epimerases|UDP-glucose 4-epimerase
PRABACTJOHN2720|CDS|CDS	44.5	6.0	24.5	M|G	COG3507|COG5520|COG3940	Beta-xylosidase|O-Glycosyl hydrolase|Predicted beta-xylosidase
Cspi0135|CDS|CDS	7.0	1.0	23.1	M|G	COG2222|COG4573	Predicted phosphosugar isomerases|Predicted tagatose 6-phosphate kinase
Pmer3398|CDS|CDS	55.5	9.0	20.4	M|G	COG3507|COG5520|COG3940	Beta-xylosidase|O-Glycosyl hydrolase|Predicted beta-xylosidase
Bdor0471|CDS|CDS	16.7	3.0	18.4	M|G	COG1210|COG1109	UDP-glucose pyrophosphorylase|Phosphomannomutase
Acol2236|CDS|CDS	5.0	1.0	16.5	M|G	COG1210|COG1109	UDP-glucose pyrophosphorylase|Phosphomannomutase
Msmi751388|CDS|CDS	1.5	0.3	14.9	M|G	COG1210|COG1109	UDP-glucose pyrophosphorylase|Phosphomannomutase
Robe0434|CDS|CDS	8.5	2.0	14.1	M|G	COG1134	ABC-type polysaccharide/polyol phosphate transport system, ATPase component
Msmi740460|CDS|CDS	7.0	1.7	13.9	M|G	COG0463|COG3594|COG1216	Glycosyltransferases involved in cell wall biogenesis|Fucose 4-O-acetylase and related acetyltransferases|Predicted glycosyltransferases
BactD13805|CDS|CDS	2.0	0.5	13.2	M|G	COG0463|COG3594|COG1887|COG1442	Glycosyltransferases involved in cell wall biogenesis|Fucose 4-O-acetylase and related acetyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
Msmi741141|CDS|CDS	3.0	0.8	13.2	M|G	COG0463|COG3594|COG1887|COG1442|COG4641	Glycosyltransferases involved in cell wall biogenesis|Fucose 4-O-acetylase and related acetyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases|Uncharacterized protein conserved in bacteria
BactD11859|CDS|CDS	4.0	1.0	13.2	M|G	COG0451|COG1088|COG1087	Nucleoside-diphosphate-sugar epimerases|dTDP-D-glucose 4,6-dehydratase|UDP-glucose 4-epimerase
Msmi741166|CDS|CDS	1.3	0.3	12.4	M|G	COG1086	Predicted nucleoside-diphosphate sugar epimerases
Rtor2578|CDS|CDS	1.0	34.0	0.1	M|G	COG2730|COG3507|COG5520|COG4124	Endoglucanase|Beta-xylosidase|O-Glycosyl hydrolase|Beta-mannanase
FpraM2122432|CDS|CDS	8.7	0.5	57.3	M|I	COG0463|COG1887|COG1216|COG3754|COG1835	Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Predicted glycosyltransferases|Lipopolysaccharide biosynthesis protein|Predicted acyltransferases
Pmer0790|CDS|CDS	11.0	2.0	18.2	M|I	COG2870|COG0615	ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase|Cytidylyltransferase
Csym2684|CDS|CDS	9.0	1.0	29.8	M|O	COG0463|COG1887|COG1216|COG3754|COG3914	Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Predicted glycosyltransferases|Lipopolysaccharide biosynthesis protein|Predicted O-linked N-acetylglucosamine transferase, SPINDLY family
TS28RumUnc2054|CDS|CDS	0.7	35.0	0.1	M|T	COG3409|COG1388|COG3883|COG3103|COG0791	Putative peptidoglycan-binding domain-containing protein|FOG: LysM repeat|Uncharacterized protein conserved in bacteria|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Bac12007|CDS|CDS	7.5	1.5	16.5	M|U	COG1538	Outer membrane protein
ShigspD92426|CDS|CDS	5.0	1.0	16.5	M|U	COG1538	Outer membrane protein
Begg2377|CDS|CDS	4.0	1.0	13.2	M|U	COG0597	Lipoprotein signal peptidase
TS28Bac6385|CDS|CDS	1.0	51.0	0.1	M|U	COG1538	Outer membrane protein
ShigspD92848|CDS|CDS	3.0	0.5	19.8	M|U|W	COG5295|COG4625|COG3468	Autotransporter adhesin|Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain|Type V secretory pathway, adhesin AidA
ShigspD92357|CDS|CDS	4.5	1.0	14.9	M|U|W	COG5295|COG3468	Autotransporter adhesin|Type V secretory pathway, adhesin AidA
BactD11577|CDS|CDS	7.5	1.5	16.5	M|V|U	COG1538|COG0841	Outer membrane protein|Cation/multidrug efflux pump
BactD20059|CDS|CDS	2.5	0.5	16.5	M|V|U	COG1538|COG0841	Outer membrane protein|Cation/multidrug efflux pump
CspM6210755|CDS|CDS	14.0	1.0	46.3	N	COG5651	PPE-repeat proteins
TS28Rum13179|CDS|CDS	139.0	14.0	32.8	N	COG1344	Flagellin and related hook-associated proteins
Casp6307|CDS|CDS	14.0	2.0	23.1	N	COG5492	Bacterial surface proteins containing Ig-like domains
RintL11106|CDS|CDS	4.0	1.0	13.2	N	COG1344	Flagellin and related hook-associated proteins
TS28Fae04478|CDS|CDS	11.0	3.0	12.1	N	COG1724	Predicted periplasmic or secreted lipoprotein
TS28Eub0393|CDS|CDS	2.0	148.5	0.0	N	COG5492	Bacterial surface proteins containing Ig-like domains
TS29Met0240|CDS|CDS	5.6	1.8	10.3	N|C|L|U	COG1156|COG1372|COG1157|COG0055	Archaeal/vacuolar-type H+-ATPase subunit B|Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|F0F1-type ATP synthase, beta subunit

TS28Dor0729|CDS|CDS	0.5	38.0	0.0	N|C|L|U	COG1372|COG1157|COG1155|COG0055	Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A|F0F1-type ATP synthase, beta subunit
Ccom1873|CDS|CDS	6.0	1.0	19.8	N|E|M|O	COG5492|COG5479|COG3291|COG1404|COG3227|COG3979|COG4412	Bacterial surface proteins containing Ig-like domains|Uncharacterized protein potentially involved in peptidoglycan biosynthesis|FOG: PKD repeat|Subtilisin-like serine proteases|Zinc metalloprotease (elastase)|Uncharacterized protein contain chitin-binding domain type 3|Uncharacterized protein conserved in bacteria
Cspi1488|CDS|CDS	48.0	3.0	52.9	N|G|U	COG5492|COG3291|COG2273|COG3250|COG1501|COG1472|COG4409|COG3525|COG0823|COG4412	Bacterial surface proteins containing Ig-like domains|FOG: PKD repeat|Beta-glucanase/Beta-glucan synthetase|Beta-galactosidase/beta-glucuronidase|Alpha-glucosidases, family 31 of glycosyl hydrolases|Beta-glucosidase-related glycosidases|Neuraminidase (sialidase)|N-acetyl-beta-hexosaminidase|Periplasmic component of the Tol biopolymer transport system|Uncharacterized protein conserved in bacteria
Msmi741408|CDS|CDS	1.7	0.5	11.0	N|G|U	COG2730|COG3210|COG5651	Endoglucanase|Large exoproteins involved in heme utilization or adhesion|PPE-repeat proteins
TS29Rum13519|CDS|CDS	117.0	6.0	64.5	N|K|T	COG0642|COG0745|COG4753|COG0784|COG3279|COG3706|COG2197|COG2200|COG2201|COG3707	Signal transduction histidine kinase|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|FOG: CheY-like receiver|Response regulator of the LytR/AlgR family|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|FOG: EAL domain|Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain|Response regulator with putative antiterminator output domain
TS28Fae17369|CDS|CDS	0.5	33.0	0.1	N|K|U|T	COG3437|COG2804	Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB
Aput2338|CDS|CDS	10.0	1.0	33.1	N|L|C|U	COG1372|COG0055|COG1157|COG1155	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A
Csci0942|CDS|CDS	9.0	1.0	29.8	N|L|C|U	COG1372|COG1156|COG1157	Intein/homing endonuclease|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
Msmi740101|CDS|CDS	11.4	2.1	17.6	N|L|C|U	COG1372|COG0055|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
Msmi751598|CDS|CDS	11.4	3.1	12.0	N|L|C|U	COG1372|COG0055|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
TS28Dor1097|CDS|CDS	0.5	36.0	0.0	N|M	COG5492|COG3409|COG1376	Bacterial surface proteins containing Ig-like domains|Putative peptidoglycan-binding domain-containing protein|Uncharacterized protein conserved in bacteria
Bdor3263|CDS|CDS	15.0	3.0	16.5	N|M|O|U	COG1705|COG5632|COG3942|COG3951	Muramidase (flagellum-specific)|N-acetylmuramoyl-L-alanine amidase|Surface antigen|Rod binding protein
TS28Bac5806|CDS|CDS	1.0	119.0	0.0	N|T	COG0642|COG5002|COG2202|COG0784|COG4252|COG2198|COG2203|COG3300|COG3292|COG3447|COG1352	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Predicted transmembrane sensor domain|FOG: HPt domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted integral membrane sensor domain|Methylase of chemotaxis methyl-accepting proteins
ShigspD91374|CDS|CDS	8.0	0.5	52.9	N|U	COG3188	P pilus assembly protein, porin PapC
ShigspD90563|CDS|CDS	7.5	1.0	24.8	N|U	COG3188	P pilus assembly protein, porin PapC
TS29Dor1540|CDS|CDS	6.0	1.0	19.8	N|U	COG1886	Flagellar motor switch/type III secretory pathway protein
TS28Clo00554|CDS|CDS	4.0	203.0	0.1	N|U	COG1459	Type II secretory pathway, component PulF
TS28Bif3174|CDS|CDS	0.3	30.7	0.0	N|U	COG2805|COG5008	Tfp pilus assembly protein, pilus retraction ATPase PilT|Tfp pilus assembly protein, ATPase PilU
Bfin0905|CDS|CDS	14.3	0.3	188.5	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Fae10145|CDS|CDS	9.3	0.3	92.6	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
PRABACTJOHN3634|CDS|CDS	28.0	1.0	92.6	O	COG3187	Heat shock protein
Bthe3732369|CDS|CDS	14.3	0.6	80.8	O	COG0071	Molecular chaperone (small heat shock protein)
Bthe7331683|CDS|CDS	14.3	0.6	80.8	O	COG0071	Molecular chaperone (small heat shock protein)
BactD12632|CDS|CDS	14.3	0.6	80.8	O	COG0071	Molecular chaperone (small heat shock protein)
Pmer1175|CDS|CDS	65.0	3.0	71.7	O	COG3187	Heat shock protein
Pmer2683|CDS|CDS	19.0	1.0	62.8	O	COG0450	Peroxiredoxin
TS29Fae09025|CDS|CDS	25.6	1.5	56.4	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Rum01962|CDS|CDS	16.0	1.0	52.9	O	COG0465	ATP-dependent Zn proteases
Casp3984|CDS|CDS	23.0	1.5	50.7	O	COG0443	Molecular chaperone
TS28Fae14370|CDS|CDS	693.5	48.0	47.8	O	COG0071	Molecular chaperone (small heat shock protein)
BactD14216|CDS|CDS	12.0	0.8	47.6	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
Bste3230|CDS|CDS	21.5	1.5	47.4	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
Bdor1245|CDS|CDS	26.5	2.0	43.8	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Fae21987|CDS|CDS	131.8	10.0	43.6	O	COG0071	Molecular chaperone (small heat shock protein)
Pmer2603|CDS|CDS	6.5	0.5	43.0	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
Cnex0251|CDS|CDS	13.0	1.0	43.0	O	COG0443	Molecular chaperone
Pmer3472|CDS|CDS	86.0	7.0	40.6	O	COG0330	Membrane protease subunits, stomatin/prohibitin homologs
Bdor3868|CDS|CDS	66.5	6.0	36.7	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Par2214|CDS|CDS	5.0	0.5	33.1	O	COG0576	Molecular chaperone GrpE (heat shock protein)
BactD10814|CDS|CDS	10.0	1.0	33.1	O	COG0071	Molecular chaperone (small heat shock protein)
PRABACTJOHN0976|CDS|CDS	19.5	2.0	32.2	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Casp2870|CDS|CDS	9.0	1.0	29.8	O	COG0466	ATP-dependent Lon protease, bacterial type
TS29Bac10141|CDS|CDS	52.5	6.0	28.9	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Rum12156|CDS|CDS	17.0	2.0	28.1	O	COG0691	tmRNA-binding protein

Bxyl3171|CDS|CDS	2.8	0.3	28.1	O	COG0612|COG1025	Predicted Zn-dependent peptidases|Secreted/periplasmic Zn-dependent peptidases, insulinase-like
TS28Ali1994|CDS|CDS	408.0	49.0	27.5	O	COG1572|COG1404|COG4935	Uncharacterized conserved protein|Subtilisin-like serine proteases|Regulatory P domain of the subtilisin-like proprotein convertases and other proteases
Bdor0083|CDS|CDS	89.7	11.0	27.0	O	COG0459	Chaperonin GroEL (HSP60 family)
Pmer2685|CDS|CDS	8.0	1.0	26.5	O	COG1180	Pyruvate-formate lyase-activating enzyme
RintL11446|CDS|CDS	8.0	1.0	26.5	O	COG1180	Pyruvate-formate lyase-activating enzyme
TS29Bac00096|CDS|CDS	8.0	1.0	26.5	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Rgna3169|CDS|CDS	4.0	0.5	26.5	O	COG0465	ATP-dependent Zn proteases
Caer1725|CDS|CDS	2.0	0.3	26.5	O	COG0443	Molecular chaperone
Bste0559|CDS|CDS	15.5	2.0	25.6	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Msmi740182|CDS|CDS	3.8	0.5	25.4	O	COG1222	ATP-dependent 26S proteasome regulatory subunit
Pmer1047|CDS|CDS	7.5	1.0	24.8	O	COG0501|COG4783|COG4784	Zn-dependent protease with chaperone function|Putative Zn-dependent protease, contains TPR repeats|Putative Zn-dependent protease
Pmer0348|CDS|CDS	25.0	3.5	23.6	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Bste2071|CDS|CDS	7.0	1.0	23.1	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS29Bac00073|CDS|CDS	3.5	0.5	23.1	O	COG0443	Molecular chaperone
Rgna0855|CDS|CDS	7.0	1.0	23.1	O	COG0071	Molecular chaperone (small heat shock protein)
Pmer0928|CDS|CDS	23.3	3.5	22.0	O	COG0459	Chaperonin GroEL (HSP60 family)
Msmi740920|CDS|CDS	16.4	2.5	21.6	O	COG0071	Molecular chaperone (small heat shock protein)
Bdor3251|CDS|CDS	26.0	4.0	21.5	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Msmi750995|CDS|CDS	3.3	0.5	21.5	O	COG0068|COG0298	Hydrogenase maturation factor|Hydrogenase maturation factor
TS28Fae20436|CDS|CDS	216.3	35.0	20.4	O	COG0071	Molecular chaperone (small heat shock protein)
Msmi750701|CDS|CDS	11.1	1.8	20.0	O	COG4070	Predicted peptidyl-prolyl cis-trans isomerase (rotamase), cyclophilin family
Bryfor2652|CDS|CDS	6.0	1.0	19.8	O	COG1219	ATP-dependent protease Clp, ATPase subunit
Bdor3252|CDS|CDS	21.0	3.5	19.8	O	COG0576	Molecular chaperone GrpE (heat shock protein)
Rbro0804|CDS|CDS	3.0	0.5	19.8	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Ehal0046|CDS|CDS	3.0	0.5	19.8	O	COG0409	Hydrogenase maturation factor
Pmer3440|CDS|CDS	23.5	4.0	19.4	O	COG2077	Peroxiredoxin
Msmi750927|CDS|CDS	3.8	0.7	18.6	O	COG0638	20S proteasome, alpha and beta subunits
Ceut2654|CDS|CDS	5.5	1.0	18.3	O	COG0443	Molecular chaperone
Bdor1200|CDS|CDS	86.0	16.3	17.4	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Fae17572|CDS|CDS	187.5	36.0	17.2	O	COG0071	Molecular chaperone (small heat shock protein)
Bste0743|CDS|CDS	51.0	10.0	16.9	O	COG0443	Molecular chaperone
TS28Fae11914|CDS|CDS	10.0	2.0	16.5	O	COG0691	tmRNA-binding protein
CspSS22208|CDS|CDS	2.5	0.5	16.5	O	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
Pmer0297|CDS|CDS	10.0	2.0	16.5	O	COG0602|COG3759	Organic radical activating enzymes|Predicted membrane protein
Hfil2561|CDS|CDS	5.0	1.0	16.5	O	COG0326	Molecular chaperone, HSP90 family
TS28Rum01574|CDS|CDS	10.0	2.0	16.5	O	COG0234	Co-chaperonin GroES (HSP10)
TS28Fae09723|CDS|CDS	19.3	4.0	16.0	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
Pmer1290|CDS|CDS	9.5	2.0	15.7	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS29Fae06754|CDS|CDS	11.8	2.5	15.7	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Rum16009|CDS|CDS	33.0	7.0	15.6	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS29Fae05844|CDS|CDS	9.3	2.0	15.4	O	COG0459	Chaperonin GroEL (HSP60 family)
Bste1251|CDS|CDS	70.0	15.0	15.4	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Ali0411|CDS|CDS	102.0	23.0	14.7	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
TS28Ali2164|CDS|CDS	39.0	9.0	14.3	O	COG0234	Co-chaperonin GroES (HSP10)
Bova3457|CDS|CDS	4.3	1.0	14.1	O	COG0459	Chaperonin GroEL (HSP60 family)
CspM6211052|CDS|CDS	4.3	1.0	14.1	O	COG0326	Molecular chaperone, HSP90 family
Bdor3308|CDS|CDS	8.0	2.0	13.2	O	COG3187	Heat shock protein
Bste2831|CDS|CDS	8.0	2.0	13.2	O	COG1076	DnaJ-domain-containing proteins 1
Bste1613|CDS|CDS	28.0	7.0	13.2	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Cbol0967|CDS|CDS	6.0	1.5	13.2	O	COG0465	ATP-dependent Zn proteases
TS29Bif0496|CDS|CDS	1.3	0.3	13.2	O	COG0450	Peroxiredoxin
Bcat1012|CDS|CDS	1.0	0.3	13.2	O	COG0443	Molecular chaperone
CspSS20336|CDS|CDS	2.0	0.5	13.2	O	COG0425	Predicted redox protein, regulator of disulfide bond formation
TS29Fae04889|CDS|CDS	2.0	0.5	13.2	O	COG0326	Molecular chaperone, HSP90 family
Rbro0565|CDS|CDS	3.3	0.8	13.2	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Dfor0868|CDS|CDS	4.0	1.0	13.2	O	COG0234	Co-chaperonin GroES (HSP10)
Dfor0429|CDS|CDS	4.0	1.0	13.2	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Clo02161|CDS|CDS	11.5	3.0	12.7	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Bac6715|CDS|CDS	119.5	31.3	12.6	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Fae13136|CDS|CDS	49.1	13.0	12.5	O	COG0071	Molecular chaperone (small heat shock protein)
Bdor3309|CDS|CDS	63.2	17.0	12.3	O	COG0443	Molecular chaperone
Bdor0014|CDS|CDS	11.0	3.0	12.1	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
Casp4535|CDS|CDS	11.0	3.0	12.1	O	COG0465	ATP-dependent Zn proteases
Bste1996|CDS|CDS	11.0	3.0	12.1	O	COG0450	Peroxiredoxin
TS28Eub1085|CDS|CDS	18.0	5.0	11.9	O	COG1180	Pyruvate-formate lyase-activating enzyme
BactD11022|CDS|CDS	2.4	0.7	11.9	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
TS29Bac09228|CDS|CDS	2.4	0.7	11.9	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
Bxyl1307|CDS|CDS	2.4	0.7	11.9	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
BactD11682|CDS|CDS	1.2	0.3	11.9	O	COG0465	ATP-dependent Zn proteases
TS29Eub2133|CDS|CDS	7.0	2.0	11.6	O	COG0443	Molecular chaperone
BactD23099|CDS|CDS	3.5	1.0	11.6	O	COG0326	Molecular chaperone, HSP90 family
TS28Rum16008|CDS|CDS	17.0	5.0	11.2	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Bdor0305|CDS|CDS	10.0	3.0	11.0	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
Csci3642|CDS|CDS	10.0	3.0	11.0	O	COG0326	Molecular chaperone, HSP90 family

TS28Met0924|CDS|CDS	6.6	2.0	10.9	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Rum21190|CDS|CDS	91.5	28.0	10.8	O	COG0071	Molecular chaperone (small heat shock protein)
TS28RumUnc0269|CDS|CDS	16.0	5.0	10.6	O	COG1066	Predicted ATP-dependent serine protease
TS28Eub1364|CDS|CDS	1.0	34.0	0.1	O	COG0326	Molecular chaperone, HSP90 family
TS28Met0899|CDS|CDS	1.0	35.0	0.1	O	COG0826	Collagenase and related proteases
TS28Rum07430|CDS|CDS	0.5	18.0	0.1	O	COG0443	Molecular chaperone
Robe1902|CDS|CDS	1.0	36.0	0.1	O	COG0326	Molecular chaperone, HSP90 family
TS28Eub1127|CDS|CDS	0.5	18.5	0.1	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
TS28Fae21746|CDS|CDS	1.0	37.0	0.1	O	COG0465	ATP-dependent Zn proteases
TS29Rum00846|CDS|CDS	2.0	79.0	0.1	O	COG0465	ATP-dependent Zn proteases
TS28Fae22203|CDS|CDS	1.0	40.0	0.1	O	COG0561|COG0652	Predicted hydrolases of the HAD superfamily|Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
TS28Bif4106|CDS|CDS	1.3	51.0	0.1	O	COG0465	ATP-dependent Zn proteases
TS28Fae10193|CDS|CDS	1.0	41.0	0.1	O	COG0464|COG0790	ATPases of the AAA+ class|FOG: TPR repeat, SEL1 subfamily
TS29Bif0183|CDS|CDS	0.7	27.7	0.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Fae03681|CDS|CDS	0.4	17.5	0.1	O	COG0459	Chaperonin GroEL (HSP60 family)
TS28Fae07842|CDS|CDS	0.5	22.0	0.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Bac6015|CDS|CDS	0.5	22.3	0.1	O	COG1404|COG3291	Subtilisin-like serine proteases|FOG: PKD repeat
Robe3122|CDS|CDS	1.0	45.0	0.1	O	COG1975	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family
TS28Fae12518|CDS|CDS	2.0	92.5	0.1	O	COG0464|COG0790	ATPases of the AAA+ class|FOG: TPR repeat, SEL1 subfamily
TS28Fae01994|CDS|CDS	0.5	23.5	0.1	O	COG0606	Predicted ATPase with chaperone activity
TS29Rum00031|CDS|CDS	1.0	48.5	0.1	O	COG0326	Molecular chaperone, HSP90 family
TS28Met0355|CDS|CDS	0.3	16.7	0.1	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS28Fae16667|CDS|CDS	1.5	76.0	0.1	O	COG0443	Molecular chaperone
TS29Fae05133|CDS|CDS	0.5	25.5	0.1	O	COG1219	ATP-dependent protease Clp, ATPase subunit
TS28Clo00661|CDS|CDS	5.0	261.0	0.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Bif5205|CDS|CDS	0.3	17.5	0.1	O	COG0602	Organic radical activating enzymes
Ebif0548|CDS|CDS	0.5	27.0	0.1	O	COG2020	Putative protein-S-isoprenylcysteine methyltransferase
TS28Rum14890|CDS|CDS	0.5	27.0	0.1	O	COG0826	Collagenase and related proteases
TS28Met0103|CDS|CDS	0.3	18.0	0.1	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Eub1030|CDS|CDS	1.0	55.0	0.1	O	COG0561|COG4696|COG0652	Predicted hydrolases of the HAD superfamily|Uncharacterized protein conserved in bacteria|Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
TS29Bif1463|CDS|CDS	0.3	14.0	0.1	O	COG0465	ATP-dependent Zn proteases
TS28Fae17720|CDS|CDS	1.5	86.5	0.1	O	COG0606	Predicted ATPase with chaperone activity
TS28Fae07982|CDS|CDS	0.7	41.0	0.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Eub4241|CDS|CDS	0.3	21.5	0.1	O	COG0826	Collagenase and related proteases
TS28Clo01165|CDS|CDS	3.0	194.0	0.1	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS28Clo01078|CDS|CDS	4.0	259.0	0.1	O	COG0826	Collagenase and related proteases
TS29Rum13627|CDS|CDS	0.3	22.0	0.1	O	COG0826	Collagenase and related proteases
TS28Fae11996|CDS|CDS	1.0	66.0	0.1	O	COG0484|COG2214|COG4930|COG3671	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone|Predicted ATP-dependent Lon-type protease|Predicted membrane protein
TS28Bif2933|CDS|CDS	0.5	35.0	0.0	O	COG4930	Predicted ATP-dependent Lon-type protease
TS29Bif3617|CDS|CDS	0.2	12.3	0.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Fae21021|CDS|CDS	0.7	49.5	0.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Eub8507|CDS|CDS	1.0	75.5	0.0	O	COG1975|COG2258	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family|Uncharacterized protein conserved in bacteria
TS28Fae00462|CDS|CDS	0.5	38.5	0.0	O	COG0326	Molecular chaperone, HSP90 family
TS28Clo01582|CDS|CDS	4.0	314.5	0.0	O	COG0466	ATP-dependent Lon protease, bacterial type
TS28Fae20118|CDS|CDS	0.5	39.5	0.0	O	COG1219	ATP-dependent protease Clp, ATPase subunit
TS28Clo00707|CDS|CDS	3.0	246.0	0.0	O	COG0443	Molecular chaperone
TS28Clo01090|CDS|CDS	2.0	165.0	0.0	O	COG0826	Collagenase and related proteases
TS28Clo01685|CDS|CDS	3.0	248.0	0.0	O	COG0326	Molecular chaperone, HSP90 family
TS28Eub8725|CDS|CDS	1.0	84.5	0.0	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Fae21766|CDS|CDS	0.2	17.0	0.0	O	COG0826	Collagenase and related proteases
TS28Eub6418|CDS|CDS	1.0	87.0	0.0	O	COG0606	Predicted ATPase with chaperone activity
TS28Fae22642|CDS|CDS	0.5	55.5	0.0	O	COG0465	ATP-dependent Zn proteases
TS28Eub5093|CDS|CDS	0.3	71.5	0.0	O	COG4826	Serine protease inhibitor
TS28Bif2086|CDS|CDS	0.2	36.9	0.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Ali2039|CDS|CDS	273.0	8.0	112.8	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS29Bac07744|CDS|CDS	9.7	0.3	95.9	O|C	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
TS28Ali1087|CDS|CDS	61.0	10.0	20.2	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS29Bac06013|CDS|CDS	18.0	3.0	19.8	O|C	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
TS28Fae10126|CDS|CDS	28.2	5.0	18.6	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS28Met0329|CDS|CDS	14.5	3.3	14.8	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS28Fae21085|CDS|CDS	25.2	7.0	11.9	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS28Clo00713|CDS|CDS	1.0	35.0	0.1	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS28Met0648|CDS|CDS	0.3	11.3	0.1	O|C	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
TS29Clo0596|CDS|CDS	1.5	72.0	0.1	O|C	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
TS28Fae07912|CDS|CDS	11.0	2.0	18.2	O|C|V	COG2274|COG1132|COG5265|COG4987	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
TS28Eub6176|CDS|CDS	2.0	67.0	0.1	O|C|V	COG1132|COG4987	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components

TS28Clo00459|CDS|CDS	4.0	143.0	0.1	O|C|V	COG1132|COG5265|COG4988|COG4987	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
TS28Fae16675|CDS|CDS	1.5	58.5	0.1	O|C|V	COG2274|COG1132|COG5265|COG4988	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components
TS28Clo00625|CDS|CDS	1.0	217.0	0.0	O|C|V	COG2274|COG1132|COG5265|COG4987	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
ShigspD91627|CDS|CDS	4.9	0.5	32.5	O|I	COG0826|COG3154	Collagenase and related proteases|Putative lipid carrier protein
TS28Met1564|CDS|CDS	0.5	26.3	0.1	O|L	COG0464|COG1372	ATPases of the AAA+ class|Intein/homing endonuclease
TS28Fae01888|CDS|CDS	0.5	17.0	0.1	O|M	COG3914|COG0463|COG1215|COG1216|COG1442	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family|Glycosyltransferases involved in cell wall biogenesis|Glycosyltransferases, probably involved in cell wall biogenesis|Predicted glycosyltransferases|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
Bryfor2651|CDS|CDS	3.0	0.2	49.6	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
Bste2437|CDS|CDS	15.0	3.0	16.5	O|U	COG0616	Periplasmic serine proteases (ClpP class)
TS28Rum06260|CDS|CDS	9.0	2.0	14.9	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
TS29Fae07669|CDS|CDS	12.0	3.0	13.2	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
b1978|CDS|adhesin	21.0	1.0	69.4	O|U|W	COG1404|COG3210|COG5295	Subtilisin-like serine proteases|Large exoproteins involved in heme utilization or adhesion|Autotransporter adhesin
TS29Fae08957|CDS|CDS	4.5	0.5	29.8	O|V	COG2274|COG1132|COG5265	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS28Clo03028|CDS|CDS	0.3	12.0	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
Msmi740561|CDS|CDS	44.3	0.3	585.3	P	COG0288	Carbonic anhydrase
Msmi750397|CDS|CDS	20.8	0.7	102.9	P	COG1528	Ferritin-like protein
TS28Met0681|CDS|CDS	20.8	0.7	102.9	P	COG1528	Ferritin-like protein
Msmi741285|CDS|CDS	20.8	0.7	102.9	P	COG1528	Ferritin-like protein
ShigspD90636|CDS|CDS	14.3	0.5	94.8	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
Pmer2111|CDS|CDS	22.5	1.0	74.4	P	COG0605	Superoxide dismutase
TS28Met0788|CDS|CDS	43.7	2.0	72.2	P	COG1930	ABC-type cobalt transport system, periplasmic component
TS29Met1084|CDS|CDS	12.2	0.7	60.4	P	COG0310	ABC-type Co2+ transport system, permease component
Pmer2304|CDS|CDS	472.5	26.0	60.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi740636|CDS|CDS	4.5	0.3	59.5	P	COG2217	Cation transport ATPase
Pmer2291|CDS|CDS	17.7	1.0	58.4	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi740532|CDS|CDS	8.0	0.5	52.9	P	COG2217|COG4087	Cation transport ATPase|Soluble P-type ATPase
PRABACTJOHN0577|CDS|CDS	7.0	0.5	46.3	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
BactD12567|CDS|CDS	6.5	0.5	43.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac03737|CDS|CDS	24.0	2.0	39.7	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
TS29Bac11512|CDS|CDS	3.8	0.3	38.0	P	COG0855	Polyphosphate kinase
Pmer1792|CDS|CDS	22.2	2.0	36.7	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
TS28Par2210|CDS|CDS	22.2	2.0	36.7	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
Bste2867|CDS|CDS	71.5	6.5	36.4	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
BactD12886|CDS|CDS	5.0	0.5	33.1	P	COG4771|COG2304	Outer membrane receptor for ferrienterochelin and colicins|Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Bthe7331666|CDS|CDS	2.5	0.3	33.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bdor1624|CDS|CDS	77.0	8.0	31.8	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
BactD11067|CDS|CDS	3.0	0.3	29.8	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac06023|CDS|CDS	9.0	1.0	29.8	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi750140|CDS|CDS	2.3	0.3	29.8	P	COG0004	Ammonia permease
TS28Met0787|CDS|CDS	13.7	1.7	27.1	P	COG0310	ABC-type Co2+ transport system, permease component
TS29Bac01385|CDS|CDS	58.6	7.2	27.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
BactD13475|CDS|CDS	13.3	1.7	26.5	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
BactD11759|CDS|CDS	4.0	0.5	26.5	P	COG3004	Na+/H+ antiporter
TS29Bac07385|CDS|CDS	4.0	0.5	26.5	P	COG3004	Na+/H+ antiporter
Bdor3002|CDS|CDS	2.7	0.3	26.5	P	COG0735	Fe2+/Zn2+ uptake regulation proteins
BactD12620|CDS|CDS	3.5	0.5	25.7	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bdor3289|CDS|CDS	15.5	2.0	25.6	P	COG0735	Fe2+/Zn2+ uptake regulation proteins
BactD21974|CDS|CDS	7.5	1.0	24.8	P	COG1785	Alkaline phosphatase
Bova2659|CDS|CDS	7.5	1.0	24.8	P	COG1785	Alkaline phosphatase
TS29Fae03267|CDS|CDS	3.7	0.5	24.3	P	COG1283	Na+/phosphate symporter
BactD12607|CDS|CDS	1.8	0.3	23.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi751111|CDS|CDS	12.3	1.8	23.1	P	COG0288	Carbonic anhydrase
Cspi0989|CDS|CDS	7.0	1.0	23.1	P	COG0053|COG1433	Predicted Co/Zn/Cd cation transporters|Uncharacterized conserved protein
Bdor0040|CDS|CDS	147.3	21.5	22.7	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bdor2203|CDS|CDS	41.0	6.0	22.6	P	COG0605	Superoxide dismutase
TS28Bac3758|CDS|CDS	10.0	1.5	22.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Pmer3368|CDS|CDS	30.0	4.5	22.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi750959|CDS|CDS	1.6	0.3	21.2	P	COG2111	Multisubunit Na+/H+ antiporter, MnhB subunit
Msmi740720|CDS|CDS	1.6	0.3	21.2	P	COG2111	Multisubunit Na+/H+ antiporter, MnhB subunit
Msmi751040|CDS|CDS	4.5	0.8	19.8	P	COG2217	Cation transport ATPase
Bdor3898|CDS|CDS	20.0	3.5	18.9	P	COG1528	Ferritin-like protein

Rtor0313|CDS|CDS	17.0	3.0	18.7	P	COG0735	Fe2+/Zn2+ uptake regulation proteins
Bova3996|CDS|CDS	5.3	1.0	17.6	P	COG4771|COG2304	Outer membrane receptor for ferrienterochelin and colicins|Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Msmi741248|CDS|CDS	4.2	0.8	16.8	P	COG0619	ABC-type cobalt transport system, permease component CbiQ and related transporters
Msmi740662|CDS|CDS	9.3	1.8	16.7	P	COG2217	Cation transport ATPase
TS28Met1730|CDS|CDS	44.3	8.8	16.7	P	COG0288	Carbonic anhydrase
Cbol6451|CDS|CDS	5.0	1.0	16.5	P	COG1528	Ferritin-like protein
TS29Rum19985|CDS|CDS	2.5	0.5	16.5	P	COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component
Msmi741246|CDS|CDS	13.0	2.7	16.1	P	COG0310	ABC-type Co2+ transport system, permease component
TS28Fae06803|CDS|CDS	14.0	3.0	15.4	P	COG0855	Polyphosphate kinase
TS28Bac4742|CDS|CDS	65.0	14.0	15.4	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi740386|CDS|CDS	16.9	3.7	15.3	P	COG2116	Formate/nitrite family of transporters
Ehal0947|CDS|CDS	4.5	1.0	14.9	P	COG3853	Uncharacterized protein involved in tellurite resistance
Bste1998|CDS|CDS	13.5	3.0	14.9	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
Msmi750917|CDS|CDS	2.3	0.5	14.9	P	COG0530	Ca2+/Na+ antiporter
BactD24083|CDS|CDS	17.6	4.0	14.6	P	COG4771|COG2304	Outer membrane receptor for ferrienterochelin and colicins|Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Bova4000|CDS|CDS	17.6	4.0	14.6	P	COG4771|COG2304	Outer membrane receptor for ferrienterochelin and colicins|Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Bbre0868|CDS|CDS	4.3	1.0	14.3	P	COG0306	Phosphate/sulphate permeases
PRABACTJOHN1943|CDS|CDS	8.5	2.0	14.1	P	COG0605	Superoxide dismutase
Bova3101|CDS|CDS	47.3	11.2	14.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bdor1761|CDS|CDS	9.3	2.3	13.2	P	COG3119	Arylsulfatase A and related enzymes
BVU1159|CDS|sulfatase	9.3	2.3	13.2	P	COG3119	Arylsulfatase A and related enzymes
TS29Bac03441|CDS|CDS	2.0	0.5	13.2	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bxyl0175|CDS|CDS	4.0	1.0	13.2	P	COG3004	Na+/H+ antiporter
TS28Met1345|CDS|CDS	8.0	2.0	13.2	P	COG2217	Cation transport ATPase
TS29Bac01872|CDS|CDS	2.7	0.7	13.2	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
BVU3788|CDS|choline-sulfatase	5.8	1.5	12.9	P	COG3119	Arylsulfatase A and related enzymes
TS28RumUnc1292|CDS|CDS	19.0	5.0	12.6	P	COG2239	Mg/Co/Ni transporter MgtE (contains CBS domain)
Bste2173|CDS|CDS	35.5	9.5	12.4	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Msmi751291|CDS|CDS	20.5	5.8	11.6	P	COG2116	Formate/nitrite family of transporters
TS28Met1184|CDS|CDS	20.5	5.8	11.6	P	COG2116	Formate/nitrite family of transporters
TS29Rum18984|CDS|CDS	14.0	4.0	11.6	P	COG3853	Uncharacterized protein involved in tellurite resistance
Bste0051|CDS|CDS	3.5	1.0	11.6	P	COG1629	Outer membrane receptor proteins, mostly Fe transport
HPAG10858|CDS|catalase	7.0	2.0	11.6	P	COG0753	Catalase
TS29Bac10370|CDS|CDS	26.0	7.5	11.5	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bdor1762|CDS|CDS	26.5	7.8	11.2	P	COG3119	Arylsulfatase A and related enzymes
TS28Par0863|CDS|CDS	40.0	12.0	11.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Pmer2906|CDS|CDS	5.0	1.5	11.0	P	COG1629	Outer membrane receptor proteins, mostly Fe transport
FpraM2120733|CDS|CDS	5.0	1.5	11.0	P	COG0581|COG0573	ABC-type phosphate transport system, permease component|ABC-type phosphate transport system, permease component
TS29Bac11284|CDS|CDS	9.4	3.0	10.4	P	COG4771|COG2304	Outer membrane receptor for ferrienterochelin and colicins|Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
TS28Bac3900|CDS|CDS	22.0	7.0	10.4	P	COG2382|COG0627	Enterochelin esterase and related enzymes|Predicted esterase
TS28Ali1512|CDS|CDS	56.0	18.0	10.3	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
TS28Bac3290|CDS|CDS	0.5	17.0	0.1	P	COG3119	Arylsulfatase A and related enzymes
Dfor0464|CDS|CDS	1.3	46.0	0.1	P	COG2217	Cation transport ATPase
TS28Bac7182|CDS|CDS	0.3	11.5	0.1	P	COG2193|COG2406	Bacterioferritin (cytochrome b1)|Protein distantly related to bacterial ferritins
Bdor1151|CDS|CDS	0.5	17.5	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae22200|CDS|CDS	0.5	17.5	0.1	P	COG3853	Uncharacterized protein involved in tellurite resistance
TS29Fae01503|CDS|CDS	0.5	18.0	0.1	P	COG3853	Uncharacterized protein involved in tellurite resistance
CspSS22626|CDS|CDS	0.5	18.0	0.1	P	COG2217	Cation transport ATPase
TS28Eub6792|CDS|CDS	1.5	56.0	0.1	P	COG0619|COG1122	ABC-type cobalt transport system, permease component CbiQ and related transporters|ABC-type cobalt transport system, ATPase component
Buni2918|CDS|CDS	0.5	19.5	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Col1623|CDS|CDS	1.0	39.0	0.1	P	COG1283	Na+/phosphate symporter
TS28Clo01553|CDS|CDS	1.0	39.0	0.1	P	COG1116|COG4525	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component|ABC-type taurine transport system, ATPase component
TS28Bac7031|CDS|CDS	2.0	79.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae20847|CDS|CDS	1.0	41.0	0.1	P	COG2059	Chromate transport protein ChrA
TS28Bac5935|CDS|CDS	2.0	83.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae10820|CDS|CDS	1.0	41.7	0.1	P	COG0471	Di- and tricarboxylate transporters
TS28Met1630|CDS|CDS	0.8	31.6	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS29Bac02568|CDS|CDS	0.2	8.5	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Rum14164|CDS|CDS	1.0	42.5	0.1	P	COG0471	Di- and tricarboxylate transporters
TS28Fae16665|CDS|CDS	0.6	25.0	0.1	P	COG1135	ABC-type metal ion transport system, ATPase component
TS29Bac02235|CDS|CDS	0.3	14.4	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Dlon1970|CDS|CDS	0.5	22.0	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS28Fae08974|CDS|CDS	1.3	56.0	0.1	P	COG1253|COG4536|COG4535	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB|Putative Mg2+ and Co2+ transporter CorC
TS28Rum12972|CDS|CDS	0.5	22.5	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS28Dor3136|CDS|CDS	0.5	22.5	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
Pmer0173|CDS|CDS	0.5	23.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae12094|CDS|CDS	0.6	27.0	0.1	P	COG1135	ABC-type metal ion transport system, ATPase component

TS28Fae17447|CDS|CDS	1.0	47.0	0.1	P	COG2217	Cation transport ATPase
TS28Fae19575|CDS|CDS	1.0	49.0	0.1	P	COG0855	Polyphosphate kinase
Rlac0825|CDS|CDS	1.3	67.3	0.1	P	COG2217	Cation transport ATPase
TS28Fae09808|CDS|CDS	0.4	19.0	0.1	P	COG0855	Polyphosphate kinase
FpraM2121804|CDS|CDS	0.3	12.8	0.1	P	COG1253|COG4536|COG4535	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB|Putative Mg2+ and Co2+ transporter CorC
TS28Eub3915|CDS|CDS	1.0	52.3	0.1	P	COG0581|COG0573	ABC-type phosphate transport system, permease component|ABC-type phosphate transport system, permease component
TS29Rum21104|CDS|CDS	1.0	53.0	0.1	P	COG3853	Uncharacterized protein involved in tellurite resistance
TS28Eub6790|CDS|CDS	1.0	53.0	0.1	P	COG1122	ABC-type cobalt transport system, ATPase component
TS28Bac6265|CDS|CDS	0.5	27.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae13172|CDS|CDS	0.5	29.0	0.1	P	COG0475	Kef-type K+ transport systems, membrane components
TS28Rum14589|CDS|CDS	0.5	31.0	0.1	P	COG0569	K+ transport systems, NAD-binding component
TS28Fae18320|CDS|CDS	0.3	15.8	0.1	P	COG1253|COG4536|COG4535	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB|Putative Mg2+ and Co2+ transporter CorC
TS29Bif3314|CDS|CDS	0.3	16.4	0.1	P	COG0474	Cation transport ATPase
TS28Eub6616|CDS|CDS	1.5	99.0	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
Bdor1140|CDS|CDS	0.3	22.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Bac6503|CDS|CDS	1.0	67.0	0.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae02501|CDS|CDS	1.0	68.0	0.0	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS28Fae22782|CDS|CDS	0.5	34.5	0.0	P	COG2217	Cation transport ATPase
CspSS21658|CDS|CDS	1.3	96.5	0.0	P	COG2217	Cation transport ATPase
TS28Eub8823|CDS|CDS	1.5	120.5	0.0	P	COG2217	Cation transport ATPase
TS28Fae01193|CDS|CDS	0.3	27.0	0.0	P	COG2239	Mg/Co/Ni transporter MgtE (contains CBS domain)
TS28Bac5338|CDS|CDS	0.3	28.0	0.0	P	COG0475|COG1226|COG4651	Kef-type K+ transport systems, membrane components|Kef-type K+ transport systems, predicted NAD-binding component|Kef-type K+ transport system, predicted NAD-binding component
TS28Bif4716|CDS|CDS	0.3	22.4	0.0	P	COG0474	Cation transport ATPase
TS28Eub8292|CDS|CDS	1.0	106.5	0.0	P	COG0855	Polyphosphate kinase
TS28Fae22049|CDS|CDS	0.5	73.0	0.0	P	COG0569	K+ transport systems, NAD-binding component
TS28Bac0741|CDS|CDS	0.5	76.5	0.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae20104|CDS|CDS	0.4	70.0	0.0	P	COG0855	Polyphosphate kinase
RintL12242|CDS|CDS	4.0	1.0	13.2	P|D	COG1135|COG2884|COG2177	ABC-type metal ion transport system, ATPase component|Predicted ATPase involved in cell division|Cell division protein
TS28Clo01379|CDS|CDS	1.0	128.0	0.0	P|D	COG2884|COG2177|COG1135	Predicted ATPase involved in cell division|Cell division protein|ABC-type metal ion transport system, ATPase component
Casp5378|CDS|CDS	6.0	1.0	19.8	P|E	COG0444|COG1123	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component|ATPase components of various ABC-type transport systems, contain duplicated ATPase
Bryfor1877|CDS|CDS	4.0	1.0	13.2	P|E	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
Rumhyd2304|CDS|CDS	3.0	0.5	19.8	P|E|F	COG0503|COG0601	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins|ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
Csp3530|CDS|CDS	2.3	0.1	92.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
Ecan0984|CDS|CDS	2.3	0.1	92.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
DpigATC0313|CDS|CDS	2.3	0.1	92.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
Ppen0002|CDS|CDS	2.3	0.1	92.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
CspM6211669|CDS|CDS	2.3	0.1	92.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
Cnex0444|CDS|CDS	2.3	0.1	92.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
Begg3358|CDS|CDS	1.8	0.1	70.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
ShigspD91992|CDS|CDS	14.5	1.0	48.0	P|E|G	COG0477	Permeases of the major facilitator superfamily
Prus2866|CDS|CDS	1.1	0.1	44.7	P|E|G	COG0477	Permeases of the major facilitator superfamily
Msmi751681|CDS|CDS	1.1	0.1	44.7	P|E|G	COG0477	Permeases of the major facilitator superfamily
Bcac0408|CDS|CDS	11.0	1.0	36.4	P|E|G	COG0477	Permeases of the major facilitator superfamily
Msmi740185|CDS|CDS	0.3	0.1	12.2	P|E|G	COG0477	Permeases of the major facilitator superfamily
Bova1303|CDS|CDS	1.8	0.5	12.1	P|E|G	COG0477	Permeases of the major facilitator superfamily
Cste0061|CDS|CDS	3.5	1.0	11.6	P|E|G	COG0477	Permeases of the major facilitator superfamily
Bdor0617|CDS|CDS	17.5	5.0	11.6	P|E|G	COG0477|COG2271|COG2814	Permeases of the major facilitator superfamily|Sugar phosphate permease|Arabinose efflux permease
Bste2908|CDS|CDS	10.0	3.0	11.0	P|E|G	COG0477	Permeases of the major facilitator superfamily
Bdor0274|CDS|CDS	9.7	3.0	10.7	P|E|G	COG0477	Permeases of the major facilitator superfamily
Msmi740824|CDS|CDS	7.9	1.0	26.2	P|E|G|V	COG1131|COG3842|COG3839|COG1126|COG1125|COG1123|COG4172|COG1135|COG4175	ABC-type multidrug transport system, ATPase component|ABC-type spermidine/putrescine transport systems, ATPase components|ABC-type sugar transport systems, ATPase components|ABC-type polar amino acid transport system, ATPase component|ABC-type proline/glycine betaine transport systems, ATPase components|ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type uncharacterized transport system, duplicated ATPase component|ABC-type metal ion transport system, ATPase component|ABC-type proline/glycine betaine transport system, ATPase component
Cspi0889|CDS|CDS	14.0	1.0	46.3	P|E|V|Q	COG1136|COG4181|COG1126|COG1135|COG4598	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component|ABC-type polar amino acid transport system, ATPase component|ABC type metal ion transport system, ATPase component|ABC-type histidine transport system, ATPase component
ShigspD90220|CDS|CDS	5.5	1.0	18.2	P|F	COG0248	Exopolyphosphatase
Bcap2857|CDS|CDS	6.5	0.5	43.0	P|G	COG1629|COG1312	Outer membrane receptor proteins, mostly Fe transport|D-mannonate dehydratase

<table>
<tr><td>Bdor0021|CDS|CDS</td><td>11.7</td><td>1.0</td><td>38.6</td><td>P|G</td><td>COG1218|COG0483</td><td>3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase|Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family</td></tr>
<tr><td>Bova1281|CDS|CDS</td><td>5.0</td><td>0.5</td><td>33.1</td><td>P|G</td><td>COG1218|COG0483</td><td>3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase|Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family</td></tr>
<tr><td>Bcap3562|CDS|CDS</td><td>7.5</td><td>1.5</td><td>16.5</td><td>P|G</td><td>COG1629|COG1312</td><td>Outer membrane receptor proteins, mostly Fe transport|D-mannonate dehydratase</td></tr>
<tr><td>Casp1491|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>P|H</td><td>COG0607|COG0301</td><td>Rhodanese-related sulfurtransferase|Thiamine biosynthesis ATP pyrophosphatase</td></tr>
<tr><td>Msmi741249|CDS|CDS</td><td>3.4</td><td>0.5</td><td>22.2</td><td>P|H</td><td>COG1122|COG1903</td><td>ABC-type cobalt transport system, ATPase component|Cobalamin biosynthesis protein CbiD</td></tr>
<tr><td>Msmi751307|CDS|CDS</td><td>2.9</td><td>0.5</td><td>18.8</td><td>P|H</td><td>COG0476|COG0607</td><td>Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2|Rhodanese-related sulfurtransferase</td></tr>
<tr><td>TS29Rum21018|CDS|CDS</td><td>10.0</td><td>3.0</td><td>11.0</td><td>P|H</td><td>COG1179|COG0607|COG0476</td><td>Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1|Rhodanese-related sulfurtransferase|Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2</td></tr>
<tr><td>TS28Rum12300|CDS|CDS</td><td>0.5</td><td>18.5</td><td>0.1</td><td>P|H</td><td>COG0607|COG0301</td><td>Rhodanese-related sulfurtransferase|Thiamine biosynthesis ATP pyrophosphatase</td></tr>
<tr><td>TS28Ali0168|CDS|CDS</td><td>1.0</td><td>39.0</td><td>0.1</td><td>P|H</td><td>COG4771|COG4206</td><td>Outer membrane receptor for ferrienterochelin and colicins|Outer membrane cobalamin receptor protein</td></tr>
<tr><td>TS28Fae01187|CDS|CDS</td><td>0.7</td><td>27.0</td><td>0.1</td><td>P|H</td><td>COG0607|COG0301</td><td>Rhodanese-related sulfurtransferase|Thiamine biosynthesis ATP pyrophosphatase</td></tr>
<tr><td>TS28Rum02826|CDS|CDS</td><td>0.5</td><td>21.5</td><td>0.1</td><td>P|H</td><td>COG1120|COG4604|COG1865</td><td>ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components|ABC-type enterochelin transport system, ATPase component|Uncharacterized conserved protein</td></tr>
<tr><td>TS28Fae14580|CDS|CDS</td><td>13.0</td><td>3.0</td><td>14.3</td><td>P|I</td><td>COG0657|COG2072</td><td>Esterase/lipase|Predicted flavoprotein involved in K+ transport</td></tr>
<tr><td>TS29RumUnc0659|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>P|J</td><td>COG0566|COG0474</td><td>rRNA methylases|Cation transport ATPase</td></tr>
<tr><td>TS28Rum16435|CDS|CDS</td><td>1.0</td><td>55.5</td><td>0.1</td><td>P|J</td><td>COG0566|COG0474</td><td>rRNA methylases|Cation transport ATPase</td></tr>
<tr><td>TS29Fae05416|CDS|CDS</td><td>4.5</td><td>1.0</td><td>14.9</td><td>P|K</td><td>COG1918|COG1321</td><td>Fe2+ transport system protein A|Mn-dependent transcriptional regulator</td></tr>
<tr><td>TS29Fae05143|CDS|CDS</td><td>15.3</td><td>0.5</td><td>101.4</td><td>P|M</td><td>COG0226|COG2885</td><td>ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins</td></tr>
<tr><td>FpraM2120301|CDS|CDS</td><td>7.3</td><td>1.5</td><td>16.2</td><td>P|M</td><td>COG0226|COG2885</td><td>ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins</td></tr>
<tr><td>Bthe3734413|CDS|CDS</td><td>1.5</td><td>0.3</td><td>14.9</td><td>P|M</td><td>COG3015</td><td>Uncharacterized lipoprotein NlpE involved in copper resistance</td></tr>
<tr><td>Bthe7331626|CDS|CDS</td><td>1.5</td><td>0.3</td><td>14.9</td><td>P|M</td><td>COG3015</td><td>Uncharacterized lipoprotein NlpE involved in copper resistance</td></tr>
<tr><td>TS29Bac08855|CDS|CDS</td><td>1.5</td><td>0.3</td><td>14.9</td><td>P|M</td><td>COG3015</td><td>Uncharacterized lipoprotein NlpE involved in copper resistance</td></tr>
<tr><td>TS28Fae12475|CDS|CDS</td><td>0.5</td><td>32.0</td><td>0.1</td><td>P|M</td><td>COG0226|COG2885</td><td>ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins</td></tr>
<tr><td>Pmer2305|CDS|CDS</td><td>584.8</td><td>6.0</td><td>322.3</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Bxyl0582|CDS|CDS</td><td>15.0</td><td>1.0</td><td>49.6</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>BactD13695|CDS|CDS</td><td>10.2</td><td>1.0</td><td>33.6</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Pmer2795|CDS|CDS</td><td>21.0</td><td>3.0</td><td>23.1</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>TS29Bac05028|CDS|CDS</td><td>10.2</td><td>1.5</td><td>22.4</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Bdor2902|CDS|CDS</td><td>3.3</td><td>0.7</td><td>16.5</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Bxyl3703|CDS|CDS</td><td>2.5</td><td>0.5</td><td>16.5</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>TS29Bac07248|CDS|CDS</td><td>2.5</td><td>0.5</td><td>16.5</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Bste3074|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>P|T</td><td>COG0517|COG0589|COG0038</td><td>FOG: CBS domain|Universal stress protein UspA and related nucleotide-binding proteins|Chloride channel protein EriC</td></tr>
<tr><td>Bdor1758|CDS|CDS</td><td>20.2</td><td>4.8</td><td>13.8</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Pmer0905|CDS|CDS</td><td>3.2</td><td>0.8</td><td>12.6</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Bova2503|CDS|CDS</td><td>5.2</td><td>1.5</td><td>11.4</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Bdor2708|CDS|CDS</td><td>19.0</td><td>6.0</td><td>10.5</td><td>P|T</td><td>COG3712</td><td>Fe2+-dicitrate sensor, membrane component</td></tr>
<tr><td>Pmer2876|CDS|CDS</td><td>13.0</td><td>3.0</td><td>14.3</td><td>P|T|E|K</td><td>COG0642|COG2202|COG0784|COG0834|COG2203|COG3437|COG3300|COG3706|COG4191|COG3899|COG2703</td><td>Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Signal transduction histidine kinase regulating C4-dicarboxylate transport system|Predicted ATPase|Hemerythrin</td></tr>
<tr><td>Csym0350|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>P|V</td><td>COG0841|COG3696</td><td>Cation/multidrug efflux pump|Putative silver efflux pump</td></tr>
<tr><td>TS28Col0898|CDS|CDS</td><td>2.0</td><td>68.0</td><td>0.1</td><td>P|V</td><td>COG0841|COG3696</td><td>Cation/multidrug efflux pump|Putative silver efflux pump</td></tr>
<tr><td>TS28Bac7939|CDS|CDS</td><td>1.0</td><td>44.5</td><td>0.1</td><td>P|V</td><td>COG0841|COG3696</td><td>Cation/multidrug efflux pump|Putative silver efflux pump</td></tr>
<tr><td>TS28Rum04557|CDS|CDS</td><td>5.0</td><td>0.5</td><td>33.1</td><td>Q</td><td>COG0500</td><td>SAM-dependent methyltransferases</td></tr>
<tr><td>TS28Rum14910|CDS|CDS</td><td>5.0</td><td>0.5</td><td>33.1</td><td>Q</td><td>COG0500</td><td>SAM-dependent methyltransferases</td></tr>
<tr><td>ShigspD91724|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>Q</td><td>COG2132</td><td>Putative multicopper oxidases</td></tr>
<tr><td>ShigspD91231|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>Q</td><td>COG2015</td><td>Alkyl sulfatase and related hydrolases</td></tr>
<tr><td>Robe3274|CDS|CDS</td><td>10.0</td><td>2.0</td><td>16.5</td><td>Q</td><td>COG4869</td><td>Propanediol utilization protein</td></tr>
<tr><td>TS29Bac07694|CDS|CDS</td><td>1.7</td><td>0.3</td><td>16.5</td><td>Q</td><td>COG0500</td><td>SAM-dependent methyltransferases</td></tr>
<tr><td>Cspi1235|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>Q</td><td>COG0561|COG2050</td><td>Predicted hydrolases of the HAD superfamily|Uncharacterized protein, possibly involved in aromatic compounds catabolism</td></tr>
<tr><td>Ehal0409|CDS|CDS</td><td>7.5</td><td>2.0</td><td>12.4</td><td>Q</td><td>COG4910</td><td>Propanediol dehydratase, small subunit</td></tr>
<tr><td>TS28Rum12776|CDS|CDS</td><td>15.0</td><td>4.0</td><td>12.4</td><td>Q</td><td>COG2015</td><td>Alkyl sulfatase and related hydrolases</td></tr>
<tr><td>TS28Rum02928|CDS|CDS</td><td>4.0</td><td>170.0</td><td>0.1</td><td>Q</td><td>COG1020|COG3321|COG3319|COG3320</td><td>Non-ribosomal peptide synthetase modules and related proteins|Polyketide synthase modules and related proteins|Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases|Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes</td></tr>
<tr><td>TS28Rum00561|CDS|CDS</td><td>0.5</td><td>22.3</td><td>0.1</td><td>Q</td><td>COG4909</td><td>Propanediol dehydratase, large subunit</td></tr>
<tr><td>TS28Rum15555|CDS|CDS</td><td>0.5</td><td>24.0</td><td>0.1</td><td>Q</td><td>COG0561|COG2050</td><td>Predicted hydrolases of the HAD superfamily|Uncharacterized protein, possibly involved in aromatic compounds catabolism</td></tr>
<tr><td>TS28Met1416|CDS|CDS</td><td>0.3</td><td>13.3</td><td>0.1</td><td>Q</td><td>COG1228</td><td>Imidazolonepropionase and related amidohydrolases</td></tr>
</table>

TS28Clo01626|CDS|CDS	1.0	75.0	0.0	Q	COG1335	Amidases related to nicotinamidase
TS28Eub8595|CDS|CDS	1.0	172.0	0.0	Q	COG2931	RTX toxins and related Ca2+-binding proteins
TS29Bif3494|CDS|CDS	0.3	46.5	0.0	Q	COG2931	RTX toxins and related Ca2+-binding proteins
TS28Eub5422|CDS|CDS	1.0	274.5	0.0	Q	COG1020|COG3321|COG3319|COG3320	Non-ribosomal peptide synthetase modules and related proteins|Polyketide synthase modules and related proteins|Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases|Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes
TS28Fae22148|CDS|CDS	1.0	41.0	0.1	Q|V	COG1136|COG4181	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component
Even0449|CDS|CDS	50.7	0.5	335.1	T	COG0642|COG2202|COG5002	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase
Cnex0540|CDS|CDS	50.7	0.5	335.1	T	COG0642|COG2202|COG5002	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase
Msmi750943|CDS|CDS	6.8	0.3	90.2	T	COG0517|COG0589|COG0618|COG3448	FOG: CBS domain|Universal stress protein UspA and related nucleotide-binding proteins|Exopolyphosphatase-related proteins|CBS-domain-containing membrane protein
Hfil2372|CDS|CDS	17.0	1.0	56.2	T	COG2202|COG3300|COG5001|COG2200	FOG: PAS/PAC domain|MHYT domain (predicted integral membrane sensor domain)|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain
ShigspD92172|CDS|CDS	7.5	0.5	49.6	T	COG2202|COG3447|COG3300|COG5001|COG2200|COG3614	FOG: PAS/PAC domain|Predicted integral membrane sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain|Predicted periplasmic ligand-binding sensor domain
CspM6212495|CDS|CDS	14.0	1.0	46.3	T	COG1217	Predicted membrane GTPase involved in stress response
TS29Fae00912|CDS|CDS	6.5	0.5	43.0	T	COG0642|COG5002|COG2202	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain
Bdor2976|CDS|CDS	11.0	1.0	36.4	T	COG0642	Signal transduction histidine kinase
CspL21207|CDS|CDS	10.6	1.0	35.2	T	COG0642|COG2202|COG5002|COG2203|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: GAF domain|Osmosensitive K+ channel histidine kinase
RintL10786|CDS|CDS	3.2	0.3	31.4	T	COG0642|COG2202|COG5002|COG2203|COG3300|COG3322|COG5001|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
Pmer2757|CDS|CDS	14.0	1.5	30.9	T	COG0642|COG2202|COG5002|COG2770|COG3614|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: HAMP domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase
Begg1032|CDS|CDS	4.5	0.5	29.8	T	COG2310|COG4110	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1|Uncharacterized protein involved in stress response
TS29Par943|CDS|CDS	4.5	0.5	29.8	T	COG2310|COG4110	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1|Uncharacterized protein involved in stress response
BactD13600|CDS|CDS	4.3	0.5	28.7	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins
TS29Bac04334|CDS|CDS	4.3	0.5	28.7	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins
Ceut1555|CDS|CDS	2.0	0.3	26.5	T	COG1217	Predicted membrane GTPase involved in stress response
TS29Fae00607|CDS|CDS	4.0	0.5	26.5	T	COG2202|COG5001|COG2200	FOG: PAS/PAC domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain
ShigspD91720|CDS|CDS	7.5	1.0	24.8	T	COG0642	Signal transduction histidine kinase
TS29Fae06630|CDS|CDS	7.0	1.0	23.1	T	COG2202|COG2203|COG3300|COG5001|COG2200	FOG: PAS/PAC domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain
TS29Fae04540|CDS|CDS	3.5	0.5	23.1	T	COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism
TS29Bac01158|CDS|CDS	6.5	1.0	21.5	T	COG0618|COG3887	Exopolyphosphatase-related proteins|Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain
TS29Fae03004|CDS|CDS	8.3	1.3	20.7	T	COG2202|COG2770|COG2203|COG3322|COG5001|COG4251|COG2199|COG2200	FOG: PAS/PAC domain|FOG: HAMP domain|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: GGDEF domain|FOG: EAL domain
FpraM2122134|CDS|CDS	8.3	1.3	20.7	T	COG2202|COG2203|COG3322|COG5001|COG2199|COG4251|COG2770|COG2200	FOG: PAS/PAC domain|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain|FOG: EAL domain
Casp1960|CDS|CDS	6.0	1.0	19.8	T	COG2202|COG2203|COG5001|COG2199|COG2200	FOG: PAS/PAC domain|FOG: GAF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: GGDEF domain|FOG: EAL domain
Acol0407|CDS|CDS	6.0	1.0	19.8	T	COG0642|COG5002	Signal transduction histidine kinase|Signal transduction histidine kinase

TS28Bac4675|CDS|CDS	6.0	1.0	19.8	T	COG0642	Signal transduction histidine kinase
TS29Bac01648|CDS|CDS	6.0	1.0	19.8	T	COG0642	Signal transduction histidine kinase
Pmer1943|CDS|CDS	39.5	7.0	18.7	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase
ShigspD92677|CDS|CDS	5.5	1.0	18.2	T	COG2766	Putative Ser protein kinase
RintL11018|CDS|CDS	5.5	1.0	18.2	T	COG2202|COG3300|COG5001|COG2200|COG3614	FOG: PAS/PAC domain|MHYT domain (predicted integral membrane sensor domain)|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain|Predicted periplasmic ligand-binding sensor domain
Hfil1937|CDS|CDS	11.0	2.0	18.2	T	COG2202|COG2203|COG3300|COG3706|COG5001|COG2200	FOG: PAS/PAC domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain
TS28Rum08086|CDS|CDS	69.0	13.0	17.6	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29RumUnc1391|CDS|CDS	2.5	0.5	16.5	T	COG0642|COG5002|COG2202|COG2770|COG2203	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain|FOG: GAF domain
Pmer1554|CDS|CDS	39.0	8.0	16.1	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins
BactD23074|CDS|CDS	4.8	1.0	15.9	T	COG1217	Predicted membrane GTPase involved in stress response
Bint2045|CDS|CDS	2.3	0.5	15.4	T	COG1734	DnaK suppressor protein
BWH21305|CDS|CDS	2.3	0.5	15.4	T	COG1734	DnaK suppressor protein
BactD11172|CDS|CDS	3.0	0.7	14.9	T	COG0642|COG2198|COG2202|COG0784|COG3300|COG3452|COG3614	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain
BactD13569|CDS|CDS	4.0	1.0	13.2	T	COG5002|COG3292|COG3706	Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain
RintL12076|CDS|CDS	4.0	1.0	13.2	T	COG2202|COG3300|COG3706|COG5001|COG2200	FOG: PAS/PAC domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain
Bste0574|CDS|CDS	20.0	5.0	13.2	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase
TS29Fae08381|CDS|CDS	4.0	1.0	13.2	T	COG1217	Predicted membrane GTPase involved in stress response
Csym2462|CDS|CDS	4.0	1.0	13.2	T	COG0642|COG2202|COG5002|COG2770	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: HAMP domain
CspSS22260|CDS|CDS	2.0	0.5	13.2	T	COG0394	Protein-tyrosine-phosphatase
Bste2938|CDS|CDS	7.0	2.0	11.6	T	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
TS28Rum13628|CDS|CDS	2.0	66.5	0.1	T	COG0618|COG3887	Exopolyphosphatase-related proteins|Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain
TS29Rum21102|CDS|CDS	1.0	34.0	0.1	T	COG2310|COG4110	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1|Uncharacterized protein involved in stress response
TS28Col0398|CDS|CDS	1.0	36.0	0.1	T	COG1966	Carbon starvation protein, predicted membrane protein
TS29Rum17091|CDS|CDS	1.0	36.0	0.1	T	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
TS28Bac6860|CDS|CDS	0.7	24.0	0.1	T	COG0642	Signal transduction histidine kinase
TS28Eub1226|CDS|CDS	1.0	36.5	0.1	T	COG0784	FOG: CheY-like receiver
TS28Rum15157|CDS|CDS	1.0	37.0	0.1	T	COG2199	FOG: GGDEF domain
Cnex0560|CDS|CDS	1.9	70.7	0.1	T	COG0642|COG2202|COG5002|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
TS28Fae13067|CDS|CDS	1.0	38.0	0.1	T	COG0642|COG5002|COG2202	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain
Ehal0756|CDS|CDS	3.0	114.5	0.1	T	COG0642|COG2198|COG2202|COG0784|COG5278|COG3300|COG5001|COG3452|COG3614	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain
TS28Rum13923|CDS|CDS	0.5	20.0	0.1	T	COG1966	Carbon starvation protein, predicted membrane protein
TS28Fae11159|CDS|CDS	0.5	20.0	0.1	T	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
TS29Rum11493|CDS|CDS	2.5	100.5	0.1	T	COG2202|COG2203|COG3300|COG5278|COG5001|COG2200	FOG: PAS/PAC domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain
TS28Fae21179|CDS|CDS	0.3	13.5	0.1	T	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
TS28Eub8875|CDS|CDS	1.5	62.5	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain

TS28Rum10354|CDS|CDS	1.0	42.0	0.1	T	COG2202|COG2203|COG3300|COG3322|COG5001|COG3706|COG4251|COG2199|COG2200	FOG: PAS/PAC domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: GGDEF domain|FOG: EAL domain
CspSS20183|CDS|CDS	0.5	21.6	0.1	T	COG0642|COG2202|COG5002|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS28Bac6602|CDS|CDS	0.7	29.0	0.1	T	COG0642	Signal transduction histidine kinase
TS28Rum10926|CDS|CDS	1.0	45.0	0.1	T	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
FpraM2122506|CDS|CDS	2.8	126.8	0.1	T	COG0642|COG2202|COG5002|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
Even0457|CDS|CDS	1.7	80.4	0.1	T	COG0642|COG2202|COG5002|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
CspL21156|CDS|CDS	0.3	11.7	0.1	T	COG0642|COG2202|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
TS28Rum13607|CDS|CDS	0.5	24.5	0.1	T	COG1702	Phosphate starvation-inducible protein PhoH, predicted ATPase
Dfor0143|CDS|CDS	0.1	7.0	0.1	T	COG0642|COG2202|COG0784|COG5002|COG2203|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|FOG: GAF domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
Ccom0780|CDS|CDS	0.8	42.2	0.1	T	COG0642|COG2202|COG5002|COG2203|COG3322|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS28Eub6518|CDS|CDS	1.0	53.0	0.1	T	COG0642|COG5002|COG2202|COG2770	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain
TS28Fae02109|CDS|CDS	0.5	30.0	0.1	T	COG0642|COG5002|COG2202|COG0784|COG2203	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|FOG: GAF domain
TS28Bac0861|CDS|CDS	0.5	33.0	0.1	T	COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains
TS29Rum17077|CDS|CDS	1.0	79.0	0.0	T	COG2202|COG3300|COG3322|COG5001|COG3706|COG2200	FOG: PAS/PAC domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|FOG: EAL domain
CspSS21921|CDS|CDS	0.2	13.4	0.0	T	COG0642|COG5002|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
Ehal1717|CDS|CDS	0.2	13.4	0.0	T	COG0642|COG5002|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
Dlon2019|CDS|CDS	0.3	20.8	0.0	T	COG0642|COG2202|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
TS28Fae20439|CDS|CDS	0.3	28.0	0.0	T	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
TS29Rum17799|CDS|CDS	0.5	42.2	0.0	T	COG0642|COG5002|COG2202|COG3292|COG2205|COG4250	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
RintL10496|CDS|CDS	0.5	42.2	0.0	T	COG0642|COG2202|COG5002|COG3292|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
CspM6212140|CDS|CDS	0.5	42.2	0.0	T	COG0642|COG2202|COG5002|COG3292|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS28Eub8190|CDS|CDS	0.5	43.5	0.0	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS28Fae14486|CDS|CDS	1.0	89.5	0.0	T	COG0642|COG5002|COG2202	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain
Bcap0393|CDS|CDS	0.3	23.0	0.0	T	COG1217	Predicted membrane GTPase involved in stress response
Dfor2877|CDS|CDS	0.3	25.7	0.0	T	COG0642|COG2202|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
TS28Dor2629|CDS|CDS	0.5	57.0	0.0	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Dor2227|CDS|CDS	0.5	59.0	0.0	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS28Fae14120|CDS|CDS	0.5	59.2	0.0	T	COG0642|COG5002|COG2202|COG2205|COG4250	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain

Dlon0976|CDS|CDS	0.3	36.8	0.0	T	COG0642|COG2202|COG0784|COG5002|COG2203|COG3322|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS28Clo00099|CDS|CDS	0.3	30.0	0.0	T	COG0642|COG5002|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
Rbro0238|CDS|CDS	0.3	32.0	0.0	T	COG0642|COG2202|COG5002|COG5001|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
TS28Eub7238|CDS|CDS	0.2	21.9	0.0	T	COG0642|COG5002|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
Robe0036|CDS|CDS	0.3	33.0	0.0	T	COG0642|COG2202|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
CspM6210571|CDS|CDS	0.3	37.8	0.0	T	COG0642|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
Eeli2696|CDS|CDS	0.3	43.1	0.0	T	COG0642|COG2202|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
Ehal1316|CDS|CDS	0.3	50.8	0.0	T	COG0642|COG2202|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
FpraM2120017|CDS|CDS	0.3	50.9	0.0	T	COG0642|COG5002|COG3300|COG4251|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|MHYT domain (predicted integral membrane sensor domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
Msmi751551|CDS|CDS	43.8	0.5	289.9	T|C	COG0589|COG0633	Universal stress protein UspA and related nucleotide-binding proteins|Ferredoxin
Msmi740038|CDS|CDS	2.8	0.3	36.6	T|C	COG5635|COG1413	Predicted NTPase (NACHT family)|FOG: HEAT repeat
TS28Fae09082|CDS|CDS	1.3	49.0	0.1	T|D	COG1674|COG1716	DNA segregation ATPase FtsK/SpoIIIE and related proteins|FOG: FHA domain
Bpse1757|CDS|CDS	0.5	38.5	0.0	T|D	COG1716|COG1674	FOG: FHA domain|DNA segregation ATPase FtsK/SpoIIIE and related proteins
TS28Bif1812|CDS|CDS	0.5	74.5	0.0	T|D	COG1674|COG1716	DNA segregation ATPase FtsK/SpoIIIE and related proteins|FOG: FHA domain
BactD13268|CDS|CDS	7.0	0.3	69.4	T|E	COG0642|COG2198|COG2202|COG0784|COG0834|COG3322	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain
Msmi750695|CDS|CDS	19.8	1.6	41.2	T|E	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
Msmi740985|CDS|CDS	19.8	1.6	41.2	T|E	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
RintL13909|CDS|CDS	11.0	1.0	36.4	T|E	COG0642|COG2198|COG2202|COG0784|COG0834|COG2203|COG3300|COG3452|COG3614	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain
Msmi750694|CDS|CDS	2.5	0.3	33.1	T|E	COG0834|COG0765	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component
Msmi740986|CDS|CDS	5.0	0.6	28.3	T|E	COG0834|COG0765	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component
Hfil0004|CDS|CDS	8.0	1.0	26.5	T|E	COG0642|COG2202|COG3447|COG0784|COG5002|COG0834|COG2770|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Predicted integral membrane sensor domain|FOG: CheY-like receiver|Signal transduction histidine kinase|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: HAMP domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
ShigspD91559|CDS|CDS	5.0	1.0	16.5	T|E	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
Bova0146|CDS|CDS	5.0	1.0	16.5	T|E	COG0642|COG2198|COG2202|COG0784|COG5002|COG3292|COG0834|COG5278|COG3300|COG2770	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|FOG: HAMP domain
Svar1673|CDS|CDS	17.0	5.0	11.2	T|E	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain

CspSS22526|CDS|CDS	5.0	1.5	11.0	T|E	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
Bdor0746|CDS|CDS	22.0	6.7	10.9	T|E	COG0642|COG2198|COG0784|COG0834|COG2203|COG3300|COG4252|COG2770|COG3452	Signal transduction histidine kinase|FOG: HPt domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Predicted transmembrane sensor domain|FOG: HAMP domain|Predicted periplasmic ligand-binding sensor domain
RintL10436|CDS|CDS	8.0	1.0	26.5	T|E|K	COG0642|COG2198|COG0784|COG0834|COG2203|COG3437|COG5278|COG2770|COG3452	Signal transduction histidine kinase|FOG: HPt domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|FOG: HAMP domain|Predicted periplasmic ligand-binding sensor domain
Robe0731|CDS|CDS	1.0	39.5	0.1	T|E|K	COG0642|COG2198|COG0784|COG0834|COG2203|COG3437|COG3300|COG2770|COG3452	Signal transduction histidine kinase|FOG: HPt domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|MHYT domain (predicted integral membrane sensor domain)|FOG: HAMP domain|Predicted periplasmic ligand-binding sensor domain
Dfor0158|CDS|CDS	1.0	44.0	0.1	T|E|K	COG0642|COG2198|COG2202|COG0834|COG2203|COG3437|COG5278|COG3300|COG3452	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain
Robe3764|CDS|CDS	1.0	47.5	0.1	T|E|K	COG0642|COG2198|COG0834|COG2203|COG3437|COG5278|COG3300|COG3452|COG3614	Signal transduction histidine kinase|FOG: HPt domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain
Robe2726|CDS|CDS	1.0	98.0	0.0	T|E|K	COG0642|COG2198|COG2202|COG0784|COG0834|COG2203|COG3437|COG5278|COG3300|COG3452	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain
Pmer2994|CDS|CDS	2.0	0.5	13.2	T|E|K|L|U|Q	COG3291|COG0515|COG1506|COG4946|COG0823|COG1228|COG3710	FOG: PKD repeat|Serine/threonine protein kinase|Dipeptidyl aminopeptidases/acylaminoacyl-peptidases|Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system|Periplasmic component of the Tol biopolymer transport system|Imidazolonepropionase and related amidohydrolases|DNA-binding winged-HTH domains
ShigspD90894|CDS|CDS	3.0	0.5	19.8	T|E|K|Q	COG2204|COG1221|COG3604|COG3829|COG3284|COG3283	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain|Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains|Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains|Transcriptional activator of acetoin/glycerol metabolism|Transcriptional regulator of aromatic amino acids metabolism
Bste0121|CDS|CDS	10.0	2.0	16.5	T|F	COG0737|COG3103|COG4085	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases|SH3 domain protein|Predicted RNA-binding protein, contains TRAM domain
Even0805|CDS|CDS	66.0	2.0	109.1	T|K	COG0317|COG2357	Guanosine polyphosphate pyrophosphohydrolases/synthetases|Uncharacterized protein conserved in bacteria
Buni2044|CDS|CDS	54.0	2.0	89.3	T|K	COG3279	Response regulator of the LytR/AlgR family
Bste1223|CDS|CDS	31.0	2.0	51.3	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
BactD13575|CDS|CDS	6.2	0.5	41.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Bxyl0397|CDS|CDS	6.2	0.5	41.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Bste0986|CDS|CDS	5.5	0.5	36.4	T|K	COG0642|COG2198|COG2202|COG0784|COG5002|COG2203|COG3437|COG3322|COG4252|COG3706|COG5001|COG4585|COG0745|COG2199|COG4251|COG2208	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Signal transduction histidine kinase|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|FOG: GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Serine phosphatase RsbU, regulator of sigma subunit

FpraM2120635|CDS|CDS	4.7	0.5	30.9	T|K	COG4753|COG0745|COG2197|COG4977|COG2207|COG4936|COG3707	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain|AraC-type DNA-binding domain-containing proteins|Predicted sensor domain|Response regulator with putative antiterminator output domain
Dfor3138|CDS|CDS	18.0	2.0	29.8	T|K	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
Bcap1917|CDS|CDS	8.0	1.0	26.5	T|K	COG0642|COG2202|COG5002|COG0745	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Bxyl0974|CDS|CDS	3.7	0.5	24.3	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Msmi740688|CDS|CDS	3.5	0.5	22.8	T|K	COG2199|COG0517|COG1475|COG0618|COG1994|COG1900	FOG: GGDEF domain|FOG: CBS domain|Predicted transcriptional regulators|Exopolyphosphatase-related proteins|Zn-dependent proteases|Uncharacterized conserved protein
Msmi750991|CDS|CDS	3.5	0.5	22.8	T|K	COG2199|COG0517|COG1475|COG0618|COG1994|COG1900	FOG: GGDEF domain|FOG: CBS domain|Predicted transcriptional regulators|Exopolyphosphatase-related proteins|Zn-dependent proteases|Uncharacterized conserved protein
BactD11047|CDS|CDS	8.3	1.3	20.7	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
Bxyl1337|CDS|CDS	8.3	1.3	20.7	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
ShigspD92657|CDS|CDS	6.0	1.0	19.8	T|K	COG3300|COG3322|COG5001|COG2200|COG2771|COG4943	MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain|DNA-binding HTH domain-containing proteins|Predicted signal transduction protein containing sensor and EAL domains
RintL10372|CDS|CDS	6.0	1.0	19.8	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Msmi741242|CDS|CDS	5.3	0.9	18.9	T|K	COG0517|COG0589|COG1994|COG2524|COG3448	FOG: CBS domain|Universal stress protein UspA and related nucleotide-binding proteins|Zn-dependent proteases|Predicted transcriptional regulator, contains C-terminal CBS domains|CBS-domain-containing membrane protein
Bdor1216|CDS|CDS	5.0	1.0	16.5	T|K	COG4753|COG3279|COG3947	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator of the LytR/AlgR family|Response regulator containing CheY-like receiver and SARP domains
Bryfor2860|CDS|CDS	5.0	1.0	16.5	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
BactD12038|CDS|CDS	3.1	0.8	13.7	T|K	COG0642|COG2202|COG0784|COG5002|COG2203|COG3437|COG2770|COG3614|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|FOG: HAMP domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase
Acac1083|CDS|CDS	4.0	1.0	13.2	T|K	COG3437|COG4252|COG3706|COG5001|COG2199|COG2770|COG2200|COG3614|COG2206	Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: GGDEF domain|FOG: HAMP domain|FOG: EAL domain|Predicted periplasmic ligand-binding sensor domain|HD-GYP domain
RintL12135|CDS|CDS	4.0	1.0	13.2	T|K	COG3437|COG3706|COG2770|COG4936|COG2206	Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|FOG: HAMP domain|Predicted sensor domain|HD-GYP domain
Cbol5796|CDS|CDS	2.0	0.5	13.2	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Pmer0794|CDS|CDS	15.0	4.0	12.4	T|K	COG2204|COG1221|COG3604|COG3829	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain|Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains|Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains
Bova2377|CDS|CDS	3.7	1.0	12.1	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Bdor0494|CDS|CDS	47.5	13.0	12.1	T|K	COG0642|COG2202|COG5002|COG2203|COG3437|COG2770|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|FOG: HAMP domain|Osmosensitive K+ channel histidine kinase
Dfor0997|CDS|CDS	3.5	1.0	11.6	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Acol1347|CDS|CDS	10.0	3.0	11.0	T|K	COG4624|COG3604|COG3829|COG2000	Iron only hydrogenase large subunit, C-terminal domain|Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains|Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains|Predicted Fe-S protein
RintL13835|CDS|CDS	2.5	83.0	0.1	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain

Rlac0025|CDS|CDS	0.3	9.6	0.1	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Ehal0295|CDS|CDS	0.5	23.0	0.1	T|K	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
Dlon2015|CDS|CDS	1.0	47.5	0.1	T|K	COG0317|COG2357	Guanosine polyphosphate pyrophosphohydrolases/synthetases|Uncharacterized protein conserved in bacteria
Even0023|CDS|CDS	2.0	97.5	0.1	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Buni2842|CDS|CDS	0.2	10.5	0.1	T|K	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
Ehal1052|CDS|CDS	0.6	39.5	0.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Even1454|CDS|CDS	0.3	20.6	0.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Ccom0781|CDS|CDS	0.6	51.0	0.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
PRABACTJOHN0673|CDS|CDS	9.0	1.0	29.8	T|K|G	COG0642|COG2198|COG2202|COG0784|COG5002|COG3292|COG3322|COG4753|COG3706|COG5001|COG0745|COG2972|COG1879|COG2114|COG4251|COG2770|COG2172	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain|Anti-sigma regulatory factor (Ser/Thr protein kinase)
Buni2328|CDS|CDS	181.0	32.0	18.7	T|K|G	COG0642|COG2202|COG0784|COG5002|COG3292|COG3322|COG4753|COG3706|COG5001|COG0745|COG2972|COG1879|COG2114|COG4251|COG2770	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain
PRABACTJOHN0019|CDS|CDS	5.0	1.0	16.5	T|K|G	COG4753|COG2207|COG3664	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Beta-xylosidase
Bova2147|CDS|CDS	2.5	0.5	16.5	T|K|G	COG0642|COG2198|COG2202|COG0784|COG5002|COG3292|COG4753|COG3706|COG5001|COG4585|COG0745|COG2199|COG2972|COG1879|COG2114|COG4251|COG2207	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Signal transduction histidine kinase|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|FOG: GGDEF domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|AraC-type DNA-binding domain-containing proteins
Bdor1046|CDS|CDS	0.3	26.5	0.0	T|K|G	COG0642|COG2202|COG0784|COG5002|COG3292|COG3300|COG4753|COG3706|COG5001|COG0745|COG2972|COG1879|COG2114|COG4251|COG2770	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain
RintL12266|CDS|CDS	46.0	3.0	50.7	T|K|L	COG0515	Serine/threonine protein kinase
Robe0717|CDS|CDS	10.8	1.8	19.5	T|K|L	COG0515|COG3899|COG3391|COG2815|COG5616|COG2319|COG2909	Serine/threonine protein kinase|Predicted ATPase|Uncharacterized conserved protein|Uncharacterized protein conserved in bacteria|Predicted integral membrane protein|FOG: WD40 repeat|ATP-dependent transcriptional regulator

<table>
<tr><td>FpraM2121072|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>T|K|L</td><td>COG0515|COG3899|COG2815|COG0631</td><td>Serine/threonine protein kinase|Predicted ATPase|Uncharacterized protein conserved in bacteria|Serine/threonine protein phosphatase</td></tr>
<tr><td>Dfor2334|CDS|CDS</td><td>7.5</td><td>2.0</td><td>12.4</td><td>T|K|L</td><td>COG0515|COG3391|COG2815|COG5616</td><td>Serine/threonine protein kinase|Uncharacterized conserved protein|Uncharacterized protein conserved in bacteria|Predicted integral membrane protein</td></tr>
<tr><td>Bpse1732|CDS|CDS</td><td>10.0</td><td>3.2</td><td>10.4</td><td>T|K|L</td><td>COG0515|COG3899|COG3391|COG2815|COG5616|COG1262|COG2909</td><td>Serine/threonine protein kinase|Predicted ATPase|Uncharacterized conserved protein|Uncharacterized protein conserved in bacteria|Predicted integral membrane protein|Uncharacterized conserved protein|ATP-dependent transcriptional regulator</td></tr>
<tr><td>Bryfor1746|CDS|CDS</td><td>11.0</td><td>1.0</td><td>36.4</td><td>T|L|G</td><td>COG1372|COG0574|COG1080|COG4668|COG3412|COG3605|COG1925</td><td>Intein/homing endonuclease|Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria|Signal transduction protein containing GAF and PtsI domains|Phosphotransferase system, HPr-related proteins</td></tr>
<tr><td>Ehal1148|CDS|CDS</td><td>10.0</td><td>3.0</td><td>11.0</td><td>T|M</td><td>COG1388|COG3409|COG3103|COG0860|COG2861</td><td>FOG: LysM repeat|Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|N-acetylmuramoyl-L-alanine amidase|Uncharacterized protein conserved in bacteria</td></tr>
<tr><td>Rbro0064|CDS|CDS</td><td>2.5</td><td>86.5</td><td>0.1</td><td>T|M</td><td>COG1388|COG3409|COG3103|COG0791|COG3883</td><td>FOG: LysM repeat|Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria</td></tr>
<tr><td>Ehal0337|CDS|CDS</td><td>1.3</td><td>48.0</td><td>0.1</td><td>T|M</td><td>COG1388|COG3409|COG3103|COG0791|COG3883|COG0739|COG2951|COG5412</td><td>FOG: LysM repeat|Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria|Membrane proteins related to metalloendopeptidases|Membrane-bound lytic murein transglycosylase B|Phage-related protein</td></tr>
<tr><td>Ccom0346|CDS|CDS</td><td>3.8</td><td>217.5</td><td>0.1</td><td>T|M</td><td>COG1388|COG3409|COG3103|COG0791|COG3883|COG0739|COG2951|COG5412</td><td>FOG: LysM repeat|Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria|Membrane proteins related to metalloendopeptidases|Membrane-bound lytic murein transglycosylase B|Phage-related protein</td></tr>
<tr><td>RintL10418|CDS|CDS</td><td>19.0</td><td>3.0</td><td>20.9</td><td>T|N</td><td>COG2202|COG0840</td><td>FOG: PAS/PAC domain|Methyl-accepting chemotaxis protein</td></tr>
<tr><td>Eeli0733|CDS|CDS</td><td>1.0</td><td>34.0</td><td>0.1</td><td>T|N</td><td>COG2202|COG5278|COG0840</td><td>FOG: PAS/PAC domain|Predicted periplasmic ligand-binding sensor domain|Methyl-accepting chemotaxis protein</td></tr>
<tr><td>Bdor3305|CDS|CDS</td><td>9.0</td><td>1.0</td><td>29.8</td><td>T|O</td><td>COG1225|COG1391</td><td>Peroxiredoxin|Glutamine synthetase adenylyltransferase</td></tr>
<tr><td>Even1108|CDS|CDS</td><td>101.0</td><td>3.0</td><td>111.3</td><td>U</td><td>COG3451</td><td>Type IV secretory pathway, VirB4 components</td></tr>
<tr><td>Bste0764|CDS|CDS</td><td>21.0</td><td>1.0</td><td>69.4</td><td>U</td><td>COG1862</td><td>Preprotein translocase subunit YajC</td></tr>
<tr><td>Msmi751123|CDS|CDS</td><td>5.7</td><td>0.3</td><td>56.2</td><td>U</td><td>COG0681</td><td>Signal peptidase I</td></tr>
<tr><td>Pmer2423|CDS|CDS</td><td>13.0</td><td>1.0</td><td>43.0</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>Bste2988|CDS|CDS</td><td>16.0</td><td>2.0</td><td>26.5</td><td>U</td><td>COG2095</td><td>Multiple antibiotic transporter</td></tr>
<tr><td>Bdor1195|CDS|CDS</td><td>8.0</td><td>1.0</td><td>26.5</td><td>U</td><td>COG1862</td><td>Preprotein translocase subunit YajC</td></tr>
<tr><td>TS29Fae09073|CDS|CDS</td><td>7.5</td><td>1.0</td><td>24.8</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>Bste1204|CDS|CDS</td><td>7.5</td><td>1.0</td><td>24.8</td><td>U</td><td>COG0552</td><td>Signal recognition particle GTPase</td></tr>
<tr><td>Cbol5940|CDS|CDS</td><td>11.0</td><td>1.5</td><td>24.3</td><td>U</td><td>COG0653</td><td>Preprotein translocase subunit SecA (ATPase, RNA helicase)</td></tr>
<tr><td>BactD14280|CDS|CDS</td><td>3.7</td><td>0.5</td><td>24.3</td><td>U</td><td>COG0342</td><td>Preprotein translocase subunit SecD</td></tr>
<tr><td>TS29Bac09291|CDS|CDS</td><td>3.6</td><td>0.5</td><td>23.7</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>Pmer2943|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>U</td><td>COG2095</td><td>Multiple antibiotic transporter</td></tr>
<tr><td>Bdor2771|CDS|CDS</td><td>14.0</td><td>2.0</td><td>23.1</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>Acol2083|CDS|CDS</td><td>6.5</td><td>1.0</td><td>21.5</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>TS29RumUnc1729|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>U</td><td>COG3451</td><td>Type IV secretory pathway, VirB4 components</td></tr>
<tr><td>Bxyl1665|CDS|CDS</td><td>1.6</td><td>0.3</td><td>15.7</td><td>U</td><td>COG0201</td><td>Preprotein translocase subunit SecY</td></tr>
<tr><td>TS29Fae03868|CDS|CDS</td><td>2.3</td><td>0.5</td><td>15.4</td><td>U</td><td>COG0653</td><td>Preprotein translocase subunit SecA (ATPase, RNA helicase)</td></tr>
<tr><td>Hfil2919|CDS|CDS</td><td>2.2</td><td>0.5</td><td>14.3</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>Msmi740423|CDS|CDS</td><td>5.8</td><td>1.3</td><td>14.3</td><td>U</td><td>COG0541</td><td>Signal recognition particle GTPase</td></tr>
<tr><td>Bste2609|CDS|CDS</td><td>20.0</td><td>5.0</td><td>13.3</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>TS29Fae10381|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>Bxyl1500|CDS|CDS</td><td>1.3</td><td>0.3</td><td>13.2</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>TS29Bac07504|CDS|CDS</td><td>1.3</td><td>0.3</td><td>13.2</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>BactD11207|CDS|CDS</td><td>1.3</td><td>0.3</td><td>13.2</td><td>U</td><td>COG0811</td><td>Biopolymer transport proteins</td></tr>
<tr><td>Bdor2413|CDS|CDS</td><td>8.0</td><td>2.0</td><td>13.2</td><td>U</td><td>COG0552</td><td>Signal recognition particle GTPase</td></tr>
<tr><td>TS29RumUnc0587|CDS|CDS</td><td>11.0</td><td>3.0</td><td>12.1</td><td>U</td><td>COG0653</td><td>Preprotein translocase subunit SecA (ATPase, RNA helicase)</td></tr>
<tr><td>Bdor4320|CDS|CDS</td><td>17.3</td><td>5.0</td><td>11.5</td><td>U</td><td>COG0201</td><td>Preprotein translocase subunit SecY</td></tr>
<tr><td>Msmi751254|CDS|CDS</td><td>5.8</td><td>1.7</td><td>11.4</td><td>U</td><td>COG0541</td><td>Signal recognition particle GTPase</td></tr>
<tr><td>TS28Rum13871|CDS|CDS</td><td>8.0</td><td>275.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS28Bif3690|CDS|CDS</td><td>1.0</td><td>34.5</td><td>0.1</td><td>U</td><td>COG0552</td><td>Signal recognition particle GTPase</td></tr>
<tr><td>TS28Fae13999|CDS|CDS</td><td>2.0</td><td>71.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>Clep1867|CDS|CDS</td><td>0.7</td><td>24.5</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS28Rum00163|CDS|CDS</td><td>1.0</td><td>37.0</td><td>0.1</td><td>U</td><td>COG3451</td><td>Type IV secretory pathway, VirB4 components</td></tr>
<tr><td>TS28Eub4514|CDS|CDS</td><td>2.0</td><td>77.0</td><td>0.1</td><td>U</td><td>COG3210</td><td>Large exoproteins involved in heme utilization or adhesion</td></tr>
<tr><td>Cnex1094|CDS|CDS</td><td>1.1</td><td>44.4</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS28Rum14281|CDS|CDS</td><td>3.0</td><td>118.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS28Eub6448|CDS|CDS</td><td>3.0</td><td>121.5</td><td>0.1</td><td>U</td><td>COG0342|COG0341</td><td>Preprotein translocase subunit SecD|Preprotein translocase subunit SecF</td></tr>
<tr><td>TS28Dor2920|CDS|CDS</td><td>4.0</td><td>163.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>Clep1850|CDS|CDS</td><td>4.0</td><td>164.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS28Fae14315|CDS|CDS</td><td>0.5</td><td>21.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS28Fae17111|CDS|CDS</td><td>0.5</td><td>21.0</td><td>0.1</td><td>U</td><td>COG0805</td><td>Sec-independent protein secretion pathway component TatC</td></tr>
<tr><td>Cnex3323|CDS|CDS</td><td>27.0</td><td>1,136.0</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
<tr><td>TS29Fae10431|CDS|CDS</td><td>1.0</td><td>43.0</td><td>0.1</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>Cnex0501|CDS|CDS</td><td>0.5</td><td>21.5</td><td>0.1</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>Bcap2364|CDS|CDS</td><td>2.0</td><td>87.3</td><td>0.1</td><td>U</td><td>COG3451</td><td>Type IV secretory pathway, VirB4 components</td></tr>
<tr><td>TS29Rum11722|CDS|CDS</td><td>2.5</td><td>111.0</td><td>0.1</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>Casp0367|CDS|CDS</td><td>0.3</td><td>15.0</td><td>0.1</td><td>U</td><td>COG3451</td><td>Type IV secretory pathway, VirB4 components</td></tr>
<tr><td>TS28Eub3948|CDS|CDS</td><td>0.7</td><td>31.0</td><td>0.1</td><td>U</td><td>COG3505</td><td>Type IV secretory pathway, VirD4 components</td></tr>
<tr><td>TS29Rum18654|CDS|CDS</td><td>1.0</td><td>47.0</td><td>0.1</td><td>U</td><td>COG0706</td><td>Preprotein translocase subunit YidC</td></tr>
<tr><td>Cbol3916|CDS|CDS</td><td>1.9</td><td>90.8</td><td>0.1</td><td>U</td><td>COG3843</td><td>Type IV secretory pathway, VirD2 components (relaxase)</td></tr>
</table>

Rbro0069|CDS|CDS	3.3	159.5	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Rum16825|CDS|CDS	2.0	99.0	0.1	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
TS28Clo01318|CDS|CDS	3.0	151.0	0.1	U	COG0706	Preprotein translocase subunit YidC
TS29Rum11866|CDS|CDS	2.5	129.8	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
FpraM2122489|CDS|CDS	1.3	66.0	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Clo02892|CDS|CDS	1.0	53.0	0.1	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
TS28Fae08945|CDS|CDS	0.3	18.0	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS28Clo01712|CDS|CDS	3.0	166.0	0.1	U	COG0681	Signal peptidase I
Pmer1017|CDS|CDS	0.2	11.1	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS28Rum10355|CDS|CDS	0.5	28.0	0.1	U	COG0552	Signal recognition particle GTPase
FpraM2120047|CDS|CDS	0.6	36.7	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Csci2501|CDS|CDS	0.2	11.6	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
FpraM2122523|CDS|CDS	0.6	39.2	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS28Clo00923|CDS|CDS	1.0	63.0	0.1	U	COG0681	Signal peptidase I
CspL20091|CDS|CDS	1.3	79.5	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Clo01547|CDS|CDS	3.0	196.0	0.1	U	COG0541	Signal recognition particle GTPase
Buni1972|CDS|CDS	0.2	13.6	0.0	U	COG3505	Type IV secretory pathway, VirD4 components
Rgna0455|CDS|CDS	1.0	70.0	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Rum11468|CDS|CDS	0.3	23.7	0.0	U	COG0201	Preprotein translocase subunit SecY
TS29Rum18923|CDS|CDS	2.0	156.0	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Fae19272|CDS|CDS	1.0	102.0	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Dor3154|CDS|CDS	2.5	275.8	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Eub5038|CDS|CDS	1.0	113.8	0.0	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
Acac2246|CDS|CDS	0.1	13.4	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
CspM6211845|CDS|CDS	0.1	14.2	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Dfor2038|CDS|CDS	0.1	14.2	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Ceut2222|CDS|CDS	0.1	14.2	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Cbol3082|CDS|CDS	0.1	16.5	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Cnex2291|CDS|CDS	0.1	24.2	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Rbro1718|CDS|CDS	0.1	24.5	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Cbol3071|CDS|CDS	0.2	57.5	0.0	U	COG3505	Type IV secretory pathway, VirD4 components
Csci3146|CDS|CDS	0.1	35.4	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Rbro0062|CDS|CDS	0.5	226.3	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Acol2774|CDS|CDS	0.1	62.3	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS29Bac02191|CDS|CDS	4.5	0.5	29.8	U|D|W	COG1674|COG5295	DNA segregation ATPase FtsK/SpoIIIE and related proteins|Autotransporter adhesin
Msmi740474|CDS|CDS	13.0	3.0	14.3	U|W	COG3291|COG3210|COG5295	FOG: PKD repeat|Large exoproteins involved in heme utilization or adhesion|Autotransporter adhesin
TS28Rum01438|CDS|CDS	2,466.0	24.7	330.6	V	COG0534	Na+-driven multidrug efflux pump
Even0818|CDS|CDS	50.0	1.0	165.3	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Met1299|CDS|CDS	396.0	12.0	109.1	V	COG3587	Restriction endonuclease
Robe2548|CDS|CDS	7.0	0.5	46.3	V	COG1131|COG4152	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component
Msmi740122|CDS|CDS	4.1	0.3	40.2	V	COG0534	Na+-driven multidrug efflux pump
Msmi741123|CDS|CDS	3.0	0.3	39.7	V	COG0842	ABC-type multidrug transport system, permease component
FpraM2121867|CDS|CDS	5.5	0.5	36.4	V	COG0534	Na+-driven multidrug efflux pump
RintL13181|CDS|CDS	9.0	1.0	29.8	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Bryfor2551|CDS|CDS	7.5	1.0	24.8	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Bova1791|CDS|CDS	6.5	1.0	21.5	V	COG0534	Na+-driven multidrug efflux pump
Even0349|CDS|CDS	6.0	1.0	19.8	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Fae05553|CDS|CDS	6.0	1.0	19.8	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Casp3525|CDS|CDS	6.0	1.0	19.8	V	COG0841	Cation/multidrug efflux pump
Pmer1810|CDS|CDS	12.0	2.0	19.8	V	COG0841	Cation/multidrug efflux pump
TS29Rum14589|CDS|CDS	6.0	1.0	19.8	V	COG0732	Restriction endonuclease S subunits
TS29Fae01573|CDS|CDS	1.7	0.3	16.5	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
Bryfor4221|CDS|CDS	5.0	1.0	16.5	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Fae03472|CDS|CDS	5.0	1.0	16.5	V	COG0732	Restriction endonuclease S subunits
TS28Bac3367|CDS|CDS	2.5	0.5	16.5	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae09897|CDS|CDS	2.5	0.5	16.5	V	COG0534	Na+-driven multidrug efflux pump
TS28Bac4876|CDS|CDS	29.0	6.0	16.0	V	COG0732	Restriction endonuclease S subunits
Msmi750115|CDS|CDS	4.8	1.0	15.7	V	COG0534	Na+-driven multidrug efflux pump
BactD24599|CDS|CDS	2.2	0.5	14.3	V	COG0842	ABC-type multidrug transport system, permease component
Bova1144|CDS|CDS	4.0	1.0	13.2	V	COG1136|COG0577	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type antimicrobial peptide transport system, permease component
Casp5521|CDS|CDS	4.0	1.0	13.2	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
Hfil2705|CDS|CDS	4.0	1.0	13.2	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Pmer3426|CDS|CDS	12.0	3.0	13.2	V	COG0534	Na+-driven multidrug efflux pump
BactD10601|CDS|CDS	2.0	0.5	13.2	V	COG0534	Na+-driven multidrug efflux pump
Even0909|CDS|CDS	11.0	3.0	12.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Bste0127|CDS|CDS	14.5	4.0	12.0	V	COG1136|COG0577	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type antimicrobial peptide transport system, permease component
TS28Bac1132|CDS|CDS	14.0	4.0	11.6	V	COG1136|COG0577	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type antimicrobial peptide transport system, permease component
Pmer0214|CDS|CDS	5.0	1.5	11.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Rum00794|CDS|CDS	23.0	7.0	10.9	V	COG2367	Beta-lactamase class A
TS28Eub0144|CDS|CDS	49.0	15.0	10.8	V	COG0286	Type I restriction-modification system methyltransferase subunit

TS28Bac0944|CDS|CDS	6.5	2.0	10.7	V	COG0841	Cation/multidrug efflux pump
TS28Eub8425|CDS|CDS	1.3	44.7	0.1	V	COG0534	Na+-driven multidrug efflux pump
Ehal2443|CDS|CDS	0.5	17.5	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Bac7466|CDS|CDS	1.0	36.5	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Eub3905|CDS|CDS	1.0	38.0	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS28Fae16454|CDS|CDS	1.0	38.0	0.1	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS28Clo10877|CDS|CDS	1.5	57.5	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Rum00725|CDS|CDS	0.5	19.5	0.1	V	COG1131|COG4152	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component
Msmi751116|CDS|CDS	0.3	9.8	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Eub8422|CDS|CDS	1.3	53.3	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Clo01250|CDS|CDS	4.0	160.5	0.1	V	COG2348	Uncharacterized protein involved in methicillin resistance
TS29Rum17071|CDS|CDS	2.0	81.0	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS28Fae12157|CDS|CDS	2.0	82.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Bif2291|CDS|CDS	1.5	62.5	0.1	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS29Fae02252|CDS|CDS	1.0	41.8	0.1	V	COG0286	Type I restriction-modification system methyltransferase subunit
TS28Rum09994|CDS|CDS	1.0	42.0	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS28Dor0838|CDS|CDS	0.5	21.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Fae17020|CDS|CDS	0.5	21.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Clo01720|CDS|CDS	2.0	89.5	0.1	V	COG4845	Chloramphenicol O-acetyltransferase
TS28Clo01668|CDS|CDS	7.0	314.0	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS28Rum16352|CDS|CDS	1.0	47.0	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS28Clo00560|CDS|CDS	6.0	296.0	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Bac0364|CDS|CDS	0.5	25.0	0.1	V	COG0841	Cation/multidrug efflux pump
TS28Fae21402|CDS|CDS	1.0	50.5	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Even0576|CDS|CDS	2.5	127.5	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Dor3087|CDS|CDS	0.5	26.0	0.1	V	COG1680	Beta-lactamase class C and other penicillin binding proteins
TS28Fae17738|CDS|CDS	1.0	53.0	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS28Fae18163|CDS|CDS	1.5	84.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Clo01224|CDS|CDS	3.0	171.0	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Bdor0611|CDS|CDS	0.3	19.0	0.1	V	COG0841	Cation/multidrug efflux pump
TS29Fae09506|CDS|CDS	0.5	29.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
FpraM2121439|CDS|CDS	2.0	116.8	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Eub4121|CDS|CDS	1.0	62.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Clo00788|CDS|CDS	3.0	187.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
Ccom0777|CDS|CDS	0.2	10.5	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Rum01570|CDS|CDS	0.5	31.5	0.1	V	COG0488|COG0534	ATPase components of ABC transporters with duplicated ATPase domains|Na+-driven multidrug efflux pump
TS29Clo4619|CDS|CDS	1.5	101.0	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Dlon0974|CDS|CDS	0.4	30.3	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Fae07372|CDS|CDS	1.0	73.0	0.0	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS29Bif3552|CDS|CDS	0.3	26.4	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
RintL13838|CDS|CDS	2.0	159.5	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Fae20830|CDS|CDS	1.5	123.5	0.0	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS28Met1736|CDS|CDS	0.3	21.3	0.0	V	COG0534	Na+-driven multidrug efflux pump
TS29Fae05124|CDS|CDS	0.5	45.0	0.0	V	COG1131	ABC-type multidrug transport system, ATPase component
Robe3755|CDS|CDS	0.3	31.5	0.0	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
CspL21209|CDS|CDS	0.4	41.1	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Fae18246|CDS|CDS	0.7	67.0	0.0	V	COG0534	Na+-driven multidrug efflux pump
TS28Eub4375|CDS|CDS	0.5	53.0	0.0	V	COG1968	Uncharacterized bacitracin resistance protein
TS28Fae12266|CDS|CDS	0.5	54.0	0.0	V	COG0534	Na+-driven multidrug efflux pump
TS28Bif2178|CDS|CDS	0.3	39.3	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
FpraM2122471|CDS|CDS	1.0	118.2	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Ccom2341|CDS|CDS	1.0	123.0	0.0	V	COG1002	Type II restriction enzyme, methylase subunits
Ehal1055|CDS|CDS	0.2	24.3	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Eub6501|CDS|CDS	0.5	73.0	0.0	V	COG0534	Na+-driven multidrug efflux pump
TS28Eub8030|CDS|CDS	0.5	73.5	0.0	V	COG0534	Na+-driven multidrug efflux pump
Eeli0031|CDS|CDS	0.4	78.6	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Robe3151|CDS|CDS	0.4	89.1	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Clo00915|CDS|CDS	1.0	256.0	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components

<table>
<tr><td>TS28Eub3906|CDS|CDS</td><td>0.5</td><td>193.5</td><td>0.0</td><td>V</td><td>COG0577</td><td>ABC-type antimicrobial peptide transport system, permease component</td></tr>
<tr><td>TS28Rum01059|CDS|CDS</td><td>0.3</td><td>161.5</td><td>0.0</td><td>V</td><td>COG0610</td><td>Type I site-specific restriction-modification system, R (restriction) subunit and related helicases</td></tr>
<tr><td>Robe3150|CDS|CDS</td><td>0.7</td><td>67.5</td><td>0.0</td><td>V|Q</td><td>COG1136|COG4181</td><td>ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component</td></tr>
<tr><td>TS28Fae15596|CDS|CDS</td><td>0.5</td><td>59.0</td><td>0.0</td><td>R</td><td>COG0073</td><td>EMAP domain</td></tr>
<tr><td>Msmi741535|CDS|CDS</td><td>7.8</td><td>0.5</td><td>51.8</td><td>R</td><td>COG0110</td><td>Acetyltransferase (isoleucine patch superfamily)</td></tr>
<tr><td>Bdor2243|CDS|CDS</td><td>12.1</td><td>4.0</td><td>10.0</td><td>R</td><td>COG0217</td><td>Uncharacterized conserved protein</td></tr>
<tr><td>TS28Eub4538|CDS|CDS</td><td>0.3</td><td>24.0</td><td>0.0</td><td>R</td><td>COG0217</td><td>Uncharacterized conserved protein</td></tr>
<tr><td>TS28Fae07816|CDS|CDS</td><td>0.2</td><td>9.0</td><td>0.1</td><td>R</td><td>COG0218</td><td>Predicted GTPase</td></tr>
<tr><td>Bste2188|CDS|CDS</td><td>5.0</td><td>0.5</td><td>33.1</td><td>R</td><td>COG0312</td><td>Predicted Zn-dependent proteases and their inactivated homologs</td></tr>
<tr><td>Ebif1781|CDS|CDS</td><td>6.0</td><td>1.0</td><td>19.8</td><td>R</td><td>COG0312</td><td>Predicted Zn-dependent proteases and their inactivated homologs</td></tr>
<tr><td>Msmi750752|CDS|CDS</td><td>7.9</td><td>1.5</td><td>17.4</td><td>R</td><td>COG0312</td><td>Predicted Zn-dependent proteases and their inactivated homologs</td></tr>
<tr><td>Msmi740927|CDS|CDS</td><td>7.9</td><td>2.0</td><td>13.1</td><td>R</td><td>COG0312</td><td>Predicted Zn-dependent proteases and their inactivated homologs</td></tr>
<tr><td>Pmer3547|CDS|CDS</td><td>20.0</td><td>6.0</td><td>11.0</td><td>R</td><td>COG0312</td><td>Predicted Zn-dependent proteases and their inactivated homologs</td></tr>
<tr><td>BVU1837|CDS|methyltransferase</td><td>29.7</td><td>2.0</td><td>49.1</td><td>R</td><td>COG0313</td><td>Predicted methyltransferases</td></tr>
<tr><td>Bdor2872|CDS|CDS</td><td>17.7</td><td>3.0</td><td>19.5</td><td>R</td><td>COG0313</td><td>Predicted methyltransferases</td></tr>
<tr><td>Pmer2668|CDS|CDS</td><td>8.0</td><td>2.0</td><td>13.2</td><td>R</td><td>COG0313</td><td>Predicted methyltransferases</td></tr>
<tr><td>Bste0572|CDS|CDS</td><td>12.0</td><td>2.0</td><td>19.8</td><td>R</td><td>COG0325</td><td>Predicted enzyme with a TIM-barrel fold</td></tr>
<tr><td>TS28Met1314|CDS|CDS</td><td>5.5</td><td>1.5</td><td>12.1</td><td>R</td><td>COG0375</td><td>Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)</td></tr>
<tr><td>TS28Bac6214|CDS|CDS</td><td>0.5</td><td>31.2</td><td>0.1</td><td>R</td><td>COG0388</td><td>Predicted amidohydrolase</td></tr>
<tr><td>TS28Clo00936|CDS|CDS</td><td>1.0</td><td>60.0</td><td>0.1</td><td>R</td><td>COG0398</td><td>Uncharacterized conserved protein</td></tr>
<tr><td>ShigspD90733|CDS|CDS</td><td>17.0</td><td>0.5</td><td>112.4</td><td>R</td><td>COG0457</td><td>FOG: TPR repeat</td></tr>
<tr><td>BactD11202|CDS|CDS</td><td>2.7</td><td>0.3</td><td>26.5</td><td>R</td><td>COG0457</td><td>FOG: TPR repeat</td></tr>
<tr><td>TS29Bac00353|CDS|CDS</td><td>2.7</td><td>0.3</td><td>26.5</td><td>R</td><td>COG0457</td><td>FOG: TPR repeat</td></tr>
<tr><td>Pmer1450|CDS|CDS</td><td>29.0</td><td>5.0</td><td>19.2</td><td>R</td><td>COG0457</td><td>FOG: TPR repeat</td></tr>
<tr><td>TS28Ali0823|CDS|CDS</td><td>46.5</td><td>12.0</td><td>12.8</td><td>R</td><td>COG0457</td><td>FOG: TPR repeat</td></tr>
<tr><td>Bdor2397|CDS|CDS</td><td>30.5</td><td>10.0</td><td>10.1</td><td>R</td><td>COG0457</td><td>FOG: TPR repeat</td></tr>
<tr><td>Aput2126|CDS|CDS</td><td>13.5</td><td>4.0</td><td>11.2</td><td>R</td><td>COG0457|COG0666</td><td>FOG: TPR repeat|FOG: Ankyrin repeat</td></tr>
<tr><td>b3706|CDS|GTPase</td><td>5.0</td><td>1.0</td><td>16.5</td><td>R</td><td>COG0486</td><td>Predicted GTPase</td></tr>
<tr><td>TS29Fae08493|CDS|CDS</td><td>0.3</td><td>8.5</td><td>0.1</td><td>R</td><td>COG0486</td><td>Predicted GTPase</td></tr>
<tr><td>TS28Rum13685|CDS|CDS</td><td>1.0</td><td>53.0</td><td>0.1</td><td>R</td><td>COG0486</td><td>Predicted GTPase</td></tr>
<tr><td>TS28Fae12679|CDS|CDS</td><td>0.3</td><td>36.0</td><td>0.0</td><td>R</td><td>COG0486</td><td>Predicted GTPase</td></tr>
<tr><td>Cbol3211|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>Bdor3253|CDS|CDS</td><td>32.0</td><td>10.2</td><td>10.4</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>Dlon0788|CDS|CDS</td><td>1.0</td><td>35.0</td><td>0.1</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>TS28Bac1770|CDS|CDS</td><td>0.3</td><td>10.0</td><td>0.1</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>TS28Fae10321|CDS|CDS</td><td>0.3</td><td>22.3</td><td>0.0</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>TS28Bif2589|CDS|CDS</td><td>0.3</td><td>36.3</td><td>0.0</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>TS28Bif4112|CDS|CDS</td><td>0.3</td><td>44.7</td><td>0.0</td><td>R</td><td>COG0488</td><td>ATPase components of ABC transporters with duplicated ATPase domains</td></tr>
<tr><td>Aput1104|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>R</td><td>COG0496</td><td>Predicted acid phosphatase</td></tr>
<tr><td>Ehal2227|CDS|CDS</td><td>5.0</td><td>0.5</td><td>33.1</td><td>R</td><td>COG0517</td><td>FOG: CBS domain</td></tr>
<tr><td>Acod0213|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>R</td><td>COG0517</td><td>FOG: CBS domain</td></tr>
<tr><td>Msmi751552|CDS|CDS</td><td>4.0</td><td>1.3</td><td>10.6</td><td>R</td><td>COG0517</td><td>FOG: CBS domain</td></tr>
<tr><td>TS28Fae08593|CDS|CDS</td><td>38.0</td><td>12.0</td><td>10.5</td><td>R</td><td>COG0517</td><td>FOG: CBS domain</td></tr>
<tr><td>TS28Col1732|CDS|CDS</td><td>1.0</td><td>42.0</td><td>0.1</td><td>R</td><td>COG0517</td><td>FOG: CBS domain</td></tr>
<tr><td>TS29Rum11606|CDS|CDS</td><td>1.0</td><td>42.5</td><td>0.1</td><td>R</td><td>COG0523</td><td>Putative GTPases (G3E family)</td></tr>
<tr><td>TS28Col0951|CDS|CDS</td><td>0.5</td><td>23.0</td><td>0.1</td><td>R</td><td>COG0523</td><td>Putative GTPases (G3E family)</td></tr>
<tr><td>TS29Fae09409|CDS|CDS</td><td>2.5</td><td>0.5</td><td>16.5</td><td>R</td><td>COG0535</td><td>Predicted Fe-S oxidoreductases</td></tr>
<tr><td>TS29Rum19807|CDS|CDS</td><td>0.5</td><td>18.0</td><td>0.1</td><td>R</td><td>COG0535|COG0641</td><td>Predicted Fe-S oxidoreductases|Arylsulfatase regulator (Fe-S oxidoreductase)</td></tr>
<tr><td>TS28Eub8072|CDS|CDS</td><td>1.5</td><td>56.0</td><td>0.1</td><td>R</td><td>COG0535|COG4001|COG0641</td><td>Predicted Fe-S oxidoreductases|Predicted metal-binding protein|Arylsulfatase regulator (Fe-S oxidoreductase)</td></tr>
<tr><td>Svar1269|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>R</td><td>COG0536</td><td>Predicted GTPase</td></tr>
<tr><td>TS29Bif3653|CDS|CDS</td><td>0.3</td><td>11.5</td><td>0.1</td><td>R</td><td>COG0536</td><td>Predicted GTPase</td></tr>
<tr><td>TS28Bif2044|CDS|CDS</td><td>0.3</td><td>11.5</td><td>0.1</td><td>R</td><td>COG0536</td><td>Predicted GTPase</td></tr>
<tr><td>TS29Rum12440|CDS|CDS</td><td>7.0</td><td>1.0</td><td>23.1</td><td>R</td><td>COG0546</td><td>Predicted phosphatases</td></tr>
<tr><td>TS29Rum07641|CDS|CDS</td><td>1.3</td><td>0.3</td><td>13.2</td><td>R</td><td>COG0546</td><td>Predicted phosphatases</td></tr>
<tr><td>TS28Bac6996|CDS|CDS</td><td>0.3</td><td>36.5</td><td>0.0</td><td>R</td><td>COG0546</td><td>Predicted phosphatases</td></tr>
<tr><td>TS28Bac2640|CDS|CDS</td><td>5.0</td><td>1.0</td><td>16.5</td><td>R</td><td>COG0561|COG4696</td><td>Predicted hydrolases of the HAD superfamily|Uncharacterized protein conserved in bacteria</td></tr>
<tr><td>Rumhyd3310|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>R</td><td>COG0595</td><td>Predicted hydrolase of the metallo-beta-lactamase superfamily</td></tr>
<tr><td>TS28Clo01541|CDS|CDS</td><td>7.0</td><td>254.5</td><td>0.1</td><td>R</td><td>COG0595</td><td>Predicted hydrolase of the metallo-beta-lactamase superfamily</td></tr>
<tr><td>TS28Rum12672|CDS|CDS</td><td>1.0</td><td>42.0</td><td>0.1</td><td>R</td><td>COG0595</td><td>Predicted hydrolase of the metallo-beta-lactamase superfamily</td></tr>
<tr><td>TS28Clo00946|CDS|CDS</td><td>2.0</td><td>190.0</td><td>0.0</td><td>R</td><td>COG0595</td><td>Predicted hydrolase of the metallo-beta-lactamase superfamily</td></tr>
<tr><td>TS28Dor0699|CDS|CDS</td><td>0.5</td><td>17.5</td><td>0.1</td><td>R</td><td>COG0596</td><td>Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)</td></tr>
<tr><td>TS29Bac03150|CDS|CDS</td><td>1.5</td><td>0.3</td><td>14.9</td><td>R</td><td>COG0612</td><td>Predicted Zn-dependent peptidases</td></tr>
<tr><td>TS28Fae12384|CDS|CDS</td><td>25.3</td><td>6.0</td><td>14.0</td><td>R</td><td>COG0612</td><td>Predicted Zn-dependent peptidases</td></tr>
<tr><td>Even1555|CDS|CDS</td><td>4.0</td><td>1.0</td><td>13.2</td><td>R</td><td>COG0612</td><td>Predicted Zn-dependent peptidases</td></tr>
<tr><td>Bcap1657|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.6</td><td>R</td><td>COG0612</td><td>Predicted Zn-dependent peptidases</td></tr>
<tr><td>TS28Ali1352|CDS|CDS</td><td>251.0</td><td>72.0</td><td>11.5</td><td>R</td><td>COG0612</td><td>Predicted Zn-dependent peptidases</td></tr>
<tr><td>Clep0333|CDS|CDS</td><td>7.9</td><td>1.7</td><td>15.7</td><td>R</td><td>COG0613</td><td>Predicted metal-dependent phosphoesterases (PHP family)</td></tr>
<tr><td>Robe3650|CDS|CDS</td><td>4.5</td><td>0.5</td><td>29.8</td><td>R</td><td>COG0628</td><td>Predicted permease</td></tr>
<tr><td>Msmi740750|CDS|CDS</td><td>3.3</td><td>0.7</td><td>16.5</td><td>R</td><td>COG0628</td><td>Predicted permease</td></tr>
<tr><td>TS29Fae08388|CDS|CDS</td><td>4.5</td><td>1.0</td><td>14.9</td><td>R</td><td>COG0628</td><td>Predicted permease</td></tr>
<tr><td>TS28Eub8994|CDS|CDS</td><td>0.5</td><td>17.0</td><td>0.1</td><td>R</td><td>COG0628</td><td>Predicted permease</td></tr>
</table>

TS28Clo00715|CDS|CDS	1.0	166.0	0.0	R	COG0628	Predicted permease
TS28Fae02281|CDS|CDS	0.5	22.0	0.1	R	COG0641	Arylsulfatase regulator (Fe-S oxidoreductase)
Ehal1041|CDS|CDS	3.0	0.5	19.8	R	COG0655	Multimeric flavodoxin WrbA
TS28Met0271|CDS|CDS	3.3	1.0	10.7	R	COG0655	Multimeric flavodoxin WrbA
Rlac0013|CDS|CDS	2.8	94.4	0.1	R	COG0655	Multimeric flavodoxin WrbA
TS28Met1589|CDS|CDS	0.3	11.0	0.1	R	COG0655	Multimeric flavodoxin WrbA
TS28Eub4370|CDS|CDS	1.0	80.0	0.0	R	COG0655	Multimeric flavodoxin WrbA
Robe2068|CDS|CDS	6.0	1.0	19.8	R	COG0658|COG2333	Predicted membrane metal-binding protein|Predicted hydrolase (metallo-beta-lactamase superfamily)
Bdor0468|CDS|CDS	0.3	17.5	0.1	R	COG0658|COG2333	Predicted membrane metal-binding protein|Predicted hydrolase (metallo-beta-lactamase superfamily)
Dlon1005|CDS|CDS	7.5	2.0	12.4	R	COG0661	Predicted unusual protein kinase
TS28Clo00730|CDS|CDS	5.0	185.0	0.1	R	COG0661	Predicted unusual protein kinase
Msmi740300|CDS|CDS	5.5	0.8	24.3	R	COG0663	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily
TS29Clo4769|CDS|CDS	0.5	49.5	0.0	R	COG0666	FOG: Ankyrin repeat
TS29Dor0946|CDS|CDS	9.0	1.0	29.8	R	COG0673	Predicted dehydrogenases and related proteins
TS29Fae04584|CDS|CDS	3.5	0.5	23.1	R	COG0673	Predicted dehydrogenases and related proteins
Pmer2748|CDS|CDS	30.0	5.0	19.8	R	COG0673	Predicted dehydrogenases and related proteins
Pmer1779|CDS|CDS	11.5	2.0	19.0	R	COG0673	Predicted dehydrogenases and related proteins
Bova2380|CDS|CDS	8.0	1.5	17.6	R	COG0673	Predicted dehydrogenases and related proteins
BactD21105|CDS|CDS	6.0	1.5	13.2	R	COG0673	Predicted dehydrogenases and related proteins
Pmer2911|CDS|CDS	19.0	6.0	10.5	R	COG0673	Predicted dehydrogenases and related proteins
Pmer1244|CDS|CDS	9.5	2.0	15.7	R	COG0705|COG3582	Uncharacterized membrane protein (homolog of Drosophila rhomboid)|Predicted nucleic acid binding protein containing the AN1-type Zn-finger
TS29Fae03451|CDS|CDS	7.0	1.0	23.1	R	COG0714	MoxR-like ATPases
TS28Fae08998|CDS|CDS	2.0	68.5	0.1	R	COG0714	MoxR-like ATPases
TS28Rum12513|CDS|CDS	0.5	23.8	0.1	R	COG0714	MoxR-like ATPases
Bxyl0536|CDS|CDS	21.1	0.5	139.7	R	COG0724	RNA-binding proteins (RRM domain)
TS29Bac00560|CDS|CDS	20.9	0.5	138.0	R	COG0724	RNA-binding proteins (RRM domain)
Bste3239|CDS|CDS	30.5	1.0	100.9	R	COG0724	RNA-binding proteins (RRM domain)
TS29Bac02527|CDS|CDS	35.0	2.0	57.9	R	COG0724	RNA-binding proteins (RRM domain)
PRABACTJOHN2801|CDS|CDS	12.0	1.0	39.7	R	COG0724	RNA-binding proteins (RRM domain)
Bste0102|CDS|CDS	70.0	6.0	38.6	R	COG0724	RNA-binding proteins (RRM domain)
Pmer1512|CDS|CDS	2.2	0.5	14.3	R	COG0724	RNA-binding proteins (RRM domain)
Bdor2438|CDS|CDS	11.5	3.0	12.7	R	COG0724	RNA-binding proteins (RRM domain)
TS28Par0076|CDS|CDS	5.2	1.5	11.4	R	COG0724	RNA-binding proteins (RRM domain)
Bxyl4341|CDS|CDS	1.6	0.5	10.9	R	COG0724	RNA-binding proteins (RRM domain)
BactD10044|CDS|CDS	1.6	0.5	10.9	R	COG0724	RNA-binding proteins (RRM domain)
TS29Dor1996|CDS|CDS	4.0	1.0	13.2	R	COG0733	Na+-dependent transporters of the SNF family
TS28Ali1650|CDS|CDS	1.0	35.0	0.1	R	COG0733	Na+-dependent transporters of the SNF family
TS28Eub5082|CDS|CDS	0.3	70.0	0.0	R	COG0733	Na+-dependent transporters of the SNF family
Bdor1791|CDS|CDS	11.0	1.0	36.4	R	COG0759	Uncharacterized conserved protein
Eeli1313|CDS|CDS	7.0	1.0	23.1	R	COG0779	Uncharacterized protein conserved in bacteria
TS29Rum19927|CDS|CDS	9.0	2.0	14.9	R	COG0779	Uncharacterized protein conserved in bacteria
TS28Fae06307|CDS|CDS	19.0	4.0	15.7	R	COG0790	FOG: TPR repeat, SEL1 subfamily
TS28Fae13357|CDS|CDS	53.0	15.0	11.7	R	COG0790|COG4249|COG2849	FOG: TPR repeat, SEL1 subfamily|Uncharacterized protein containing caspase domain|Uncharacterized protein conserved in bacteria
Bdor3683|CDS|CDS	3.5	0.3	34.7	R	COG0820	Predicted Fe-S-cluster redox enzyme
Msmi750558|CDS|CDS	8.7	2.2	13.2	R	COG1011	Predicted hydrolase (HAD superfamily)
Rtor1309|CDS|CDS	19.0	5.0	12.6	R	COG1011	Predicted hydrolase (HAD superfamily)
TS28Fae00613|CDS|CDS	1.0	40.5	0.1	R	COG1026	Predicted Zn-dependent peptidases, insulinase-like
CspSS21842|CDS|CDS	0.5	38.0	0.0	R	COG1026	Predicted Zn-dependent peptidases, insulinase-like
TS28Eub4362|CDS|CDS	1.0	80.5	0.0	R	COG1026	Predicted Zn-dependent peptidases, insulinase-like
TS28Eub6780|CDS|CDS	1.0	43.5	0.1	R	COG1033	Predicted exporters of the RND superfamily
TS28Fae09550|CDS|CDS	0.4	40.5	0.0	R	COG1033	Predicted exporters of the RND superfamily
TS28Fae19080|CDS|CDS	0.4	31.0	0.0	R	COG1033|COG2409	Predicted exporters of the RND superfamily|Predicted drug exporters of the RND superfamily
TS28Fae17600|CDS|CDS	0.5	37.0	0.0	R	COG1073	Hydrolases of the alpha/beta superfamily
Msmi741580|CDS|CDS	2.9	0.5	19.3	R	COG1078	HD superfamily phosphohydrolases
TS28Fae22051|CDS|CDS	1.0	42.0	0.1	R	COG1079	Uncharacterized ABC-type transport system, permease component
TS28Clo01121|CDS|CDS	2.0	78.5	0.1	R	COG1092	Predicted SAM-dependent methyltransferases
Msmi750844|CDS|CDS	9.3	2.0	15.4	R	COG1094	Predicted RNA-binding protein (contains KH domains)
TS28Met0234|CDS|CDS	10.8	3.0	11.8	R	COG1094	Predicted RNA-binding protein (contains KH domains)
TS28Met0233|CDS|CDS	3.4	1.0	11.3	R	COG1094	Predicted RNA-binding protein (contains KH domains)
TS29Fae04577|CDS|CDS	3.5	1.0	11.6	R	COG1159	GTPase
Bxyl4337|CDS|CDS	3.8	0.5	25.4	R	COG1160	Predicted GTPases
TS29Bac01265|CDS|CDS	2.0	0.5	13.2	R	COG1160	Predicted GTPases
TS28Rum10174|CDS|CDS	3.5	1.0	11.6	R	COG1160	Predicted GTPases
TS28Fae10403|CDS|CDS	1.0	35.0	0.1	R	COG1160	Predicted GTPases
TS28Col0392|CDS|CDS	0.5	22.5	0.1	R	COG1160	Predicted GTPases
TS29Fae00300|CDS|CDS	7.0	1.5	15.4	R	COG1162	Predicted GTPases
Ccom0377|CDS|CDS	7.0	2.0	11.6	R	COG1201|COG1205	Lhr-like helicases|Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster
TS28Met0165|CDS|CDS	1.3	43.8	0.1	R	COG1201|COG1205	Lhr-like helicases|Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster
TS28Fae18151|CDS|CDS	4.0	159.0	0.1	R	COG1203	Predicted helicases
Bdor3609|CDS|CDS	13.7	3.8	11.8	R	COG1234	Metal-dependent hydrolases of the beta-lactamase superfamily III
TS29Clo0772|CDS|CDS	14.0	0.5	92.6	R	COG1272	Predicted membrane protein, hemolysin III homolog
TS28Clo01378|CDS|CDS	3.0	113.0	0.1	R	COG1284	Uncharacterized conserved protein
Csym1611|CDS|CDS	14.0	1.0	46.3	R	COG1288	Predicted membrane protein
Ceut0478|CDS|CDS	0.1	3.0	0.1	R	COG1289	Predicted membrane protein
CspL21157|CDS|CDS	0.1	7.1	0.0	R	COG1289	Predicted membrane protein
Robe0037|CDS|CDS	0.1	10.1	0.0	R	COG1289	Predicted membrane protein
RintL10785|CDS|CDS	0.1	10.9	0.0	R	COG1289	Predicted membrane protein
Eeli2695|CDS|CDS	0.1	12.8	0.0	R	COG1289	Predicted membrane protein
Dlon2020|CDS|CDS	0.1	13.1	0.0	R	COG1289	Predicted membrane protein
FpraM2120019|CDS|CDS	0.1	18.9	0.0	R	COG1289	Predicted membrane protein

CspM6210573|CDS|CDS	0.1	43.7	0.0	R	COG1289	Predicted membrane protein
Ehal1317|CDS|CDS	0.1	71.3	0.0	R	COG1289	Predicted membrane protein
Rbro0237|CDS|CDS	0.1	93.7	0.0	R	COG1289	Predicted membrane protein
TS28Clo01109|CDS|CDS	2.0	110.0	0.1	R	COG1295	Predicted membrane protein
TS28Rum13104|CDS|CDS	1.3	0.3	13.2	R	COG1297	Predicted membrane protein
Ehal2353|CDS|CDS	0.5	19.5	0.1	R	COG1297	Predicted membrane protein
TS28Eub3507|CDS|CDS	0.5	20.5	0.1	R	COG1297	Predicted membrane protein
TS28Rum09255|CDS|CDS	14.0	4.0	11.6	R	COG1306	Uncharacterized conserved protein
TS28RumUnc0398|CDS|CDS	17.0	5.0	11.2	R	COG1306	Uncharacterized conserved protein
TS28Fae14048|CDS|CDS	2.0	0.5	13.2	R	COG1307	Uncharacterized protein conserved in bacteria
TS29Rum05406|CDS|CDS	2.3	0.7	11.6	R	COG1307	Uncharacterized protein conserved in bacteria
RintL12814|CDS|CDS	7.0	1.0	23.1	R	COG1307|COG1461	Uncharacterized protein conserved in bacteria|Predicted kinase related to dihydroxyacetone kinase
Bste0952|CDS|CDS	7.0	0.5	46.3	R	COG1322	Uncharacterized protein conserved in bacteria
TS28Clo01130|CDS|CDS	1.0	81.0	0.0	R	COG1354	Uncharacterized conserved protein
Bste0789|CDS|CDS	7.0	2.0	11.6	R	COG1357	Uncharacterized low-complexity proteins
TS28Met0719|CDS|CDS	8.0	1.0	26.5	R	COG1359	Uncharacterized conserved protein
Msmi751272|CDS|CDS	8.0	1.0	26.5	R	COG1359	Uncharacterized conserved protein
BactD22080|CDS|CDS	87.0	1.0	287.7	R	COG1373	Predicted ATPase (AAA+ superfamily)
Bxyl2673|CDS|CDS	87.0	2.0	143.9	R	COG1373	Predicted ATPase (AAA+ superfamily)
Bpse1851|CDS|CDS	8.0	1.0	26.5	R	COG1373	Predicted ATPase (AAA+ superfamily)
RintL13452|CDS|CDS	5.0	1.0	16.5	R	COG1373	Predicted ATPase (AAA+ superfamily)
CspL21205|CDS|CDS	3.5	0.8	13.9	R	COG1373	Predicted ATPase (AAA+ superfamily)
Ceut0345|CDS|CDS	1.0	50.0	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS28Rum16221|CDS|CDS	1.0	51.0	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS28Met0533|CDS|CDS	0.3	13.9	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS28Eub0238|CDS|CDS	0.5	98.3	0.0	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS29Rum12436|CDS|CDS	12.0	3.0	13.2	R	COG1376	Uncharacterized protein conserved in bacteria
TS28Rum13543|CDS|CDS	0.5	42.5	0.0	R	COG1376	Uncharacterized protein conserved in bacteria
Bdor1388|CDS|CDS	20.0	1.0	66.1	R	COG1385	Uncharacterized protein conserved in bacteria
TS28Eub4232|CDS|CDS	1.0	45.5	0.1	R	COG1385	Uncharacterized protein conserved in bacteria
Rtor0446|CDS|CDS	18.0	5.0	11.9	R	COG1399	Predicted metal-binding, possibly nucleic acid-binding protein
Bdor4300|CDS|CDS	2.5	0.5	16.5	R	COG1402	Uncharacterized protein, putative amidase
Msmi751052|CDS|CDS	3.8	1.0	12.4	R	COG1408	Predicted phosphohydrolases
Bbre0077|CDS|CDS	20.0	2.0	33.1	R	COG1409	Predicted phosphohydrolases
Casp0114|CDS|CDS	6.0	1.0	19.8	R	COG1409	Predicted phosphohydrolases
TS28Clo05976|CDS|CDS	1.0	54.0	0.1	R	COG1409	Predicted phosphohydrolases
TS28Ali0429|CDS|CDS	84.0	20.0	13.9	R	COG1418	Predicted HD superfamily hydrolase
Bdor0584|CDS|CDS	8.0	2.0	13.2	R	COG1418	Predicted HD superfamily hydrolase
Bdor3063|CDS|CDS	28.5	9.0	10.5	R	COG1418	Predicted HD superfamily hydrolase
TS28Clo01539|CDS|CDS	1.0	224.0	0.0	R	COG1418	Predicted HD superfamily hydrolase
TS28Bac5641|CDS|CDS	0.5	20.0	0.1	R	COG1453	Predicted oxidoreductases of the aldo/keto reductase family
TS28Eub7489|CDS|CDS	2.0	89.5	0.1	R	COG1461	Predicted kinase related to dihydroxyacetone kinase
Csym4794|CDS|CDS	6.0	1.0	19.8	R	COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase
Hfil3009|CDS|CDS	4.0	1.0	13.2	R	COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase
TS28Fae12231|CDS|CDS	1.0	60.5	0.1	R	COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase
TS29Par858|CDS|CDS	2.5	0.5	16.5	R	COG1479	Uncharacterized conserved protein
BactD10459|CDS|CDS	2.5	0.5	16.5	R	COG1479	Uncharacterized conserved protein
TS28Eub3845|CDS|CDS	3.0	108.0	0.1	R	COG1479|COG3586	Uncharacterized conserved protein|Uncharacterized conserved protein
TS28Clo01408|CDS|CDS	3.0	114.0	0.1	R	COG1481	Uncharacterized protein conserved in bacteria
Rgna3174|CDS|CDS	7.0	1.0	23.1	R	COG1511	Predicted membrane protein
TS28Fae11799|CDS|CDS	1.0	50.0	0.1	R	COG1511|COG2409	Predicted membrane protein|Predicted drug exporters of the RND superfamily
Msmi751396|CDS|CDS	5.0	0.5	33.1	R	COG1537	Predicted RNA-binding proteins
TS28Clo01096|CDS|CDS	4.0	138.0	0.1	R	COG1559	Predicted periplasmic solute-binding protein
TS28Eub5217|CDS|CDS	1.0	65.0	0.1	R	COG1559	Predicted periplasmic solute-binding protein
TS28Eub7485|CDS|CDS	0.5	51.0	0.0	R	COG1561	Uncharacterized stress-induced protein
Msmi751191|CDS|CDS	8.9	2.5	11.8	R	COG1571	Predicted DNA-binding protein containing a Zn-ribbon domain
Msmi740195|CDS|CDS	2.3	0.6	13.2	R	COG1578	Uncharacterized conserved protein
Msmi751485|CDS|CDS	2.3	0.6	13.2	R	COG1578	Uncharacterized conserved protein
TS28Bac5013|CDS|CDS	21.2	3.5	20.0	R	COG1579	Zn-ribbon protein, possibly nucleic acid-binding
Bdor2041|CDS|CDS	38.5	3.0	42.4	R	COG1610	Uncharacterized conserved protein
Bdor1880|CDS|CDS	14.7	3.7	13.2	R	COG1611	Predicted Rossmann fold nucleotide-binding protein
TS28Eub1511|CDS|CDS	1.0	41.5	0.1	R	COG1624	Uncharacterized conserved protein
TS28Clo00505|CDS|CDS	2.0	75.5	0.1	R	COG1636	Uncharacterized protein conserved in bacteria
TS28Eub3862|CDS|CDS	0.5	30.0	0.1	R	COG1636	Uncharacterized protein conserved in bacteria
Ehal1108|CDS|CDS	9.0	2.5	11.9	R	COG1641	Uncharacterized conserved protein
Bste2176|CDS|CDS	8.5	2.0	14.1	R	COG1649	Uncharacterized protein conserved in bacteria
Buni0908|CDS|CDS	18.7	5.0	12.3	R	COG1649	Uncharacterized protein conserved in bacteria
TS28Bac2304|CDS|CDS	18.7	5.0	12.3	R	COG1649	Uncharacterized protein conserved in bacteria
TS28Bac4526|CDS|CDS	20.0	6.5	10.2	R	COG1649	Uncharacterized protein conserved in bacteria
TS28Clo00572|CDS|CDS	2.0	153.0	0.0	R	COG1649	Uncharacterized protein conserved in bacteria
TS29Rum12932|CDS|CDS	2.0	0.3	19.8	R	COG1660	Predicted P-loop-containing kinase
TS29Fae08070|CDS|CDS	0.5	28.0	0.1	R	COG1672	Predicted ATPase (AAA+ superfamily)
TS28Fae17290|CDS|CDS	0.5	28.0	0.1	R	COG1672	Predicted ATPase (AAA+ superfamily)
TS29Fae06825|CDS|CDS	1.0	86.0	0.0	R	COG1672	Predicted ATPase (AAA+ superfamily)
TS28Fae19056|CDS|CDS	3.5	0.5	23.1	R	COG1683	Uncharacterized conserved protein
Msmi740313|CDS|CDS	7.0	0.3	92.6	R	COG1690	Uncharacterized conserved protein
Msmi751369|CDS|CDS	7.5	1.8	14.2	R	COG1690	Uncharacterized conserved protein
Msmi751569|CDS|CDS	5.8	0.5	38.6	R	COG1712	Predicted dinucleotide-utilizing enzyme
TS28Met0460|CDS|CDS	3.1	0.7	15.3	R	COG1719	Predicted hydrocarbon binding protein (contains V4R domain)
TS29Rum00049|CDS|CDS	0.3	25.0	0.0	R	COG1720	Uncharacterized conserved protein
BactD12067|CDS|CDS	2.0	0.5	13.2	R	COG1721	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)
FpraM2121018|CDS|CDS	9.8	0.5	65.0	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
Bcap2813|CDS|CDS	90.6	6.0	50.0	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS28RumUnc1427|CDS|CDS	118.5	8.0	49.0	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein

TS29Fae02846|CDS|CDS	3.5	0.5	23.1	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS28RumUnc0265|CDS|CDS	35.0	6.0	19.3	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS29Rum17154|CDS|CDS	4.5	1.0	14.9	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS29Fae05803|CDS|CDS	5.5	1.5	12.1	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
Svar1090|CDS|CDS	3.4	1.0	11.2	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
Msmi741444|CDS|CDS	6.0	0.7	29.8	R	COG1745	Predicted metal-binding protein
TS28Met1087|CDS|CDS	6.0	0.7	29.8	R	COG1745	Predicted metal-binding protein
Msmi740033|CDS|CDS	15.0	4.0	12.4	R	COG1759	ATP-utilizing enzymes of ATP-grasp superfamily (probably carboligases)
TS28Fae20114|CDS|CDS	1.0	46.0	0.1	R	COG1768	Predicted phosphohydrolase
Msmi741426|CDS|CDS	5.1	1.3	12.6	R	COG1771	Uncharacterized protein conserved in archaea
Dlon2630|CDS|CDS	6.0	0.5	39.7	R	COG1774	Uncharacterized homolog of PSP1
FpraM2120675|CDS|CDS	6.0	0.5	39.7	R	COG1774	Uncharacterized homolog of PSP1
Bdor2879|CDS|CDS	0.3	13.0	0.1	R	COG1774	Uncharacterized homolog of PSP1
TS28Bac5737|CDS|CDS	0.3	20.0	0.1	R	COG1774	Uncharacterized homolog of PSP1
TS29Fae00492|CDS|CDS	4.5	0.5	29.8	R	COG1799	Uncharacterized protein conserved in bacteria
Dlon2201|CDS|CDS	5.5	1.0	18.2	R	COG1799	Uncharacterized protein conserved in bacteria
Rtor2147|CDS|CDS	5.0	1.0	16.5	R	COG1799	Uncharacterized protein conserved in bacteria
TS28Clo00516|CDS|CDS	1.0	68.0	0.0	R	COG1799	Uncharacterized protein conserved in bacteria
Msmi750254|CDS|CDS	2.3	0.3	29.8	R	COG1817	Uncharacterized protein conserved in archaea
Msmi740225|CDS|CDS	3.5	0.5	23.1	R	COG1822	Predicted archaeal membrane protein
Msmi751377|CDS|CDS	4.9	0.3	48.8	R	COG1836	Predicted membrane protein
TS28Rum09890|CDS|CDS	6.5	1.5	14.3	R	COG1837	Predicted RNA-binding protein (contains KH domain)
Rtor1397|CDS|CDS	6.5	1.5	14.3	R	COG1837	Predicted RNA-binding protein (contains KH domain)
TS29Rum05911|CDS|CDS	4.9	0.7	24.5	R	COG1847	Predicted RNA-binding protein
Rtor0909|CDS|CDS	4.9	1.2	14.0	R	COG1847	Predicted RNA-binding protein
Msmi750077|CDS|CDS	6.0	1.0	19.0	R	COG1860	Uncharacterized protein conserved in archaea
Msmi741633|CDS|CDS	6.0	1.0	19.0	R	COG1860	Uncharacterized protein conserved in archaea
TS28Fae09811|CDS|CDS	7.0	2.0	11.6	R	COG1873	Uncharacterized conserved protein
Msmi740789|CDS|CDS	10.0	3.0	11.0	R	COG1873	Uncharacterized conserved protein
Msmi741256|CDS|CDS	4.0	0.8	15.9	R	COG1891	Uncharacterized protein conserved in archaea
Msmi741440|CDS|CDS	3.8	0.3	37.2	R	COG1900	Uncharacterized conserved protein
Casp1085|CDS|CDS	6.0	1.0	19.8	R	COG1915	Uncharacterized conserved protein
Robe2729|CDS|CDS	0.5	18.5	0.1	R	COG1917|COG0599	Uncharacterized conserved protein, contains double-stranded beta-helix domain|Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit
TS28RumUnc0997|CDS|CDS	7.0	1.0	23.1	R	COG1923	Uncharacterized host factor I protein
TS28Dor2914|CDS|CDS	0.5	18.0	0.1	R	COG1964	Predicted Fe-S oxidoreductases
Pmer2384|CDS|CDS	10.0	3.0	11.0	R	COG1971	Predicted membrane protein
TS28Rum05141|CDS|CDS	5.4	1.0	17.9	R	COG2001	Uncharacterized protein conserved in bacteria
Dfor0850|CDS|CDS	10.0	3.0	11.0	R	COG2001	Uncharacterized protein conserved in bacteria
TS28Rum13912|CDS|CDS	0.5	26.0	0.1	R	COG2005|COG2068	N-terminal domain of molybdenum-binding protein|Uncharacterized MobA-related protein
Pmer1803|CDS|CDS	8.0	2.0	13.2	R	COG2006	Uncharacterized conserved protein
Ccom2285|CDS|CDS	5.0	1.0	16.5	R	COG2013	Uncharacterized conserved protein
TS28Fae06758|CDS|CDS	8.0	2.0	13.2	R	COG2013	Uncharacterized conserved protein
Msmi751431|CDS|CDS	2.3	0.3	29.8	R	COG2054	Uncharacterized archaeal kinase related to aspartokinases, uridylate kinases
TS29Rum14664|CDS|CDS	10.0	2.0	16.5	R	COG2068	Uncharacterized MobA-related protein
TS28Fae16637|CDS|CDS	0.5	69.5	0.0	R	COG2070	Dioxygenases related to 2-nitropropane dioxygenase
Msmi750753|CDS|CDS	6.6	0.5	43.3	R	COG2078|COG3885	Uncharacterized conserved protein|Uncharacterized conserved protein
TS29Met0119|CDS|CDS	4.1	0.9	14.6	R	COG2078|COG3885	Uncharacterized conserved protein|Uncharacterized conserved protein
Msmi740926|CDS|CDS	2.8	0.9	10.1	R	COG2078|COG3885	Uncharacterized conserved protein|Uncharacterized conserved protein
Msmi740549|CDS|CDS	2.5	0.3	24.8	R	COG2081	Predicted flavoproteins
Msmi750311|CDS|CDS	14.0	0.5	92.6	R	COG2085	Predicted dinucleotide-binding enzymes
Robe3263|CDS|CDS	5.3	1.5	11.8	R	COG2096|COG3193	Uncharacterized conserved protein|Uncharacterized protein, possibly involved in utilization of glycolate and propanediol
Msmi741493|CDS|CDS	5.0	0.3	66.1	R	COG2102	Predicted ATPases of PP-loop superfamily
Msmi750220|CDS|CDS	3.0	0.3	39.7	R	COG2102	Predicted ATPases of PP-loop superfamily
ShigspD92223|CDS|CDS	6.8	1.0	22.6	R	COG2103	Predicted sugar phosphate isomerase
Bste2157|CDS|CDS	19.0	6.0	10.5	R	COG2103	Predicted sugar phosphate isomerase
Msmi741031|CDS|CDS	5.7	0.9	20.4	R	COG2106	Uncharacterized conserved protein
Msmi741001|CDS|CDS	1.8	0.3	18.2	R	COG2129	Predicted phosphoesterases, related to the Icc protein
Msmi740500|CDS|CDS	9.5	0.8	37.7	R	COG2138	Uncharacterized conserved protein
TS28Clo00802|CDS|CDS	1.0	52.0	0.1	R	COG2179	Predicted hydrolase of the HAD superfamily
Msmi750666|CDS|CDS	6.0	0.3	79.4	R	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold
Msmi741015|CDS|CDS	6.0	0.3	79.4	R	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold
BactD20437|CDS|CDS	2.0	0.5	13.2	R	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold
BVU1865|CDS|aminopeptidase	0.3	11.7	0.1	R	COG2234	Predicted aminopeptidases
TS28Bac0940|CDS|CDS	0.3	18.7	0.1	R	COG2234	Predicted aminopeptidases
TS28Fae01749|CDS|CDS	1.0	35.5	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS28Clo00691|CDS|CDS	4.0	154.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS29Rum16015|CDS|CDS	1.0	41.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS28Fae15753|CDS|CDS	1.0	44.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS28Eub0884|CDS|CDS	1.0	51.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS28Fae20409|CDS|CDS	1.0	66.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS28Fae17143|CDS|CDS	1.0	83.0	0.0	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid

TS29Rum11095|CDS|CDS	20.0	3.0	22.0	R	COG2252	Permeases
TS28Rum08091|CDS|CDS	15.0	4.0	12.4	R	COG2257	Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB
Pmer1168|CDS|CDS	6.5	1.0	21.5	R	COG2259	Predicted membrane protein
Bova2305|CDS|CDS	2.0	0.3	19.8	R	COG2262	GTPases
TS28Fae08961|CDS|CDS	2.0	74.0	0.1	R	COG2262	GTPases
BactD13474|CDS|CDS	13.3	0.5	87.6	R	COG2304	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Bova0525|CDS|CDS	6.0	1.0	19.7	R	COG2304	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Bste1197|CDS|CDS	26.0	8.0	10.7	R	COG2304	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
TS28RumUnc1238|CDS|CDS	4.0	1.0	13.2	R	COG2333	Predicted hydrolase (metallo-beta-lactamase superfamily)
PRABACTJOHN3210|CDS|CDS	27.5	8.0	11.4	R	COG2333	Predicted hydrolase (metallo-beta-lactamase superfamily)
TS28Par0106|CDS|CDS	1.0	41.0	0.1	R	COG2339	Predicted membrane protein
TS28Rum12178|CDS|CDS	21.0	3.0	23.1	R	COG2344	AT-rich DNA-binding protein
TS28CloUnc091|CDS|CDS	20.0	6.0	11.0	R	COG2357	Uncharacterized protein conserved in bacteria
TS28Clo00938|CDS|CDS	1.0	100.0	0.0	R	COG2357	Uncharacterized protein conserved in bacteria
TS28Col1689|CDS|CDS	124.0	23.0	17.8	R	COG2358	TRAP-type uncharacterized transport system, periplasmic component
TS28Clo01118|CDS|CDS	1.0	40.0	0.1	R	COG2359	Uncharacterized protein conserved in bacteria
Pmer2942|CDS|CDS	16.0	3.0	17.6	R	COG2364	Predicted membrane protein
TS28Dor2922|CDS|CDS	0.5	35.0	0.0	R	COG2364	Predicted membrane protein
ShigspD92361|CDS|CDS	7.0	1.0	23.1	R	COG2373	Large extracellular alpha-helical protein
TS29Rum19899|CDS|CDS	5.0	1.0	16.5	R	COG2384	Predicted SAM-dependent methyltransferase
Bdor3073|CDS|CDS	4.5	1.0	14.9	R	COG2388	Predicted acetyltransferase
Msmi750271|CDS|CDS	4.3	0.6	24.1	R	COG2403	Predicted GTPase
TS28Met0926|CDS|CDS	0.3	10.0	0.1	R	COG2457	Uncharacterized conserved protein
TS29Fae10244|CDS|CDS	6.0	1.0	19.8	R	COG2501	Uncharacterized conserved protein
TS28Fae01729|CDS|CDS	17.0	4.0	14.1	R	COG2501	Uncharacterized conserved protein
CspSS22369|CDS|CDS	2.0	0.5	13.2	R	COG2501	Uncharacterized conserved protein
TS29Clo0901|CDS|CDS	11.0	3.0	12.1	R	COG2509	Uncharacterized FAD-dependent dehydrogenases
TS28Eub6395|CDS|CDS	1.0	101.5	0.0	R	COG2509	Uncharacterized FAD-dependent dehydrogenases
TS29Clo1899|CDS|CDS	1.7	0.3	16.5	R	COG2607	Predicted ATPase (AAA+ superfamily)
TS28Rum13839|CDS|CDS	5.0	1.0	16.5	R	COG2607	Predicted ATPase (AAA+ superfamily)
Bdor0061|CDS|CDS	21.5	3.0	23.7	R	COG2738	Predicted Zn-dependent protease
TS29Fae00713|CDS|CDS	11.5	0.5	76.1	R	COG2739	Uncharacterized protein conserved in bacteria
ShigspD90529|CDS|CDS	10.5	1.0	34.7	R	COG2828|COG3181	Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria
Acol0604|CDS|CDS	5.0	1.0	16.5	R	COG2848	Uncharacterized conserved protein
Casp2540|CDS|CDS	4.0	1.0	13.2	R	COG2848	Uncharacterized conserved protein
TS29Rum20177|CDS|CDS	0.5	17.0	0.1	R	COG2848	Uncharacterized conserved protein
TS28Rum15365|CDS|CDS	0.5	36.0	0.0	R	COG2848	Uncharacterized conserved protein
Bste0757|CDS|CDS	20.0	5.0	13.2	R	COG2855	Predicted membrane protein
TS28Bac0869|CDS|CDS	0.3	19.5	0.1	R	COG2908	Uncharacterized protein conserved in bacteria
TS29Fae06188|CDS|CDS	38.0	2.0	62.8	R	COG2929	Uncharacterized protein conserved in bacteria
Bdor2857|CDS|CDS	0.3	14.5	0.1	R	COG2936	Predicted acyl esterases
Pmer2441|CDS|CDS	5.0	1.0	16.5	R	COG2954	Uncharacterized protein conserved in bacteria
BactD11837|CDS|CDS	4.0	1.0	13.2	R	COG2985	Predicted permease
TS29Rum11762|CDS|CDS	1.0	38.0	0.1	R	COG2996	Uncharacterized protein conserved in bacteria
ShigspD92643|CDS|CDS	6.5	1.0	21.5	R	COG3008	Paraquat-inducible protein B
TS28Bac7399|CDS|CDS	12.0	1.0	39.7	R	COG3041	Uncharacterized protein conserved in bacteria
TS29Clo4944|CDS|CDS	6.3	2.0	10.3	R	COG3041	Uncharacterized protein conserved in bacteria
Bdor0596|CDS|CDS	21.0	3.0	23.1	R	COG3055	Uncharacterized protein conserved in bacteria
Bdor2055|CDS|CDS	3.0	0.7	14.9	R	COG3176	Putative hemolysin
Bxyl2352|CDS|CDS	5.0	1.0	16.5	R	COG3177	Uncharacterized conserved protein
ShigspD90379|CDS|CDS	8.0	0.5	52.9	R	COG3214	Uncharacterized protein conserved in bacteria
Msmi751170|CDS|CDS	5.5	1.7	10.8	R	COG3273	Uncharacterized conserved protein
TS28Fae15688|CDS|CDS	191.0	55.0	11.5	R	COG3291	FOG: PKD repeat
TS28Rum02197|CDS|CDS	34.0	10.0	11.2	R	COG3291	FOG: PKD repeat
TS28Fae11308|CDS|CDS	1.0	44.0	0.1	R	COG3291	FOG: PKD repeat
TS28Met1107|CDS|CDS	0.3	15.5	0.1	R	COG3291	FOG: PKD repeat
TS28Clo01735|CDS|CDS	2.0	209.0	0.0	R	COG3291	FOG: PKD repeat
TS28Bac4220|CDS|CDS	8.0	2.0	13.2	R	COG3304	Predicted membrane protein
Bdor2382|CDS|CDS	12.3	3.0	13.6	R	COG3323|COG0327	Uncharacterized protein conserved in bacteria|Uncharacterized conserved protein
Msmi750663|CDS|CDS	2.9	0.3	37.7	R	COG3356	Predicted membrane protein
TS29Met0772|CDS|CDS	5.6	1.0	18.5	R	COG3356	Predicted membrane protein
TS28Ali1508|CDS|CDS	126.3	10.0	41.8	R	COG3391	Uncharacterized conserved protein
TS28Ali1510|CDS|CDS	161.0	28.0	19.0	R	COG3391	Uncharacterized conserved protein
Pmer3415|CDS|CDS	57.5	6.0	31.7	R	COG3533	Uncharacterized protein conserved in bacteria
Bdor2171|CDS|CDS	44.5	8.0	18.4	R	COG3560	Predicted oxidoreductase related to nitroreductase
Pmer1538|CDS|CDS	9.0	2.0	14.9	R	COG3560	Predicted oxidoreductase related to nitroreductase
TS28Fae08800|CDS|CDS	1.0	34.0	0.1	R	COG3567	Uncharacterized protein conserved in bacteria
Pmer2293|CDS|CDS	7.5	1.0	24.8	R	COG3568|COG4412	Metal-dependent hydrolase|Uncharacterized protein conserved in bacteria
TS28Clo00886|CDS|CDS	1.0	108.0	0.0	R	COG3581|COG3580	Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria
TS28RumUnc0714|CDS|CDS	11.0	2.0	18.2	R	COG3641	Predicted membrane protein, putative toxin regulator
TS28Dor0443|CDS|CDS	0.5	17.5	0.1	R	COG3681	Uncharacterized conserved protein
TS29Fae06454|CDS|CDS	0.5	40.5	0.0	R	COG3786	Uncharacterized protein conserved in bacteria
TS28Fae08484|CDS|CDS	0.5	40.5	0.0	R	COG3786	Uncharacterized protein conserved in bacteria
TS28Eub4416|CDS|CDS	4.0	132.5	0.1	R	COG3858	Predicted glycosyl hydrolase
TS28Fae21833|CDS|CDS	4.0	1.0	13.2	R	COG3862	Uncharacterized protein with conserved CXXC pairs
TS29Fae05457|CDS|CDS	15.0	2.0	24.8	R	COG3876	Uncharacterized protein conserved in bacteria
TS29Bac01591|CDS|CDS	4.7	0.7	23.1	R	COG3876	Uncharacterized protein conserved in bacteria
Msmi751519|CDS|CDS	16.2	4.3	12.3	R	COG3894	Uncharacterized metal-binding protein
TS28Clo00424|CDS|CDS	3.0	117.0	0.1	R	COG3910	Predicted ATPase
TS29LacUnc011|CDS|CDS	14.0	3.0	15.4	R	COG3937	Uncharacterized conserved protein
TS28Bac8004|CDS|CDS	1.0	33.7	0.1	R	COG3940	Predicted beta-xylosidase
TS29Fae03489|CDS|CDS	12.0	2.0	19.8	R	COG3943	Virulence protein
Casp5726|CDS|CDS	5.0	1.0	16.5	R	COG3968	Uncharacterized protein related to glutamine synthetase

TS28Fae20021|CDS|CDS	1.0	39.0	0.1	R	COG3968	Uncharacterized protein related to glutamine synthetase
TS28Fae20568|CDS|CDS	1.0	63.5	0.1	R	COG3968	Uncharacterized protein related to glutamine synthetase
BactD13448|CDS|CDS	3.3	0.5	22.0	R	COG3969	Predicted phosphoadenosine phosphosulfate sulfotransferase
TS28Bif3124|CDS|CDS	1.3	44.7	0.1	R	COG3973	Superfamily I DNA and RNA helicases
TS28Clo00690|CDS|CDS	5.0	232.0	0.1	R	COG3973	Superfamily I DNA and RNA helicases
TS28Eub1029|CDS|CDS	1.0	164.0	0.0	R	COG3973	Superfamily I DNA and RNA helicases
BactD13488|CDS|CDS	7.0	1.0	23.1	R	COG3979	Uncharacterized protein contain chitin-binding domain type 3
Msmi750405|CDS|CDS	1.0	0.3	13.2	R	COG4026	Uncharacterized protein containing TOPRIM domain, potential nuclease
Msmi750038|CDS|CDS	4.7	0.3	46.6	R	COG4030	Uncharacterized protein conserved in archaea
Msmi741676|CDS|CDS	4.7	1.3	11.7	R	COG4030	Uncharacterized protein conserved in archaea
TS28Met0625|CDS|CDS	8.9	0.3	117.9	R	COG4036	Predicted membrane protein
Msmi741687|CDS|CDS	9.6	0.8	42.3	R	COG4036	Predicted membrane protein
Msmi741689|CDS|CDS	2.0	0.2	33.1	R	COG4038	Predicted membrane protein
Msmi750025|CDS|CDS	3.8	0.5	27.6	R	COG4038	Predicted membrane protein
TS29Met0091|CDS|CDS	3.8	0.8	15.8	R	COG4038	Predicted membrane protein
TS28Met0628|CDS|CDS	3.8	0.8	15.8	R	COG4038	Predicted membrane protein
Msmi741692|CDS|CDS	4.3	1.0	14.1	R	COG4041	Predicted membrane protein
Msmi740981|CDS|CDS	2.0	0.3	19.8	R	COG4050	Uncharacterized protein conserved in archaea
TS28Met1260|CDS|CDS	0.3	17.9	0.0	R	COG4071	Uncharacterized protein conserved in archaea
Msmi741110|CDS|CDS	8.5	1.6	17.8	R	COG4079	Uncharacterized protein conserved in archaea
Msmi750566|CDS|CDS	10.8	2.3	15.9	R	COG4079	Uncharacterized protein conserved in archaea
Msmi750257|CDS|CDS	10.0	0.3	99.2	R	COG4081	Uncharacterized protein conserved in archaea
TS28Met1320|CDS|CDS	10.0	2.3	14.2	R	COG4081	Uncharacterized protein conserved in archaea
TS29Rum03113|CDS|CDS	38.0	7.0	18.0	R	COG4086	Predicted secreted protein
Bdor2615|CDS|CDS	39.3	7.7	17.0	R	COG4105	DNA uptake lipoprotein
Pmer1141|CDS|CDS	20.5	2.0	33.9	R	COG4185	Uncharacterized protein conserved in bacteria
TS29Bac09669|CDS|CDS	2.0	0.5	13.2	R	COG4198	Uncharacterized conserved protein
TS28Bac2502|CDS|CDS	36.5	10.0	12.1	R	COG4198	Uncharacterized conserved protein
TS28Fae22118|CDS|CDS	1.0	43.5	0.1	R	COG4200	Uncharacterized protein conserved in bacteria
TS29Bac05446|CDS|CDS	2.7	0.3	26.5	R	COG4225	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins
TS28Fae18169|CDS|CDS	1.0	39.5	0.1	R	COG4260	Putative virion core protein (lumpy skin disease virus)
TS28Eub5894|CDS|CDS	0.5	20.0	0.1	R	COG4260	Putative virion core protein (lumpy skin disease virus)
TS28Clo00615|CDS|CDS	3.0	157.0	0.1	R	COG4260	Putative virion core protein (lumpy skin disease virus)
TS28Dor0344|CDS|CDS	0.5	24.5	0.1	R	COG4277	Predicted DNA-binding protein with the Helix-hairpin-helix motif
TS28Eub7197|CDS|CDS	1.0	86.0	0.0	R	COG4277	Predicted DNA-binding protein with the Helix-hairpin-helix motif
Bste2159|CDS|CDS	2.5	0.5	16.5	R	COG4299	Uncharacterized conserved protein
TS29Bif0648|CDS|CDS	0.3	11.3	0.1	R	COG4393	Predicted membrane protein
Even1979|CDS|CDS	0.8	32.4	0.1	R	COG4422	Bacteriophage protein gp37
Dfor0888|CDS|CDS	10.0	1.0	33.1	R	COG4472	Uncharacterized protein conserved in bacteria
TS28Rum02946|CDS|CDS	9.0	1.0	29.8	R	COG4485	Predicted membrane protein
TS28Clo00565|CDS|CDS	8.0	277.0	0.1	R	COG4485	Predicted membrane protein
TS28Dor1957|CDS|CDS	1.0	45.0	0.1	R	COG4485	Predicted membrane protein
TS28Eub5363|CDS|CDS	2.0	95.3	0.1	R	COG4485	Predicted membrane protein
TS28Fae12026|CDS|CDS	1.0	58.5	0.1	R	COG4485	Predicted membrane protein
TS28Clo00756|CDS|CDS	1.0	49.0	0.1	R	COG4495	Uncharacterized protein conserved in bacteria
TS28RumUnc0548|CDS|CDS	0.5	25.0	0.1	R	COG4603	ABC-type uncharacterized transport system, permease component
Bdor2372|CDS|CDS	19.5	2.0	32.2	R	COG4642	Uncharacterized protein conserved in bacteria
TS29Rum10308|CDS|CDS	6.0	1.0	19.8	R	COG4667	Predicted esterase of the alpha-beta hydrolase superfamily
TS29Rum00611|CDS|CDS	2.0	0.3	19.8	R	COG4716	Myosin-crossreactive antigen
TS28Clo00490|CDS|CDS	5.0	211.5	0.1	R	COG4716	Myosin-crossreactive antigen
TS28Fae13726|CDS|CDS	1.0	50.0	0.1	R	COG4716	Myosin-crossreactive antigen
TS28Clo00736|CDS|CDS	1.0	37.0	0.1	R	COG4728	Uncharacterized protein conserved in bacteria
Msmi741293|CDS|CDS	4.3	0.3	42.2	R	COG4744	Uncharacterized conserved protein
Msmi750390|CDS|CDS	3.3	0.3	32.2	R	COG4744	Uncharacterized conserved protein
BactD11694|CDS|CDS	14.3	1.0	47.4	R	COG4747	ACT domain-containing protein
Bdor0570|CDS|CDS	5.2	1.0	17.2	R	COG4804	Uncharacterized conserved protein
TS29Bac00982|CDS|CDS	5.0	1.0	16.5	R	COG4804	Uncharacterized conserved protein
Bsp1161711|CDS|CDS	2.3	0.5	14.9	R	COG4804	Uncharacterized conserved protein
TS29Bac01072|CDS|CDS	2.3	0.5	14.9	R	COG4804	Uncharacterized conserved protein
TS28Bac5883|CDS|CDS	0.5	52.0	0.0	R	COG4804	Uncharacterized conserved protein
CspSS21123|CDS|CDS	0.3	23.0	0.0	R	COG4805	Uncharacterized protein conserved in bacteria
Csci0185|CDS|CDS	6.0	1.0	19.8	R	COG4824	Phage-related holin (Lysis protein)
TS28Fae21267|CDS|CDS	26.0	3.0	28.7	R	COG4832	Uncharacterized conserved protein
Cspi1195|CDS|CDS	63.0	1.0	208.3	R	COG4856	Uncharacterized protein conserved in bacteria
Acol0976|CDS|CDS	7.0	2.0	11.6	R	COG4857	Predicted kinase
Buni1154|CDS|CDS	8.8	2.5	11.7	R	COG4864	Uncharacterized protein conserved in bacteria
TS28Bac3330|CDS|CDS	8.8	2.5	11.7	R	COG4864	Uncharacterized protein conserved in bacteria
Bdor1122|CDS|CDS	8.3	2.7	10.3	R	COG4866	Uncharacterized conserved protein
TS28Bif5376|CDS|CDS	0.7	26.2	0.1	R	COG4868	Uncharacterized protein conserved in bacteria
Clep0429|CDS|CDS	163.0	8.5	63.4	R	COG4880	Secreted protein containing C-terminal beta-propeller domain distantly related to WD-40 repeats
Dfor2715|CDS|CDS	73.0	10.0	24.1	R	COG4880	Secreted protein containing C-terminal beta-propeller domain distantly related to WD-40 repeats
TS28Dor1882|CDS|CDS	172.0	39.0	14.6	R	COG4880	Secreted protein containing C-terminal beta-propeller domain distantly related to WD-40 repeats
Msmi740702|CDS|CDS	11.8	0.3	116.9	R	COG4883	Uncharacterized protein conserved in archaea
Msmi750976|CDS|CDS	21.5	3.3	21.3	R	COG4883	Uncharacterized protein conserved in archaea
Rtor0725|CDS|CDS	30.3	9.8	10.2	R	COG4886	Leucine-rich repeat (LRR) protein
Msmi750615|CDS|CDS	4.0	0.6	22.7	R	COG4907	Predicted membrane protein
Msmi741063|CDS|CDS	4.0	1.1	12.2	R	COG4907	Predicted membrane protein
TS28Fae21583|CDS|CDS	3.0	183.3	0.1	R	COG4913	Uncharacterized protein conserved in bacteria
TS28Bac6589|CDS|CDS	6.3	1.5	14.0	R	COG4946	Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system
TS28Eub7288|CDS|CDS	0.5	34.5	0.0	R	COG4951	Uncharacterized protein conserved in bacteria
TS28Clo01183|CDS|CDS	2.0	67.0	0.1	R	COG5017	Uncharacterized conserved protein
Csym0815|CDS|CDS	7.0	1.0	23.2	R	COG5263	FOG: Glucan-binding domain (YG repeat)
Cbol1236|CDS|CDS	32.8	5.0	21.7	R	COG5263	FOG: Glucan-binding domain (YG repeat)

TS29Clo2651|CDS|CDS	9.0	2.0	14.9	R	COG5263	FOG: Glucan-binding domain (YG repeat)
TS28Rum03315|CDS|CDS	2.0	74.0	0.1	R	COG5283|COG5412	Phage-related tail protein|Phage-related protein
TS28Fae04439|CDS|CDS	1.0	46.0	0.1	R	COG5283|COG5412|COG5280	Phage-related tail protein|Phage-related protein|Phage-related minor tail protein
TS28RumUnc1879|CDS|CDS	2.0	135.0	0.0	R	COG5283|COG5412|COG5280	Phage-related tail protein|Phage-related protein|Phage-related minor tail protein
Dfor1552|CDS|CDS	9.0	2.0	14.9	R	COG5341	Uncharacterized protein conserved in bacteria
TS28Fae01808|CDS|CDS	0.5	75.0	0.0	R	COG5412|COG5280	Phage-related protein|Phage-related minor tail protein
TS29Fae10219|CDS|CDS	8.0	2.0	13.2	R	COG5438	Predicted multitransmembrane protein
Bdor3895|CDS|CDS	11.5	1.5	25.4	R	COG5464	Uncharacterized conserved protein
Bxyl0019|CDS|CDS	2.7	0.5	17.6	R	COG5464	Uncharacterized conserved protein
Bste1283|CDS|CDS	24.0	6.0	13.2	R	COG5464	Uncharacterized conserved protein
Acol2972|CDS|CDS	3.0	104.0	0.1	R	COG5511	Bacteriophage capsid protein
Bova2285|CDS|CDS	6.0	1.0	19.8	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Bxyl0884|CDS|CDS	6.0	1.0	19.8	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Cnex2744|CDS|CDS	2.2	94.4	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Ccom0763|CDS|CDS	0.8	38.9	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Even0585|CDS|CDS	2.5	149.8	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
FpraM2120212|CDS|CDS	0.4	26.9	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Cnex1526|CDS|CDS	0.4	28.5	0.0	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Ceut1813|CDS|CDS	0.3	97.2	0.0	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Bdor2374|CDS|CDS	41.5	3.0	45.7	R	COG5587	Uncharacterized conserved protein
TS28Fae04289|CDS|CDS	27,602.0	2.0	45,639.0	NA	NA	hypothetical protein
TS28Par2562|CDS|CDS	4,019.0	1.0	13,290.6	NA	NA	hypothetical protein
TS28Fae17789|CDS|CDS	7,989.0	2.0	13,209.5	NA	NA	hypothetical protein
TS29Fae02022|CDS|CDS	11,443.5	5.0	7,568.6	NA	NA	hypothetical protein
Ccom1560|CDS|CDS	2,277.9	1.0	7,532.9	NA	NA	hypothetical protein
TS29Rum02227|CDS|CDS	1,723.0	1.0	5,697.8	NA	NA	hypothetical protein
TS29Fae02023|CDS|CDS	1,595.7	1.0	5,276.8	NA	NA	hypothetical protein
Robe2147|CDS|CDS	4,405.1	3.0	4,855.8	NA	NA	hypothetical protein
TS29Fae01517|CDS|CDS	31,785.2	28.0	3,754.0	NA	NA	hypothetical protein
TS29Fae05352|CDS|CDS	2,249.0	2.0	3,718.6	NA	NA	hypothetical protein
Rgna2691|CDS|CDS	5,387.0	5.0	3,562.9	NA	NA	hypothetical protein
TS29Fae09565|CDS|CDS	13,183.0	15.0	2,906.4	NA	NA	hypothetical protein
TS28Fae18234|CDS|CDS	2,812.0	4.0	2,324.8	NA	NA	hypothetical protein
TS29Fae00793|CDS|CDS	1,851.0	3.0	2,040.4	NA	NA	hypothetical protein
TS29Fae05351|CDS|CDS	912.5	1.5	2,011.7	NA	NA	hypothetical protein
TS28Fae18841|CDS|CDS	912.5	1.5	2,011.7	NA	NA	hypothetical protein
TS28Rum15487|CDS|CDS	592.0	1.0	1,957.7	NA	NA	hypothetical protein
TS28Rum10074|CDS|CDS	553.0	1.0	1,828.7	NA	NA	hypothetical protein
TS29Fae03670|CDS|CDS	1,536.0	3.0	1,693.1	NA	NA	hypothetical protein
TS28Bac7805|CDS|CDS	2,025.0	4.0	1,674.1	NA	NA	hypothetical protein
BDI0358|CDS|hypothetical	982.0	2.0	1,623.7	NA	NA	hypothetical protein
TS28Rum13907|CDS|CDS	1,918.5	5.5	1,153.5	NA	NA	hypothetical protein
TS29Rum16880|CDS|CDS	1,918.5	5.5	1,153.5	NA	NA	hypothetical protein
TS29Fae04643|CDS|CDS	1,286.5	4.0	1,063.6	NA	NA	hypothetical protein
Acod0202|CDS|CDS	312.0	1.0	1,031.8	NA	NA	hypothetical protein
TS28Rum04305|CDS|CDS	310.0	1.0	1,025.1	NA	NA	hypothetical protein
TS28Rum10982|CDS|CDS	305.0	1.0	1,008.6	NA	NA	hypothetical protein
Msm1017|CDS|methyl-coenzyme	196.8	0.7	976.0	NA	NA	hypothetical protein
Bste1270|CDS|CDS	143.0	0.5	945.8	NA	NA	hypothetical protein
TS29Bac03469|CDS|CDS	143.0	0.5	945.8	NA	NA	hypothetical protein
Bden1557|CDS|CDS	129.0	0.5	853.2	NA	NA	hypothetical protein
TS28Rum04833|CDS|CDS	368.0	1.5	811.3	NA	NA	hypothetical protein
Rtor0713|CDS|CDS	368.0	1.5	811.3	NA	NA	hypothetical protein
TS29Rum18028|CDS|CDS	483.0	2.0	798.6	NA	NA	hypothetical protein
Msm1018|CDS|methyl-coenzyme	54.0	0.3	714.3	NA	NA	hypothetical protein
Rbro1223|CDS|CDS	1,928.0	9.0	708.4	NA	NA	hypothetical protein
TS29Fae06146|CDS|CDS	203.0	1.0	671.3	NA	NA	hypothetical protein
TS28Ali2041|CDS|CDS	1,001.5	5.0	662.4	NA	NA	hypothetical protein
TS29Fae05350|CDS|CDS	1,394.0	7.0	658.6	NA	NA	hypothetical protein
TS29Fae07012|CDS|CDS	2,822.0	15.0	622.1	NA	NA	hypothetical protein
Bxyl0898|CDS|CDS	91.4	0.5	604.6	NA	NA	hypothetical protein
TS28EryUnc75|CDS|CDS	836.0	5.0	552.9	NA	NA	hypothetical protein
Msm0884|CDS|adhesin-like	133.7	0.8	530.5	NA	NA	hypothetical protein
TS29Dor0588|CDS|CDS	316.0	2.0	522.5	NA	NA	hypothetical protein
Bdor2038|CDS|CDS	157.0	1.0	519.2	NA	NA	hypothetical protein
TS29Rum16879|CDS|CDS	1,458.0	10.0	482.2	NA	NA	hypothetical protein
TS29Fae05353|CDS|CDS	1,248.0	9.0	458.6	NA	NA	hypothetical protein
BFych462748|CDS|hypothetical	402.5	3.0	443.7	NA	NA	hypothetical protein
Acod1370|CDS|CDS	122.0	1.0	403.4	NA	NA	hypothetical protein
TS29Fae02024|CDS|CDS	363.3	3.0	400.5	NA	NA	hypothetical protein
TS28RumUnc0888|CDS|CDS	119.0	1.0	393.5	NA	NA	hypothetical protein
TS28Rum04903|CDS|CDS	2,822.0	24.0	388.8	NA	NA	hypothetical protein
TS28Col1110|CDS|CDS	884.0	8.0	365.4	NA	NA	hypothetical protein
Rlac1489|CDS|CDS	651.5	6.0	359.1	NA	NA	hypothetical protein
TS28Fae04055|CDS|CDS	106.0	1.0	350.5	NA	NA	hypothetical protein
TS28Eub3781|CDS|CDS	106.0	1.0	350.5	NA	NA	hypothetical protein
TS29Rum18027|CDS|CDS	201.0	2.0	332.3	NA	NA	hypothetical protein
TS29Fae01516|CDS|CDS	1,280.5	13.5	313.7	NA	NA	hypothetical protein
TS28Fae00002|CDS|CDS	187.0	2.0	309.1	NA	NA	hypothetical protein
TS28Clo06847|CDS|CDS	170.0	2.0	281.1	NA	NA	hypothetical protein
BDI0370|CDS|hypothetical	675.0	8.0	279.0	NA	NA	hypothetical protein
Msm0542|CDS|methylenetetrahydromethanopterin	151.0	1.8	272.5	NA	NA	hypothetical protein
Msm0221|CDS|adhesin-like	81.8	1.0	270.5	NA	NA	hypothetical protein
BL1101|CDS|hypothetical	230.0	3.0	253.5	NA	NA	hypothetical protein
TS29Bac00036|CDS|CDS	141.5	2.0	234.0	NA	NA	hypothetical protein
BFych461128|CDS|hypothetical	210.0	3.0	231.5	NA	NA	hypothetical protein
BFnctc1040|CDS|hypothetical	210.0	3.0	231.5	NA	NA	hypothetical protein
Cbar0702|CDS|CDS	70.0	1.0	231.5	NA	NA	hypothetical protein
TS28RumUnc0887|CDS|CDS	70.0	1.0	231.5	NA	NA	hypothetical protein
TS29Fae08572|CDS|CDS	554.0	8.0	229.0	NA	NA	hypothetical protein

Msm1349|CDS|F420H2-oxidase/flavoprotein,	57.1	0.8	226.7	NA	NA	hypothetical protein
Dlon0995|CDS|CDS	135.0	2.0	223.2	NA	NA	hypothetical protein
Msmi750779|CDS|CDS	176.5	2.7	218.9	NA	NA	hypothetical protein
Msm0844|CDS|histone,	82.2	1.3	217.3	NA	NA	hypothetical protein
TS29Fae00137|CDS|CDS	65.5	1.0	216.6	NA	NA	hypothetical protein
Bste1533|CDS|CDS	128.5	2.0	212.5	NA	NA	hypothetical protein
TS29Fae08622|CDS|CDS	64.2	1.0	212.2	NA	NA	hypothetical protein
TS29Fae08440|CDS|CDS	62.0	1.0	205.0	NA	NA	hypothetical protein
Msm1009|CDS|tetrahydromethanopterin	15.3	0.3	201.7	NA	NA	hypothetical protein
TS28Met0362|CDS|CDS	15.3	0.3	201.7	NA	NA	hypothetical protein
TS28Fae19195|CDS|CDS	302.0	5.0	199.7	NA	NA	hypothetical protein
TS28Par0058|CDS|CDS	29.2	0.5	192.9	NA	NA	hypothetical protein
RintL13873|CDS|CDS	57.5	1.0	190.1	NA	NA	hypothetical protein
EUBREC1396|CDS|hypothetical	27.5	0.5	181.9	NA	NA	hypothetical protein
Pmer2646|CDS|CDS	27.2	0.5	179.7	NA	NA	hypothetical protein
BVU2266|CDS|hypothetical	27.0	0.5	178.6	NA	NA	hypothetical protein
Msm1019|CDS|methyl-coenzyme	175.4	3.3	178.5	NA	NA	hypothetical protein
b3498|CDS|oligopeptidase	26.0	0.5	172.0	NA	NA	hypothetical protein
Bdor0668|CDS|CDS	50.5	1.0	167.0	NA	NA	hypothetical protein
Msm0550|CDS|protein	12.5	0.3	165.3	NA	NA	hypothetical protein
BVU1389|CDS|30S	641.3	13.0	163.1	NA	NA	hypothetical protein
TS28Col0962|CDS|CDS	529.0	11.0	159.0	NA	NA	hypothetical protein
TS28Fae18976|CDS|CDS	480.0	10.0	158.7	NA	NA	hypothetical protein
Msmi741566|CDS|CDS	111.3	2.3	157.7	NA	NA	hypothetical protein
Msmi750152|CDS|CDS	111.3	2.3	157.7	NA	NA	hypothetical protein
Bdor0683|CDS|CDS	190.5	4.0	157.5	NA	NA	hypothetical protein
TS28Clo02074|CDS|CDS	136.0	3.0	149.9	NA	NA	hypothetical protein
Msm0666|CDS|hypothetical	11.0	0.3	145.5	NA	NA	hypothetical protein
TS28Fae16003|CDS|CDS	171.0	4.0	141.4	NA	NA	hypothetical protein
Msm1544|CDS|lipopolysaccharide	10.7	0.3	141.1	NA	NA	hypothetical protein
TS28Ali0695|CDS|CDS	169.0	4.0	139.7	NA	NA	hypothetical protein
TS29Rum17607|CDS|CDS	83.0	2.0	137.2	NA	NA	hypothetical protein
TS28Ali0057|CDS|CDS	124.0	3.0	136.7	NA	NA	hypothetical protein
Msm1223|CDS|carbonic	10.3	0.3	135.6	NA	NA	hypothetical protein
Pmer0925|CDS|CDS	41.0	1.0	135.6	NA	NA	hypothetical protein
TS28Dor0749|CDS|CDS	122.0	3.0	134.5	NA	NA	hypothetical protein
EUBREC3394|CDS|hypothetical	20.0	0.5	132.3	NA	NA	hypothetical protein
Msmi750378|CDS|CDS	26.3	0.7	130.2	NA	NA	hypothetical protein
Bdor0047|CDS|CDS	39.0	1.0	129.0	NA	NA	hypothetical protein
Bdor2768|CDS|CDS	77.3	2.0	127.7	NA	NA	hypothetical protein
b3476|CDS|nickel	19.0	0.5	125.7	NA	NA	hypothetical protein
TS29Fae08068|CDS|CDS	76.0	2.0	125.7	NA	NA	hypothetical protein
TS28Ali0655|CDS|CDS	600.0	16.0	124.0	NA	NA	hypothetical protein
Bste1192|CDS|CDS	36.0	1.0	119.0	NA	NA	hypothetical protein
TS28Col0105|CDS|CDS	35.0	1.0	115.7	NA	NA	hypothetical protein
b3056|CDS|fused	17.5	0.5	115.7	NA	NA	hypothetical protein
TS29Rum07439|CDS|CDS	11.2	0.3	110.8	NA	NA	hypothetical protein
Rtor0839|CDS|CDS	11.2	0.3	110.8	NA	NA	hypothetical protein
Rtor2195|CDS|CDS	11.2	0.3	110.8	NA	NA	hypothetical protein
TS29Bif3379|CDS|CDS	230.0	7.0	108.7	NA	NA	hypothetical protein
TS28Bac5720|CDS|CDS	16.3	0.5	108.0	NA	NA	hypothetical protein
Msmi741305|CDS|CDS	32.6	1.0	107.8	NA	NA	hypothetical protein
Msm1008|CDS|tetrahydromethanopterin	48.8	1.5	107.5	NA	NA	hypothetical protein
Pmer2753|CDS|CDS	65.0	2.0	107.5	NA	NA	hypothetical protein
b3530|CDS|cellulose	16.0	0.5	105.8	NA	NA	hypothetical protein
TS28Fae11007|CDS|CDS	32.0	1.0	105.8	NA	NA	hypothetical protein
Dfor0044|CDS|CDS	32.0	1.0	105.8	NA	NA	hypothetical protein
TS28Rum15904|CDS|CDS	222.0	7.0	104.9	NA	NA	hypothetical protein
FpraM2121587|CDS|CDS	62.8	2.0	103.8	NA	NA	hypothetical protein
TS28Fae15723|CDS|CDS	313.2	10.0	103.6	NA	NA	hypothetical protein
BVU3832|CDS|hypothetical	46.8	1.5	103.2	NA	NA	hypothetical protein
Msmi751003|CDS|CDS	78.0	2.5	103.2	NA	NA	hypothetical protein
TS28Fae04551|CDS|CDS	248.0	8.0	102.5	NA	NA	hypothetical protein
CspM6210398|CDS|CDS	31.0	1.0	102.5	NA	NA	hypothetical protein
TS29Fae08439|CDS|CDS	216.0	7.0	102.0	NA	NA	hypothetical protein
Begg0284|CDS|CDS	10.2	0.3	101.5	NA	NA	hypothetical protein
TS29Fae08624|CDS|CDS	122.5	4.0	101.3	NA	NA	hypothetical protein
BVU1960|CDS|isocitrate	20.3	0.7	100.9	NA	NA	hypothetical protein
TS28Ali2040|CDS|CDS	1,817.5	60.0	100.2	NA	NA	hypothetical protein
CspL21891|CDS|CDS	120.3	4.0	99.5	NA	NA	hypothetical protein
Msm0104|CDS|hypothetical	10.0	0.3	99.2	NA	NA	hypothetical protein
Msm0822|CDS|photosynthetic	7.5	0.3	99.2	NA	NA	hypothetical protein
TS29Bac11180|CDS|CDS	30.0	1.0	99.2	NA	NA	hypothetical protein
Msmi740970|CDS|CDS	7.5	0.3	99.2	NA	NA	hypothetical protein
Msmi750710|CDS|CDS	7.5	0.3	99.2	NA	NA	hypothetical protein
BVU3944|CDS|putative	298.5	10.0	98.7	NA	NA	hypothetical protein
TS28Fae07911|CDS|CDS	59.0	2.0	97.6	NA	NA	hypothetical protein
Bdor2833|CDS|CDS	29.0	1.0	95.9	NA	NA	hypothetical protein
b3409|CDS|fused	14.3	0.5	94.8	NA	NA	hypothetical protein
Bdor2539|CDS|CDS	28.5	1.0	94.2	NA	NA	hypothetical protein
TS28Fae20214|CDS|CDS	28.5	1.0	94.2	NA	NA	hypothetical protein
BVU3539|CDS|superoxide	142.0	5.0	93.9	NA	NA	hypothetical protein
TS28Rum10073|CDS|CDS	85.0	3.0	93.7	NA	NA	hypothetical protein
BVU4068|CDS|hypothetical	196.5	7.0	92.8	NA	NA	hypothetical protein
Acol2751|CDS|CDS	14.0	0.5	92.6	NA	NA	hypothetical protein
Pmer0290|CDS|CDS	14.0	0.5	92.6	NA	NA	hypothetical protein
BVU3949|CDS|glucose-1-phosphate	14.0	0.5	92.6	NA	NA	hypothetical protein
Msm1015|CDS|methyl-coenzyme	106.3	3.8	91.7	NA	NA	hypothetical protein
Dfor0622|CDS|CDS	13.8	0.5	91.5	NA	NA	hypothetical protein
Dfor2068|CDS|CDS	13.8	0.5	91.5	NA	NA	hypothetical protein
TS28Fae04550|CDS|CDS	82.0	3.0	90.4	NA	NA	hypothetical protein
Buni1677|CDS|CDS	76.7	2.8	89.5	NA	NA	hypothetical protein

TS29Bac08434|CDS|CDS	76.7	2.8	89.5	NA	NA	hypothetical protein
Bdor2612|CDS|CDS	13.5	0.5	89.3	NA	NA	hypothetical protein
CspSS21224|CDS|CDS	27.0	1.0	89.3	NA	NA	hypothetical protein
TS28Par1632|CDS|CDS	13.5	0.5	89.3	NA	NA	hypothetical protein
b4117|CDS|biodegradative	13.5	0.5	89.3	NA	NA	hypothetical protein
TS28Ali0694|CDS|CDS	1,233.0	46.0	88.6	NA	NA	hypothetical protein
TS28Ali2038|CDS|CDS	562.0	21.0	88.5	NA	NA	hypothetical protein
Msm1406|CDS|molybdenum	6.7	0.3	88.2	NA	NA	hypothetical protein
TS28Rum07281|CDS|CDS	53.0	2.0	87.6	NA	NA	hypothetical protein
TS28Bac1165|CDS|CDS	26.3	1.0	87.1	NA	NA	hypothetical protein
TS29Rum10730|CDS|CDS	39.5	1.5	87.1	NA	NA	hypothetical protein
Msm0807|CDS|polar	19.8	0.8	87.1	NA	NA	hypothetical protein
Acol1441|CDS|CDS	26.0	1.0	86.0	NA	NA	hypothetical protein
TS28Clo08426|CDS|CDS	52.0	2.0	86.0	NA	NA	hypothetical protein
TS28Ali1833|CDS|CDS	26.0	1.0	86.0	NA	NA	hypothetical protein
BactD13479|CDS|CDS	13.0	0.5	86.0	NA	NA	hypothetical protein
b0586|CDS|enterobactin	13.0	0.5	86.0	NA	NA	hypothetical protein
BFych462844|CDS|hypothetical	13.0	0.5	86.0	NA	NA	hypothetical protein
TS29Bac07886|CDS|CDS	12.8	0.5	84.9	NA	NA	hypothetical protein
Bxyl3210|CDS|CDS	12.8	0.5	84.9	NA	NA	hypothetical protein
TS28Par2296|CDS|CDS	101.3	4.0	83.8	NA	NA	hypothetical protein
Msm1006|CDS|hypothetical	6.3	0.3	83.3	NA	NA	hypothetical protein
TS29Fae09944|CDS|CDS	12.5	0.5	82.7	NA	NA	hypothetical protein
Msmi750941|CDS|CDS	6.3	0.3	82.7	NA	NA	hypothetical protein
TS28Clo07265|CDS|CDS	75.0	3.0	82.7	NA	NA	hypothetical protein
Msmi740190|CDS|CDS	6.3	0.3	82.7	NA	NA	hypothetical protein
TS29Rum03677|CDS|CDS	25.0	1.0	82.7	NA	NA	hypothetical protein
Msm1016|CDS|methyl-coenzyme	112.4	4.5	82.6	NA	NA	hypothetical protein
TS28Fae22715|CDS|CDS	489.0	20.0	80.9	NA	NA	hypothetical protein
Msm1274|CDS|predicted	8.1	0.3	80.5	NA	NA	hypothetical protein
TS28Clo02078|CDS|CDS	145.0	6.0	79.9	NA	NA	hypothetical protein
Bdor3553|CDS|CDS	48.3	2.0	79.9	NA	NA	hypothetical protein
TS28Rum11980|CDS|CDS	217.0	9.0	79.7	NA	NA	hypothetical protein
Msmi740853|CDS|CDS	18.0	0.8	79.4	NA	NA	hypothetical protein
TS29Fae01541|CDS|CDS	144.0	6.0	79.4	NA	NA	hypothetical protein
TS28Fae03563|CDS|CDS	95.5	4.0	79.0	NA	NA	hypothetical protein
TS28Ali1507|CDS|CDS	286.0	12.0	78.8	NA	NA	hypothetical protein
TS29Rum03899|CDS|CDS	71.0	3.0	78.3	NA	NA	hypothetical protein
Bdor1900|CDS|CDS	508.5	22.0	76.4	NA	NA	hypothetical protein
TS28Bac6363|CDS|CDS	23.0	1.0	76.1	NA	NA	hypothetical protein
Bste2123|CDS|CDS	23.0	1.0	76.1	NA	NA	hypothetical protein
Bdor3578|CDS|CDS	11.5	0.5	76.1	NA	NA	hypothetical protein
Cbar2665|CDS|CDS	23.0	1.0	76.1	NA	NA	hypothetical protein
BVU3280|CDS|50S	45.5	2.0	75.2	NA	NA	hypothetical protein
Bova3105|CDS|CDS	34.0	1.5	75.0	NA	NA	hypothetical protein
b0497|CDS|rhsD	22.2	1.0	73.3	NA	NA	hypothetical protein
Rbro0053|CDS|CDS	14.8	0.7	73.2	NA	NA	hypothetical protein
FpraM2121034|CDS|CDS	11.0	0.5	72.8	NA	NA	hypothetical protein
TS29Clo2882|CDS|CDS	22.0	1.0	72.8	NA	NA	hypothetical protein
TS29Fae08441|CDS|CDS	11.0	0.5	72.8	NA	NA	hypothetical protein
BactD12196|CDS|CDS	22.0	1.0	72.8	NA	NA	hypothetical protein
TS29Rum14197|CDS|CDS	44.0	2.0	72.8	NA	NA	hypothetical protein
Msmi750226|CDS|CDS	5.4	0.3	71.7	NA	NA	hypothetical protein
BVU0762|CDS|putative	43.0	2.0	71.1	NA	NA	hypothetical protein
BVU2582|CDS|ribonuclease	17.7	0.8	70.1	NA	NA	hypothetical protein
TS28Bac7374|CDS|CDS	21.2	1.0	70.1	NA	NA	hypothetical protein
BactD13476|CDS|CDS	21.2	1.0	70.0	NA	NA	hypothetical protein
TS28Par1295|CDS|CDS	7.0	0.3	69.4	NA	NA	hypothetical protein
TS28RumUnc0591|CDS|CDS	21.0	1.0	69.4	NA	NA	hypothetical protein
b2503|CDS|predicted	10.5	0.5	69.4	NA	NA	hypothetical protein
TS28Fae04304|CDS|CDS	21.0	1.0	69.4	NA	NA	hypothetical protein
BVU0462|CDS|malate	72.7	3.5	68.7	NA	NA	hypothetical protein
Bova3103|CDS|CDS	10.3	0.5	68.3	NA	NA	hypothetical protein
BactD11217|CDS|CDS	6.8	0.3	67.3	NA	NA	hypothetical protein
Msm0706|CDS|ribosomal	20.3	1.0	67.2	NA	NA	hypothetical protein
RintL13367|CDS|CDS	6.7	0.3	66.1	NA	NA	hypothetical protein
Cbar0932|CDS|CDS	20.0	1.0	66.1	NA	NA	hypothetical protein
Msm0142|CDS|predicted	5.0	0.3	66.1	NA	NA	hypothetical protein
TS28Ali1674|CDS|CDS	280.0	14.0	66.1	NA	NA	hypothetical protein
TS28Clo02075|CDS|CDS	259.0	13.0	65.9	NA	NA	hypothetical protein
TS28Bac0803|CDS|CDS	9.8	0.5	65.0	NA	NA	hypothetical protein
TS28Ali1761|CDS|CDS	98.0	5.0	64.8	NA	NA	hypothetical protein
TS28Rum01946|CDS|CDS	39.0	2.0	64.5	NA	NA	hypothetical protein
TS29Bac01387|CDS|CDS	19.3	1.0	63.9	NA	NA	hypothetical protein
TS29Fae03719|CDS|CDS	9.7	0.5	63.9	NA	NA	hypothetical protein
TS28Bac8384|CDS|CDS	38.5	2.0	63.7	NA	NA	hypothetical protein
TS28Ali2037|CDS|CDS	306.0	16.0	63.2	NA	NA	hypothetical protein
TS28Ali0286|CDS|CDS	57.0	3.0	62.8	NA	NA	hypothetical protein
BVU0572|CDS|hypothetical	19.0	1.0	62.8	NA	NA	hypothetical protein
b3234|CDS|serine	19.0	1.0	62.8	NA	NA	hypothetical protein
Msm0320|CDS|predicted	4.8	0.3	62.8	NA	NA	hypothetical protein
HPAG10210|CDS|outer	19.0	1.0	62.8	NA	NA	hypothetical protein
b0436|CDS|peptidyl-prolyl	19.0	1.0	62.8	NA	NA	hypothetical protein
TS28Clo08420|CDS|CDS	94.0	5.0	62.2	NA	NA	hypothetical protein
Msm1551|CDS|glucosamine--fructose-6-phosphate	12.5	0.7	62.0	NA	NA	hypothetical protein
b3956|CDS|phosphoenolpyruvate	18.5	1.0	61.2	NA	NA	hypothetical protein
BVU3326|CDS|putative	18.5	1.0	61.2	NA	NA	hypothetical protein
TS28Fae04509|CDS|CDS	92.0	5.0	60.8	NA	NA	hypothetical protein
EUBREC1884|CDS|hypothetical	73.3	4.0	60.6	NA	NA	hypothetical protein
BVU4064|CDS|hypothetical	54.5	3.0	60.1	NA	NA	hypothetical protein
Msm1730|CDS|hypothetical	36.3	2.0	59.9	NA	NA	hypothetical protein
TS28Fae22716|CDS|CDS	163.0	9.0	59.9	NA	NA	hypothetical protein

Bova0460|CDS|CDS	18.1	1.0	59.7	NA	NA	hypothetical protein
BL1481|CDS|hypothetical	6.0	0.3	59.5	NA	NA	hypothetical protein
HPAG10035|CDS|NADH-ubiquinone	18.0	1.0	59.5	NA	NA	hypothetical protein
TS28Fae05431|CDS|CDS	90.0	5.0	59.5	NA	NA	hypothetical protein
b4317|CDS|outer	9.0	0.5	59.5	NA	NA	hypothetical protein
Msm1153|CDS|cation	4.5	0.3	59.5	NA	NA	hypothetical protein
TS29Fae09418|CDS|CDS	9.0	0.5	59.5	NA	NA	hypothetical protein
HPAG10388|CDS|Holliday	18.0	1.0	59.5	NA	NA	hypothetical protein
Dlon0992|CDS|CDS	9.0	0.5	59.5	NA	NA	hypothetical protein
Msm1336|CDS|heterodisulfide	59.2	3.3	58.7	NA	NA	hypothetical protein
PRABACTJOHN1057|CDS|CDS	53.0	3.0	58.4	NA	NA	hypothetical protein
BVU0311|CDS|putative	23.5	1.3	58.3	NA	NA	hypothetical protein
TS28Bif3719|CDS|CDS	229.0	13.0	58.3	NA	NA	hypothetical protein
BVU0325|CDS|electron	26.3	1.5	58.1	NA	NA	hypothetical protein
TS28Met1690|CDS|CDS	17.5	1.0	57.9	NA	NA	hypothetical protein
TS28Bac5675|CDS|CDS	17.5	1.0	57.9	NA	NA	hypothetical protein
Msm0515|CDS|methanol:cobalamin	25.8	1.5	57.0	NA	NA	hypothetical protein
TS28Bif3718|CDS|CDS	119.0	7.0	56.2	NA	NA	hypothetical protein
TS28Clo06517|CDS|CDS	17.0	1.0	56.2	NA	NA	hypothetical protein
TS29Fae05195|CDS|CDS	8.5	0.5	56.2	NA	NA	hypothetical protein
Bdor1541|CDS|CDS	34.0	2.0	56.2	NA	NA	hypothetical protein
Msm0933|CDS|cobalamin-5-phosphate	4.3	0.3	56.2	NA	NA	hypothetical protein
TS28Bac4438|CDS|CDS	17.0	1.0	56.2	NA	NA	hypothetical protein
Msm1562|CDS|acetyl-CoA	8.4	0.5	55.6	NA	NA	hypothetical protein
TS28Ali0449|CDS|CDS	84.0	5.0	55.6	NA	NA	hypothetical protein
BactD22816|CDS|CDS	25.0	1.5	55.1	NA	NA	hypothetical protein
TS28Clo05689|CDS|CDS	198.0	12.0	54.6	NA	NA	hypothetical protein
Pmer0292|CDS|CDS	33.0	2.0	54.6	NA	NA	hypothetical protein
BVU0477|CDS|pyridoxal	13.5	0.8	53.6	NA	NA	hypothetical protein
Msm0867|CDS|AMMECR1-related	4.1	0.3	53.6	NA	NA	hypothetical protein
BVU3983|CDS|two-component	177.0	11.0	53.2	NA	NA	hypothetical protein
TS29Bac03392|CDS|CDS	5.3	0.3	52.9	NA	NA	hypothetical protein
TS28Par0489|CDS|CDS	24.0	1.5	52.9	NA	NA	hypothetical protein
TS28Bac6789|CDS|CDS	16.0	1.0	52.9	NA	NA	hypothetical protein
HPAG10975|CDS|hypothetical	16.0	1.0	52.9	NA	NA	hypothetical protein
TS28Par0864|CDS|CDS	16.0	1.0	52.9	NA	NA	hypothetical protein
Dlon2637|CDS|CDS	32.0	2.0	52.9	NA	NA	hypothetical protein
RintL10294|CDS|CDS	16.0	1.0	52.9	NA	NA	hypothetical protein
HPAG11373|CDS|50S	16.0	1.0	52.9	NA	NA	hypothetical protein
Msm1421|CDS|hypothetical	4.0	0.3	52.9	NA	NA	hypothetical protein
Msmi741511|CDS|CDS	4.0	0.3	52.9	NA	NA	hypothetical protein
HPAG10853|CDS|flagellar	16.0	1.0	52.9	NA	NA	hypothetical protein
TS28Clo08395|CDS|CDS	32.0	2.0	52.9	NA	NA	hypothetical protein
TS28Met0841|CDS|CDS	16.0	1.0	52.9	NA	NA	hypothetical protein
b0916|CDS|conserved	8.0	0.5	52.9	NA	NA	hypothetical protein
b0830|CDS|predicted	8.0	0.5	52.9	NA	NA	hypothetical protein
Cbar2626|CDS|CDS	16.0	1.0	52.9	NA	NA	hypothetical protein
Pmer3585|CDS|CDS	16.0	1.0	52.9	NA	NA	hypothetical protein
Bdor1385|CDS|CDS	31.7	2.0	52.4	NA	NA	hypothetical protein
Msm1227|CDS|phosphoribosylamine-glycine	3.9	0.3	51.8	NA	NA	hypothetical protein
TS29Bac03345|CDS|CDS	5.2	0.3	51.5	NA	NA	hypothetical protein
TS28Clo02080|CDS|CDS	187.0	12.0	51.5	NA	NA	hypothetical protein
TS28Ali1770|CDS|CDS	77.5	5.0	51.3	NA	NA	hypothetical protein
b4242|CDS|magnesium	15.5	1.0	51.3	NA	NA	hypothetical protein
TS29Bac08221|CDS|CDS	15.5	1.0	51.3	NA	NA	hypothetical protein
TS28Ali0659|CDS|CDS	464.5	30.0	51.2	NA	NA	hypothetical protein
Msm1547|CDS|phosphoribosylaminoimidazole-succinocarboxamide	5.2	0.3	51.1	NA	NA	hypothetical protein
BVU0053|CDS|hypothetical	7.7	0.5	50.7	NA	NA	hypothetical protein
Dlon0163|CDS|CDS	23.0	1.5	50.7	NA	NA	hypothetical protein
TS28Fae22763|CDS|CDS	7.7	0.5	50.7	NA	NA	hypothetical protein
TS28Fae20009|CDS|CDS	210.5	13.8	50.3	NA	NA	hypothetical protein
TS29Fae08124|CDS|CDS	210.5	13.8	50.3	NA	NA	hypothetical protein
TS28Rum01945|CDS|CDS	196.0	13.0	49.9	NA	NA	hypothetical protein
Rbro0564|CDS|CDS	5.0	0.3	49.6	NA	NA	hypothetical protein
Vvad5483385|CDS|CDS	5.0	0.3	49.6	NA	NA	hypothetical protein
b2076|CDS|multidrug	15.0	1.0	49.6	NA	NA	hypothetical protein
TS28Ali0047|CDS|CDS	15.0	1.0	49.6	NA	NA	hypothetical protein
TS28Bac5974|CDS|CDS	7.5	0.5	49.6	NA	NA	hypothetical protein
TS28Bif1200|CDS|CDS	3.8	0.3	49.6	NA	NA	hypothetical protein
b2822|CDS|exonuclease	7.5	0.5	49.6	NA	NA	hypothetical protein
Bdor3167|CDS|CDS	15.0	1.0	49.6	NA	NA	hypothetical protein
Msm0843|CDS|2-deoxyribose-5-phosphate	3.8	0.3	49.6	NA	NA	hypothetical protein
CspM6212552|CDS|CDS	15.0	1.0	49.6	NA	NA	hypothetical protein
Msm0136|CDS|putative	3.8	0.3	49.6	NA	NA	hypothetical protein
Bova3213|CDS|CDS	14.8	1.0	49.1	NA	NA	hypothetical protein
TS28Ali2036|CDS|CDS	415.0	28.0	49.0	NA	NA	hypothetical protein
TS29Eub0956|CDS|CDS	22.2	1.5	48.9	NA	NA	hypothetical protein
BVU3197|CDS|putative	66.5	4.5	48.9	NA	NA	hypothetical protein
Msm1123|CDS|coenzyme	84.5	5.8	48.6	NA	NA	hypothetical protein
BVU0796|CDS|30S	14.7	1.0	48.5	NA	NA	hypothetical protein
Msmi740907|CDS|CDS	174.4	12.0	48.0	NA	NA	hypothetical protein
b1588|CDS|oxidoreductase	14.5	1.0	48.0	NA	NA	hypothetical protein
PRABACTJOHN3211|CDS|CDS	7.3	0.5	48.0	NA	NA	hypothetical protein
b0927|CDS|predicted	14.5	1.0	48.0	NA	NA	hypothetical protein
Msm1124|CDS|coenzyme	43.5	3.0	47.9	NA	NA	hypothetical protein
BFych464196|CDS|50S	7.2	0.5	47.8	NA	NA	hypothetical protein
BFnctc4019|CDS|50S	7.2	0.5	47.8	NA	NA	hypothetical protein
Bste2175|CDS|CDS	86.0	6.0	47.4	NA	NA	hypothetical protein
Cbar2411|CDS|CDS	43.0	3.0	47.4	NA	NA	hypothetical protein
TS29Rum17530|CDS|CDS	43.0	3.0	47.4	NA	NA	hypothetical protein
Msm1054|CDS|IMP	7.1	0.5	47.0	NA	NA	hypothetical protein

Msm0155|CDS|predicted	3.6	0.3	47.0	NA	NA	hypothetical protein
TS28Fae22762|CDS|CDS	56.5	4.0	46.7	NA	NA	hypothetical protein
Msm0309|CDS|hypothetical	4.7	0.3	46.6	NA	NA	hypothetical protein
TS28Fae19798|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
TS28Bif1935|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
TS28Clo04540|CDS|CDS	28.0	2.0	46.3	NA	NA	hypothetical protein
b0418|CDS|phosphatidylglycerophosphatase	14.0	1.0	46.3	NA	NA	hypothetical protein
BVU1364|CDS|glycoside	7.0	0.5	46.3	NA	NA	hypothetical protein
TS29Bac00469|CDS|CDS	7.0	0.5	46.3	NA	NA	hypothetical protein
Dlon1079|CDS|CDS	7.0	0.5	46.3	NA	NA	hypothetical protein
BactD10690|CDS|CDS	7.0	0.5	46.3	NA	NA	hypothetical protein
Rtor1308|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
Bste1123|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
Dfor2250|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
TS28Ali0782|CDS|CDS	28.0	2.0	46.3	NA	NA	hypothetical protein
Bova2011|CDS|CDS	3.5	0.3	46.3	NA	NA	hypothetical protein
TS28Fae20726|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
FpraM2120184|CDS|CDS	7.0	0.5	46.3	NA	NA	hypothetical protein
b4466|CDS|predicted	7.0	0.5	46.3	NA	NA	hypothetical protein
TS28Fae07168|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
TS29Rum19031|CDS|CDS	14.0	1.0	46.3	NA	NA	hypothetical protein
Msmi740351|CDS|CDS	28.0	2.0	46.3	NA	NA	hypothetical protein
BFnctc2138|CDS|carboxymuconolactone	7.0	0.5	46.3	NA	NA	hypothetical protein
Bdor2871|CDS|CDS	28.0	2.0	46.3	NA	NA	hypothetical protein
BVU0742|CDS|glycoside	7.0	0.5	46.3	NA	NA	hypothetical protein
HPAG10491|CDS|GTP-binding	14.0	1.0	46.3	NA	NA	hypothetical protein
TS28Bac0562|CDS|CDS	7.0	0.5	46.3	NA	NA	hypothetical protein
BVU3515|CDS|phosphoglycerate	3.5	0.3	46.0	NA	NA	hypothetical protein
Msm0813|CDS|hypothetical	9.3	0.7	45.9	NA	NA	hypothetical protein
Msm0918|CDS|phosphoglycerate	4.6	0.3	45.8	NA	NA	hypothetical protein
Msm0943|CDS|hypothetical	19.3	1.4	45.1	NA	NA	hypothetical protein
Msmi750833|CDS|CDS	19.3	1.4	45.1	NA	NA	hypothetical protein
CspL21862|CDS|CDS	36.3	2.7	45.0	NA	NA	hypothetical protein
Ccom0008|CDS|CDS	1.1	0.1	44.7	NA	NA	hypothetical protein
BactD12856|CDS|CDS	4.5	0.3	44.6	NA	NA	hypothetical protein
TS29Bac09576|CDS|CDS	4.5	0.3	44.6	NA	NA	hypothetical protein
b3339|CDS|protein	4.5	0.3	44.6	NA	NA	hypothetical protein
TS28Rum04583|CDS|CDS	13.5	1.0	44.6	NA	NA	hypothetical protein
TS28Ali1351|CDS|CDS	67.0	5.0	44.3	NA	NA	hypothetical protein
Msm0292|CDS|predicted	26.8	2.0	44.2	NA	NA	hypothetical protein
Msmi741640|CDS|CDS	26.8	2.0	44.2	NA	NA	hypothetical protein
Msm0560|CDS|pyruvate	15.3	1.2	43.5	NA	NA	hypothetical protein
BactD22821|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
TS28Fae03566|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
Msm0402|CDS|deoxycytidine	3.3	0.3	43.0	NA	NA	hypothetical protein
HPAG10727|CDS|rod	13.0	1.0	43.0	NA	NA	hypothetical protein
Cbol4054|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
TS29Rum17713|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
HPAG11395|CDS|type	13.0	1.0	43.0	NA	NA	hypothetical protein
Pmer1475|CDS|CDS	26.0	2.0	43.0	NA	NA	hypothetical protein
TS28Bif0202|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
Bdor3697|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
Msm1714|CDS|coenzyme	3.3	0.3	43.0	NA	NA	hypothetical protein
TS28Clo08515|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
Csci2335|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
TS28Rum07549|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
Robe3564|CDS|CDS	52.0	4.0	43.0	NA	NA	hypothetical protein
Msm0298|CDS|50S	3.3	0.3	43.0	NA	NA	hypothetical protein
Msmi741148|CDS|CDS	13.0	1.0	43.0	NA	NA	hypothetical protein
Msm1413|CDS|tungsten	5.8	0.5	42.6	NA	NA	hypothetical protein
Msm1388|CDS|thiamine	8.6	0.7	42.6	NA	NA	hypothetical protein
BVU0198|CDS|hypothetical	25.7	2.0	42.4	NA	NA	hypothetical protein
Msm1405|CDS|formate	30.9	2.4	42.2	NA	NA	hypothetical protein
Msm0999|CDS|methyl	36.2	2.8	42.2	NA	NA	hypothetical protein
Msm1620|CDS|cobalt	4.2	0.3	42.0	NA	NA	hypothetical protein
b0924|CDS|fused	6.3	0.5	41.9	NA	NA	hypothetical protein
TS28Fae17686|CDS|CDS	253.0	20.0	41.8	NA	NA	hypothetical protein
TS28Met0137|CDS|CDS	142.3	11.3	41.5	NA	NA	hypothetical protein
BVU3435|CDS|hypothetical	238.0	19.0	41.4	NA	NA	hypothetical protein
TS28Fae10756|CDS|CDS	12.5	1.0	41.3	NA	NA	hypothetical protein
TS28Fae07888|CDS|CDS	12.5	1.0	41.3	NA	NA	hypothetical protein
Dfor0627|CDS|CDS	50.0	4.0	41.3	NA	NA	hypothetical protein
TS29Fae05258|CDS|CDS	12.5	1.0	41.3	NA	NA	hypothetical protein
TS28Ali0660|CDS|CDS	854.0	69.0	40.9	NA	NA	hypothetical protein
BVU1158|CDS|putative	41.2	3.3	40.8	NA	NA	hypothetical protein
b0772|CDS|predicted	6.2	0.5	40.8	NA	NA	hypothetical protein
BVU1429|CDS|putative	37.0	3.0	40.8	NA	NA	hypothetical protein
Pmer2779|CDS|CDS	256.7	21.0	40.4	NA	NA	hypothetical protein
TS29Fae02498|CDS|CDS	36.5	3.0	40.2	NA	NA	hypothetical protein
TS28Bac3283|CDS|CDS	16.2	1.3	40.1	NA	NA	hypothetical protein
TS28Bac5722|CDS|CDS	48.5	4.0	40.1	NA	NA	hypothetical protein
BVU3347|CDS|RNA	66.7	5.5	40.1	NA	NA	hypothetical protein
Msm1550|CDS|uroporphyrin-III	4.0	0.3	39.7	NA	NA	hypothetical protein
TS28Eub8348|CDS|CDS	36.0	3.0	39.7	NA	NA	hypothetical protein
BVU0996|CDS|DNA-binding	72.0	6.0	39.7	NA	NA	hypothetical protein
b2549|CDS|conserved	12.0	1.0	39.7	NA	NA	hypothetical protein
TS29Bac03734|CDS|CDS	6.0	0.5	39.7	NA	NA	hypothetical protein
Pmer0449|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
TS28Par2430|CDS|CDS	6.0	0.5	39.7	NA	NA	hypothetical protein
TS28Fae10035|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
Pmer3017|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
TS29Met0434|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein

Cbar2386|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
TS28Rum02425|CDS|CDS	6.0	0.5	39.7	NA	NA	hypothetical protein
TS28Bac2367|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
Bcap0334|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
Robe2215|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
TS29Fae02057|CDS|CDS	6.0	0.5	39.7	NA	NA	hypothetical protein
HPAG10088|CDS|hypothetical	12.0	1.0	39.7	NA	NA	hypothetical protein
b3355|CDS|predicted	6.0	0.5	39.7	NA	NA	hypothetical protein
TS28RumUnc0868|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
TS28RumUnc1083|CDS|CDS	12.0	1.0	39.7	NA	NA	hypothetical protein
HPAG10811|CDS|thioredoxin	12.0	1.0	39.7	NA	NA	hypothetical protein
HPAG10774|CDS|outer	12.0	1.0	39.7	NA	NA	hypothetical protein
b2805|CDS|DNA-binding	12.0	1.0	39.7	NA	NA	hypothetical protein
Dlon0993|CDS|CDS	6.0	0.5	39.7	NA	NA	hypothetical protein
TS28Fae04555|CDS|CDS	264.0	22.0	39.7	NA	NA	hypothetical protein
TS29Fae02346|CDS|CDS	59.8	5.0	39.5	NA	NA	hypothetical protein
Msmi750899|CDS|CDS	20.8	1.8	39.2	NA	NA	hypothetical protein
Msmi740784|CDS|CDS	20.8	1.8	39.2	NA	NA	hypothetical protein
b3158|CDS|predicted	5.9	0.5	39.1	NA	NA	hypothetical protein
Bdor0223|CDS|CDS	35.3	3.0	38.9	NA	NA	hypothetical protein
Bxyl1100|CDS|CDS	9.8	0.8	38.8	NA	NA	hypothetical protein
Pmer3005|CDS|CDS	35.0	3.0	38.6	NA	NA	hypothetical protein
TS28Bac1144|CDS|CDS	23.3	2.0	38.6	NA	NA	hypothetical protein
TS29Fae01327|CDS|CDS	127.0	11.0	38.2	NA	NA	hypothetical protein
TS29Bac02077|CDS|CDS	11.5	1.0	38.0	NA	NA	hypothetical protein
BVU2312|CDS|hypothetical	11.5	1.0	38.0	NA	NA	hypothetical protein
TS28Fae17103|CDS|CDS	11.5	1.0	38.0	NA	NA	hypothetical protein
Bdor3903|CDS|CDS	11.5	1.0	38.0	NA	NA	hypothetical protein
Msm1359|CDS|adenine	5.8	0.5	38.0	NA	NA	hypothetical protein
TS28Clo06388|CDS|CDS	46.0	4.0	38.0	NA	NA	hypothetical protein
TS29Fae09430|CDS|CDS	11.5	1.0	38.0	NA	NA	hypothetical protein
TS28Rum04676|CDS|CDS	23.0	2.0	38.0	NA	NA	hypothetical protein
TS28Ali1509|CDS|CDS	489.0	43.0	37.6	NA	NA	hypothetical protein
Bste2342|CDS|CDS	17.0	1.5	37.5	NA	NA	hypothetical protein
Bxyl1461|CDS|CDS	5.7	0.5	37.5	NA	NA	hypothetical protein
TS29Bac03596|CDS|CDS	5.7	0.5	37.5	NA	NA	hypothetical protein
Msm0171|CDS|hypothetical	2.8	0.3	37.5	NA	NA	hypothetical protein
TS28Bac7339|CDS|CDS	5.7	0.5	37.5	NA	NA	hypothetical protein
TS28Rum09603|CDS|CDS	73.5	6.5	37.4	NA	NA	hypothetical protein
EFER3774|CDS|protein	3.7	0.3	36.9	NA	NA	hypothetical protein
Msm0501|CDS|phycocyanin	2.8	0.3	36.6	NA	NA	hypothetical protein
TS28Ali0285|CDS|CDS	94.0	8.5	36.6	NA	NA	hypothetical protein
TS28Ali1506|CDS|CDS	232.0	21.0	36.5	NA	NA	hypothetical protein
Msm0518|CDS|methylcobalamin:coenzyme	3.7	0.3	36.4	NA	NA	hypothetical protein
Msm0025|CDS|acyl-CoA	3.7	0.3	36.4	NA	NA	hypothetical protein
TS29Bac07656|CDS|CDS	3.7	0.3	36.4	NA	NA	hypothetical protein
Rtor1204|CDS|CDS	7.3	0.7	36.4	NA	NA	hypothetical protein
BVU1156|CDS|hypothetical	20.2	1.8	36.4	NA	NA	hypothetical protein
TS29Bac09800|CDS|CDS	5.5	0.5	36.4	NA	NA	hypothetical protein
TS28Fae06012|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
Dfor0045|CDS|CDS	66.0	6.0	36.4	NA	NA	hypothetical protein
Bxyl2905|CDS|CDS	5.5	0.5	36.4	NA	NA	hypothetical protein
TS29Bac01342|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
TS28Rum09199|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
Msm0262|CDS|desulfoferrodoxin	5.5	0.5	36.4	NA	NA	hypothetical protein
TS29Met1016|CDS|CDS	5.5	0.5	36.4	NA	NA	hypothetical protein
TS28Ali1870|CDS|CDS	352.0	32.0	36.4	NA	NA	hypothetical protein
HPAG11027|CDS|hypothetical	11.0	1.0	36.4	NA	NA	hypothetical protein
HPAG10265|CDS|type	11.0	1.0	36.4	NA	NA	hypothetical protein
TS28Rum09602|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
TS29Rum13936|CDS|CDS	33.0	3.0	36.4	NA	NA	hypothetical protein
TS29Bif3099|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
TS29Rum17608|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
TS29Fae08298|CDS|CDS	5.5	0.5	36.4	NA	NA	hypothetical protein
Pmer3260|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
Bcap1628|CDS|CDS	11.0	1.0	36.4	NA	NA	hypothetical protein
b2810|CDS|cysteine	5.5	0.5	36.4	NA	NA	hypothetical protein
Msm1549|CDS|phosphoribosylformylglycinamidine	2.8	0.3	36.4	NA	NA	hypothetical protein
Msm0229|CDS|hypothetical	5.5	0.5	36.4	NA	NA	hypothetical protein
HPAG11422|CDS|phosphate	11.0	1.0	36.4	NA	NA	hypothetical protein
Pmer3259|CDS|CDS	33.0	3.0	36.4	NA	NA	hypothetical protein
b4586|CDS|hypothetical	11.0	1.0	36.4	NA	NA	hypothetical protein
Msm1468|CDS|adenylosuccinate	5.5	0.5	36.4	NA	NA	hypothetical protein
Bcoproc2742|CDS|CDS	3.7	0.3	36.4	NA	NA	hypothetical protein
Msm1446|CDS|hydroxylamine	31.0	2.8	36.2	NA	NA	hypothetical protein
BactD12171|CDS|CDS	10.8	1.0	35.8	NA	NA	hypothetical protein
Msm1086|CDS|hypothetical	10.8	1.0	35.7	NA	NA	hypothetical protein
TS29Rum17529|CDS|CDS	16.0	1.5	35.3	NA	NA	hypothetical protein
Bdor0861|CDS|CDS	32.0	3.0	35.3	NA	NA	hypothetical protein
TS28Ali1871|CDS|CDS	85.0	8.0	35.1	NA	NA	hypothetical protein
TS28Clo02073|CDS|CDS	106.0	10.0	35.1	NA	NA	hypothetical protein
Bxyl4368|CDS|CDS	3.5	0.3	34.7	NA	NA	hypothetical protein
TS28Fae13859|CDS|CDS	10.5	1.0	34.7	NA	NA	hypothetical protein
TS29Fae02457|CDS|CDS	10.5	1.0	34.7	NA	NA	hypothetical protein
Msm0934|CDS|predicted	5.3	0.5	34.7	NA	NA	hypothetical protein
Bxyl1523|CDS|CDS	5.3	0.5	34.7	NA	NA	hypothetical protein
Pmer1156|CDS|CDS	26.0	2.5	34.4	NA	NA	hypothetical protein
Bste2607|CDS|CDS	10.4	1.0	34.4	NA	NA	hypothetical protein
Msm0517|CDS|methyltransferase	24.2	2.3	34.3	NA	NA	hypothetical protein
TS28Clo09195|CDS|CDS	31.0	3.0	34.2	NA	NA	hypothetical protein
BWH25667|CDS|CDS	5.2	0.5	34.2	NA	NA	hypothetical protein

Bthe3735771|CDS|CDS	5.2	0.5	34.2	NA	NA	hypothetical protein
TS28Rum09321|CDS|CDS	6.8	0.7	33.9	NA	NA	hypothetical protein
BactD13477|CDS|CDS	15.3	1.5	33.8	NA	NA	hypothetical protein
Msmi751415|CDS|CDS	2.6	0.3	33.7	NA	NA	hypothetical protein
Rbro0754|CDS|CDS	117.0	11.5	33.6	NA	NA	hypothetical protein
Rbro0865|CDS|CDS	10.2	1.0	33.6	NA	NA	hypothetical protein
Msm0056|CDS|fructose-bisphosphate	5.1	0.5	33.6	NA	NA	hypothetical protein
Pmer3255|CDS|CDS	61.0	6.0	33.6	NA	NA	hypothetical protein
BVU0052|CDS|putative	131.5	13.0	33.5	NA	NA	hypothetical protein
b3988|CDS|RNA	18.5	1.8	33.4	NA	NA	hypothetical protein
Bste1494|CDS|CDS	121.0	12.0	33.3	NA	NA	hypothetical protein
TS28Fae15213|CDS|CDS	20.1	2.0	33.2	NA	NA	hypothetical protein
stu1963|CDS|anaerobic	6.7	0.7	33.1	NA	NA	hypothetical protein
str1963|CDS|anaerobic	6.7	0.7	33.1	NA	NA	hypothetical protein
Rbro0220|CDS|CDS	3.3	0.3	33.1	NA	NA	hypothetical protein
TS29Eub1098|CDS|CDS	3.3	0.3	33.1	NA	NA	hypothetical protein
TS29Eub2139|CDS|CDS	3.3	0.3	33.1	NA	NA	hypothetical protein
TS28Fae20389|CDS|CDS	15.0	1.5	33.1	NA	NA	hypothetical protein
TS28Bac5962|CDS|CDS	3.3	0.3	33.1	NA	NA	hypothetical protein
TS28Par0865|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
HPAG10139|CDS|L-lactate	10.0	1.0	33.1	NA	NA	hypothetical protein
TS29Rum11259|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS29Dor1234|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
BVU1470|CDS|hypothetical	5.0	0.5	33.1	NA	NA	hypothetical protein
Msm0355|CDS|predicted	2.5	0.3	33.1	NA	NA	hypothetical protein
BVU1770|CDS|hypothetical	5.0	0.5	33.1	NA	NA	hypothetical protein
TS28Fae20867|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS29Bac00100|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
BVU2291|CDS|hypothetical	5.0	0.5	33.1	NA	NA	hypothetical protein
TS28Fae15810|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
Bint0432|CDS|CDS	2.5	0.3	33.1	NA	NA	hypothetical protein
M23Apeg793|CDS|Transcription	10.0	1.0	33.1	NA	NA	hypothetical protein
Msm0358|CDS|hypothetical	5.0	0.5	33.1	NA	NA	hypothetical protein
TS28Ali0215|CDS|CDS	20.0	2.0	33.1	NA	NA	hypothetical protein
TS28Ali2078|CDS|CDS	20.0	2.0	33.1	NA	NA	hypothetical protein
Pmer3266|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS28Ali1772|CDS|CDS	5.0	0.5	33.1	NA	NA	hypothetical protein
Cbar1717|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS29Fae09396|CDS|CDS	5.0	0.5	33.1	NA	NA	hypothetical protein
Bxyl2632|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
Bste2720|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS29Fae10254|CDS|CDS	5.0	0.5	33.1	NA	NA	hypothetical protein
Buni1024|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS28Bac5553|CDS|CDS	20.0	2.0	33.1	NA	NA	hypothetical protein
Bste0988|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
Bste1147|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
str0993|CDS|hypothetical	10.0	1.0	33.1	NA	NA	hypothetical protein
TS28Clo09662|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
Even1132|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
Cnex1122|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
TS28Par2128|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
BactD22540|CDS|CDS	5.0	0.5	33.1	NA	NA	hypothetical protein
Acol1276|CDS|CDS	10.0	1.0	33.1	NA	NA	hypothetical protein
HPAG10405|CDS|hypothetical	10.0	1.0	33.1	NA	NA	hypothetical protein
TS29Rum10573|CDS|CDS	5.0	0.5	33.1	NA	NA	hypothetical protein
EUBREC0301|CDS|hypothetical	5.0	0.5	33.1	NA	NA	hypothetical protein
Bdor2757|CDS|CDS	19.8	2.0	32.8	NA	NA	hypothetical protein
TS28Bac5716|CDS|CDS	19.8	2.0	32.8	NA	NA	hypothetical protein
BVU2597|CDS|glycosyltransferase	16.5	1.7	32.7	NA	NA	hypothetical protein
TS28Clo10782|CDS|CDS	108.5	11.0	32.6	NA	NA	hypothetical protein
Bste2866|CDS|CDS	49.0	5.0	32.4	NA	NA	hypothetical protein
BVU2243|CDS|hypothetical	8.2	0.8	32.4	NA	NA	hypothetical protein
Msm0002|CDS|integrase-recombinase	3.3	0.3	32.2	NA	NA	hypothetical protein
TS28Fae04554|CDS|CDS	68.0	7.0	32.1	NA	NA	hypothetical protein
Msm1332|CDS|replication	4.9	0.5	32.1	NA	NA	hypothetical protein
Bdor3171|CDS|CDS	33.8	3.5	32.0	NA	NA	hypothetical protein
TS28Ali2060|CDS|CDS	58.0	6.0	32.0	NA	NA	hypothetical protein
TS29Bac08946|CDS|CDS	4.8	0.5	32.0	NA	NA	hypothetical protein
b2616|CDS|recombination	4.8	0.5	32.0	NA	NA	hypothetical protein
BVU2271|CDS|outer	226.8	23.5	31.9	NA	NA	hypothetical protein
Bste1493|CDS|CDS	77.0	8.0	31.8	NA	NA	hypothetical protein
TS28Ali1019|CDS|CDS	67.0	7.0	31.7	NA	NA	hypothetical protein
TS28Fae12733|CDS|CDS	181.0	19.0	31.5	NA	NA	hypothetical protein
BVU2754|CDS|ferritin	100.0	10.5	31.5	NA	NA	hypothetical protein
str0255|CDS|glutamate	3.2	0.3	31.4	NA	NA	hypothetical protein
STER0302|CDS|glutamate	3.2	0.3	31.4	NA	NA	hypothetical protein
Bxyl4141|CDS|CDS	3.2	0.3	31.4	NA	NA	hypothetical protein
TS28Fae01288|CDS|CDS	14.3	1.5	31.4	NA	NA	hypothetical protein
Pmer2476|CDS|CDS	19.0	2.0	31.4	NA	NA	hypothetical protein
Bova1217|CDS|CDS	9.5	1.0	31.4	NA	NA	hypothetical protein
Bxyl0576|CDS|CDS	4.8	0.5	31.4	NA	NA	hypothetical protein
TS28Fae04361|CDS|CDS	38.0	4.0	31.4	NA	NA	hypothetical protein
TS28Clo03262|CDS|CDS	19.0	2.0	31.4	NA	NA	hypothetical protein
Buni0158|CDS|CDS	9.5	1.0	31.4	NA	NA	hypothetical protein
TS28Par0848|CDS|CDS	9.5	1.0	31.4	NA	NA	hypothetical protein
Bdor1158|CDS|CDS	19.0	2.0	31.4	NA	NA	hypothetical protein
TS29Fae06102|CDS|CDS	9.5	1.0	31.4	NA	NA	hypothetical protein
TS28Ali0287|CDS|CDS	33.0	3.5	31.2	NA	NA	hypothetical protein
Msm0923|CDS|multimeric	4.7	0.5	31.1	NA	NA	hypothetical protein
Bdor1760|CDS|CDS	40.7	4.3	31.0	NA	NA	hypothetical protein
TS29Bac00037|CDS|CDS	93.5	10.0	30.9	NA	NA	hypothetical protein
TS28Clo10781|CDS|CDS	93.5	10.0	30.9	NA	NA	hypothetical protein

TS28Fae16376|CDS|CDS	28.0	3.0	30.9	NA	NA	hypothetical protein
b3800|CDS|predicted	9.3	1.0	30.9	NA	NA	hypothetical protein
Bdor2589|CDS|CDS	9.3	1.0	30.9	NA	NA	hypothetical protein
TS28Clo02049|CDS|CDS	121.0	13.0	30.8	NA	NA	hypothetical protein
Pmer1555|CDS|CDS	46.5	5.0	30.8	NA	NA	hypothetical protein
Bste0376|CDS|CDS	55.3	6.0	30.5	NA	NA	hypothetical protein
Bste2248|CDS|CDS	55.3	6.0	30.5	NA	NA	hypothetical protein
TS28Bac3636|CDS|CDS	76.7	8.3	30.4	NA	NA	hypothetical protein
TS28Met1709|CDS|CDS	4.6	0.5	30.3	NA	NA	hypothetical protein
BVU3775|CDS|hypothetical	9.2	1.0	30.3	NA	NA	hypothetical protein
Msm0786|CDS|transglutaminase-like	13.8	1.5	30.3	NA	NA	hypothetical protein
Msm0626|CDS|cell	24.3	2.7	30.2	NA	NA	hypothetical protein
BVU3160|CDS|haloacid	18.2	2.0	30.0	NA	NA	hypothetical protein
TS28Met0541|CDS|CDS	221.9	24.5	29.9	NA	NA	hypothetical protein
BVU2897|CDS|glycosyltransferase	36.2	4.0	29.9	NA	NA	hypothetical protein
BVU2579|CDS|hypothetical	126.3	14.0	29.8	NA	NA	hypothetical protein
TS29Bac11652|CDS|CDS	3.0	0.3	29.8	NA	NA	hypothetical protein
Msm1151|CDS|adenylosuccinate	3.0	0.3	29.8	NA	NA	hypothetical protein
Bxyl3265|CDS|CDS	3.0	0.3	29.8	NA	NA	hypothetical protein
FpraM2122295|CDS|CDS	3.0	0.3	29.8	NA	NA	hypothetical protein
Msm1636|CDS|ProFAR	3.0	0.3	29.8	NA	NA	hypothetical protein
Msmi750380|CDS|CDS	3.0	0.3	29.8	NA	NA	hypothetical protein
HPAG11146|CDS|translation	9.0	1.0	29.8	NA	NA	hypothetical protein
TS28RumUnc1537|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Msm1492|CDS|hydrogenase	2.3	0.3	29.8	NA	NA	hypothetical protein
b1189|CDS|D-amino	9.0	1.0	29.8	NA	NA	hypothetical protein
TS29Fae00114|CDS|CDS	18.0	2.0	29.8	NA	NA	hypothetical protein
Msm0121|CDS|DNA	2.3	0.3	29.8	NA	NA	hypothetical protein
TS28Par0285|CDS|CDS	18.0	2.0	29.8	NA	NA	hypothetical protein
TS29Rum17013|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
b2546|CDS|predicted	4.5	0.5	29.8	NA	NA	hypothetical protein
Cbar0312|CDS|CDS	18.0	2.0	29.8	NA	NA	hypothetical protein
TS28Bac7187|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
Bste1085|CDS|CDS	18.0	2.0	29.8	NA	NA	hypothetical protein
TS29Fae06926|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
L169301|CDS|hypothetical	9.0	1.0	29.8	NA	NA	hypothetical protein
BLD1312|CDS|Heat	2.3	0.3	29.8	NA	NA	hypothetical protein
TS29Ali429|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
TS28Fae06148|CDS|CDS	27.0	3.0	29.8	NA	NA	hypothetical protein
Dfor1495|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
TS28Fae16883|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
TS28Bac7392|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Bova3279|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
TS28Par2038|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
TS29Fae05222|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
Bthe3730719|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
Bdor3226|CDS|CDS	72.0	8.0	29.8	NA	NA	hypothetical protein
Aput2127|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
Msm0604|CDS|predicted	2.3	0.3	29.8	NA	NA	hypothetical protein
Msm1279|CDS|predicted	2.3	0.3	29.8	NA	NA	hypothetical protein
TS29Rum04907|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Bste0034|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Aput1553|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
TS28Col1196|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Cbar2442|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Rgna2802|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Buni0105|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
TS28Ali0822|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
Cbar0109|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
RintL12727|CDS|CDS	2.3	0.3	29.8	NA	NA	hypothetical protein
EUBREC2855|CDS|hypothetical	81.0	9.0	29.8	NA	NA	hypothetical protein
TS28Eub6029|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Begg2395|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
Robe2671|CDS|CDS	2.3	0.3	29.8	NA	NA	hypothetical protein
BactD21542|CDS|CDS	4.5	0.5	29.8	NA	NA	hypothetical protein
b0801|CDS|predicted	9.0	1.0	29.8	NA	NA	hypothetical protein
Dfor3105|CDS|CDS	2.3	0.3	29.8	NA	NA	hypothetical protein
Begg2484|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
b2866|CDS|xanthine	4.5	0.5	29.8	NA	NA	hypothetical protein
BVU3077|CDS|putative	9.0	1.0	29.8	NA	NA	hypothetical protein
Rgna3025|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
BVU3001|CDS|ATP	9.0	1.0	29.8	NA	NA	hypothetical protein
TS28Fae01911|CDS|CDS	9.0	1.0	29.8	NA	NA	hypothetical protein
HPAG10864|CDS|hypothetical	9.0	1.0	29.8	NA	NA	hypothetical protein
Msm0090|CDS|hypothetical	6.0	0.7	29.8	NA	NA	hypothetical protein
TS28Fae14005|CDS|CDS	53.8	6.0	29.7	NA	NA	hypothetical protein
BactD22268|CDS|CDS	4.5	0.5	29.5	NA	NA	hypothetical protein
BVU0345|CDS|chaperonin	102.3	11.5	29.4	NA	NA	hypothetical protein
Bdor0313|CDS|CDS	26.7	3.0	29.4	NA	NA	hypothetical protein
TS29Bac01388|CDS|CDS	8.8	1.0	29.2	NA	NA	hypothetical protein
TS28Clo10288|CDS|CDS	97.0	11.0	29.2	NA	NA	hypothetical protein
Msm1409|CDS|tungsten	9.1	1.0	29.0	NA	NA	hypothetical protein
BVU0789|CDS|50S	43.7	5.0	28.9	NA	NA	hypothetical protein
BVU2519|CDS|hypothetical	87.3	10.0	28.9	NA	NA	hypothetical protein
TS28Rum00783|CDS|CDS	61.0	7.0	28.8	NA	NA	hypothetical protein
TS28Ali0679|CDS|CDS	165.5	19.0	28.8	NA	NA	hypothetical protein
Msm1411|CDS|tungsten	8.7	1.0	28.8	NA	NA	hypothetical protein
TS29Bac01389|CDS|CDS	13.0	1.5	28.7	NA	NA	hypothetical protein
TS28Fae01512|CDS|CDS	26.0	3.0	28.7	NA	NA	hypothetical protein
Msm0653|CDS|histidinol-phosphate	6.5	0.8	28.7	NA	NA	hypothetical protein
Msm0154|CDS|homoserine	8.7	1.0	28.7	NA	NA	hypothetical protein
Msm1013|CDS|tetrahydromethanopterin	13.7	1.6	28.5	NA	NA	hypothetical protein

BT1957|CDS|hypothetical	0.6	0.1	28.5	NA	NA	hypothetical protein
Bsp1162037|CDS|CDS	0.6	0.1	28.5	NA	NA	hypothetical protein
Msm1014|CDS|tetrahydromethanopterin	25.8	3.0	28.5	NA	NA	hypothetical protein
Bste2174|CDS|CDS	86.0	10.0	28.4	NA	NA	hypothetical protein
TS29Fae04046|CDS|CDS	43.0	5.0	28.4	NA	NA	hypothetical protein
Msm1702|CDS|UDP-glucose	24.3	2.8	28.3	NA	NA	hypothetical protein
TS29Fae01563|CDS|CDS	34.0	4.0	28.1	NA	NA	hypothetical protein
TS28Fae20365|CDS|CDS	17.0	2.0	28.1	NA	NA	hypothetical protein
Msm1024|CDS|pheromone	4.3	0.5	28.1	NA	NA	hypothetical protein
BVU0581|CDS|possible	8.5	1.0	28.1	NA	NA	hypothetical protein
HPAG10230|CDS|outer	8.5	1.0	28.1	NA	NA	hypothetical protein
TS28Bac5992|CDS|CDS	34.0	4.0	28.1	NA	NA	hypothetical protein
TS28RumUnc0539|CDS|CDS	17.0	2.0	28.1	NA	NA	hypothetical protein
Rlac0021|CDS|CDS	8.5	1.0	28.1	NA	NA	hypothetical protein
b3691|CDS|D-galactonate	8.5	1.0	28.1	NA	NA	hypothetical protein
TS28Par1032|CDS|CDS	8.5	1.0	28.1	NA	NA	hypothetical protein
TS29Fae01621|CDS|CDS	25.3	3.0	27.9	NA	NA	hypothetical protein
TS28Clo09678|CDS|CDS	59.0	7.0	27.9	NA	NA	hypothetical protein
Msm0031|CDS|adhesin-like	8.4	1.0	27.8	NA	NA	hypothetical protein
Bova3911|CDS|CDS	8.4	1.0	27.8	NA	NA	hypothetical protein
TS29Fae09675|CDS|CDS	67.0	8.0	27.7	NA	NA	hypothetical protein
TS29Rum15337|CDS|CDS	8.3	1.0	27.6	NA	NA	hypothetical protein
TS29Eub1245|CDS|CDS	8.3	1.0	27.6	NA	NA	hypothetical protein
TS29Met0211|CDS|CDS	5.4	0.7	27.5	NA	NA	hypothetical protein
BVU1027|CDS|hypothetical	54.0	6.5	27.5	NA	NA	hypothetical protein
TS28Ali0623|CDS|CDS	547.0	66.0	27.4	NA	NA	hypothetical protein
TS29Rum11874|CDS|CDS	58.0	7.0	27.4	NA	NA	hypothetical protein
Msm0457|CDS|D-3-phosphoglycerate	13.1	1.6	27.4	NA	NA	hypothetical protein
TS28Rum10231|CDS|CDS	33.0	4.0	27.3	NA	NA	hypothetical protein
TS28Ali1826|CDS|CDS	33.0	4.0	27.3	NA	NA	hypothetical protein
TS28Clo06588|CDS|CDS	33.0	4.0	27.3	NA	NA	hypothetical protein
Buni2356|CDS|CDS	24.7	3.0	27.2	NA	NA	hypothetical protein
Msm1458|CDS|hypothetical	2.1	0.3	27.1	NA	NA	hypothetical protein
Msmi741100|CDS|CDS	2.1	0.3	27.1	NA	NA	hypothetical protein
Msm1371|CDS|diaminopimelate	12.3	1.5	27.0	NA	NA	hypothetical protein
Pmer0725|CDS|CDS	49.0	6.0	27.0	NA	NA	hypothetical protein
TS28Par1198|CDS|CDS	24.5	3.0	27.0	NA	NA	hypothetical protein
Msmi751581|CDS|CDS	10.1	1.3	26.8	NA	NA	hypothetical protein
TS28Clo07264|CDS|CDS	113.0	14.0	26.7	NA	NA	hypothetical protein
BVU2338|CDS|RNA	20.2	2.5	26.7	NA	NA	hypothetical protein
BVU3343|CDS|outer	80.7	10.0	26.7	NA	NA	hypothetical protein
TS28Bac4595|CDS|CDS	2.7	0.3	26.5	NA	NA	hypothetical protein
Begg0845|CDS|CDS	0.9	0.1	26.5	NA	NA	hypothetical protein
Bxyl1212|CDS|CDS	0.9	0.1	26.5	NA	NA	hypothetical protein
Bthe3733903|CDS|CDS	0.9	0.1	26.5	NA	NA	hypothetical protein
Bfin1132|CDS|CDS	0.9	0.1	26.5	NA	NA	hypothetical protein
Bthe7332533|CDS|CDS	0.9	0.1	26.5	NA	NA	hypothetical protein
TS28Col1450|CDS|CDS	24.0	3.0	26.5	NA	NA	hypothetical protein
TS29Fae00286|CDS|CDS	40.0	5.0	26.5	NA	NA	hypothetical protein
TS29Eub1927|CDS|CDS	24.0	3.0	26.5	NA	NA	hypothetical protein
TS28Ali0678|CDS|CDS	40.0	5.0	26.5	NA	NA	hypothetical protein
Svar0834|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS28Fae18727|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS28Rum01520|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
Pmer3039|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
HPAG10684|CDS|hypothetical	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Bac06930|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Fae06071|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Rum02385|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
TS28Fae09495|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
CspM6210397|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Fae03224|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
Rbro0388|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Fae08415|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
Bste1459|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
b2700|CDS|conserved	8.0	1.0	26.5	NA	NA	hypothetical protein
Bple3171|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Fae01210|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Clo02036|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
b0037|CDS|predicted	8.0	1.0	26.5	NA	NA	hypothetical protein
Bova2456|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS28Rum04558|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Rum05387|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
BL1131|CDS|NADPH:quinone	2.0	0.3	26.5	NA	NA	hypothetical protein
TS28Bac2370|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
Cbar1309|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Col1353|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Aput0526|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
HPAG10287|CDS|hypothetical	8.0	1.0	26.5	NA	NA	hypothetical protein
b3562|CDS|conserved	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Rum18975|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
b2292|CDS|predicted	8.0	1.0	26.5	NA	NA	hypothetical protein
HPAG11445|CDS|DNA	8.0	1.0	26.5	NA	NA	hypothetical protein
Begg0450|CDS|CDS	2.0	0.3	26.5	NA	NA	hypothetical protein
TS28Clo03748|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
HPAG10640|CDS|protective	8.0	1.0	26.5	NA	NA	hypothetical protein
Bxyl2730|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Bdor2808|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
Pmer1162|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
TS28Ali2301|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS28Rum06803|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Fae02335|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein

Pmer1293|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
b2407|CDS|purine	8.0	1.0	26.5	NA	NA	hypothetical protein
TS28Par0600|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
BVU2208|CDS|hypothetical	4.0	0.5	26.5	NA	NA	hypothetical protein
TS29Bac05182|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Bac6677|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Aput0771|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Fae05270|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Aput2026|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Bac11768|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
TS29Rum13953|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
Msm0702|CDS|prefoldin	4.0	0.5	26.5	NA	NA	hypothetical protein
Pmer0379|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Eub3035|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
Cbol4849|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
Aput0909|CDS|CDS	16.0	2.0	26.5	NA	NA	hypothetical protein
Pmer1442|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
TS28Rum07351|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Msmi740568|CDS|CDS	2.0	0.3	26.5	NA	NA	hypothetical protein
EUBREC2216|CDS|ADP-glucose	16.0	2.0	26.5	NA	NA	hypothetical protein
TS29Fae02730|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Rgna1217|CDS|CDS	8.0	1.0	26.5	NA	NA	hypothetical protein
HPAG10893|CDS|rep	8.0	1.0	26.5	NA	NA	hypothetical protein
Msmi740338|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
HPAG10034|CDS|hypothetical	16.0	2.0	26.5	NA	NA	hypothetical protein
HPAG11274|CDS|cation	16.0	2.0	26.5	NA	NA	hypothetical protein
Rtor2060|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
Msm0580|CDS|putative	2.0	0.3	26.5	NA	NA	hypothetical protein
Dlon2160|CDS|CDS	4.0	0.5	26.5	NA	NA	hypothetical protein
BactD12190|CDS|CDS	2.7	0.3	26.5	NA	NA	hypothetical protein
TS29Bac08957|CDS|CDS	2.7	0.3	26.5	NA	NA	hypothetical protein
Bxyl4132|CDS|CDS	2.7	0.3	26.5	NA	NA	hypothetical protein
BVU1286|CDS|putative	712.2	90.0	26.2	NA	NA	hypothetical protein
Bova3104|CDS|CDS	11.8	1.5	26.1	NA	NA	hypothetical protein
EUBREC0542|CDS|putative	31.5	4.0	26.0	NA	NA	hypothetical protein
b3003|CDS|predicted	7.8	1.0	25.9	NA	NA	hypothetical protein
Msmi750687|CDS|CDS	6.5	0.8	25.8	NA	NA	hypothetical protein
TS28Clo03129|CDS|CDS	39.0	5.0	25.8	NA	NA	hypothetical protein
TS28Ali0408|CDS|CDS	156.0	20.0	25.8	NA	NA	hypothetical protein
BVU1050|CDS|3-oxoacyl-[acyl-carrier-protein]	23.3	3.0	25.7	NA	NA	hypothetical protein
TS28Clo02770|CDS|CDS	62.0	8.0	25.6	NA	NA	hypothetical protein
TS29Fae01743|CDS|CDS	38.8	5.0	25.6	NA	NA	hypothetical protein
BVU0800|CDS|50S	84.9	11.0	25.5	NA	NA	hypothetical protein
TS28Bac1004|CDS|CDS	39.7	5.2	25.4	NA	NA	hypothetical protein
Msm1403|CDS|formate/nitrite	12.8	1.7	25.4	NA	NA	hypothetical protein
TS28Fae18233|CDS|CDS	46.0	6.0	25.4	NA	NA	hypothetical protein
Msm1418|CDS|glutamine	3.5	0.5	25.4	NA	NA	hypothetical protein
Rtor0085|CDS|CDS	7.7	1.0	25.4	NA	NA	hypothetical protein
b1812|CDS|aminodeoxychorismate	3.8	0.5	25.4	NA	NA	hypothetical protein
Msm0622|CDS|50S	6.0	0.8	25.3	NA	NA	hypothetical protein
Msm0866|CDS|Zn	7.7	1.0	25.3	NA	NA	hypothetical protein
Msm0147|CDS|CTP	8.9	1.2	25.3	NA	NA	hypothetical protein
TS28Clo02091|CDS|CDS	61.0	8.0	25.2	NA	NA	hypothetical protein
BactD20603|CDS|CDS	3.8	0.5	25.1	NA	NA	hypothetical protein
Bova1802|CDS|CDS	3.8	0.5	25.1	NA	NA	hypothetical protein
Bdor0236|CDS|CDS	37.8	5.0	25.0	NA	NA	hypothetical protein
Msm0993|CDS|putative	5.0	0.7	24.8	NA	NA	hypothetical protein
BVU4060|CDS|putative	22.5	3.0	24.8	NA	NA	hypothetical protein
BT4738|CDS|formate	2.5	0.3	24.8	NA	NA	hypothetical protein
Msm1585|CDS|adhesin-like	60.0	8.0	24.8	NA	NA	hypothetical protein
Bste2850|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
TS28Clo02362|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
Cbar2100|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
Bint4554|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
b4334|CDS|predicted	7.5	1.0	24.8	NA	NA	hypothetical protein
TS29Bac11809|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
TS28Ali0526|CDS|CDS	7.5	1.0	24.8	NA	NA	hypothetical protein
Bova3945|CDS|CDS	7.5	1.0	24.8	NA	NA	hypothetical protein
Bste2931|CDS|CDS	7.5	1.0	24.8	NA	NA	hypothetical protein
b3589|CDS|predicted	7.5	1.0	24.8	NA	NA	hypothetical protein
b3144|CDS|predicted	7.5	1.0	24.8	NA	NA	hypothetical protein
Bste0125|CDS|CDS	7.5	1.0	24.8	NA	NA	hypothetical protein
BactD24006|CDS|CDS	7.5	1.0	24.8	NA	NA	hypothetical protein
TS29Rum09418|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
TS28Ali2080|CDS|CDS	15.0	2.0	24.8	NA	NA	hypothetical protein
Msm1472|CDS|hypothetical	6.8	0.9	24.7	NA	NA	hypothetical protein
TS28Ali2090|CDS|CDS	148.7	20.0	24.6	NA	NA	hypothetical protein
TS28Fae17636|CDS|CDS	37.0	5.0	24.5	NA	NA	hypothetical protein
TS28Ali0070|CDS|CDS	74.0	10.0	24.5	NA	NA	hypothetical protein
Bste0575|CDS|CDS	3.7	0.5	24.3	NA	NA	hypothetical protein
FpraM2121052|CDS|CDS	7.3	1.0	24.3	NA	NA	hypothetical protein
Msm0654|CDS|carbonic	5.5	0.8	24.3	NA	NA	hypothetical protein
TS28Clo02775|CDS|CDS	22.0	3.0	24.3	NA	NA	hypothetical protein
BVU3859|CDS|hypothetical	40.3	5.5	24.3	NA	NA	hypothetical protein
str1542|CDS|cytoplasmic	3.7	0.5	24.251	NA	NA	hypothetical protein
Msm0932|CDS|hypothetical	3.7	0.5	24.251	NA	NA	hypothetical protein
Bxyl1657|CDS|CDS	3.7	0.5	24.251	NA	NA	hypothetical protein
stu1542|CDS|cytoplasmic	3.7	0.5	24.251	NA	NA	hypothetical protein
BVU3269|CDS|two-component	14.5	2.0	23.975	NA	NA	hypothetical protein
Bdor3704|CDS|CDS	14.5	2.0	23.975	NA	NA	hypothetical protein
Bdor3607|CDS|CDS	58.0	8.0	23.975	NA	NA	hypothetical protein
Bdor4064|CDS|CDS	29.0	4.0	23.975	NA	NA	hypothetical protein

TS29Fae01016|CDS|CDS	7.3	1.0	23.975	NA	NA	hypothetical protein
Bxyl2080|CDS|CDS	1.5	0.2	23.975	NA	NA	hypothetical protein
Msm0954|CDS|predicted	14.5	2.0	23.975	NA	NA	hypothetical protein
Msm0439|CDS|vacuolar-type	2.9	0.4	23.975	NA	NA	hypothetical protein
BactD11293|CDS|CDS	1.8	0.3	23.936	NA	NA	hypothetical protein
BVU3610|CDS|hypothetical	10.8	1.5	23.883	NA	NA	hypothetical protein
BactD12055|CDS|CDS	2.4	0.3	23.810	NA	NA	hypothetical protein
Bxyl0959|CDS|CDS	2.4	0.3	23.810	NA	NA	hypothetical protein
Msm0796|CDS|heterodisulfide	23.3	3.3	23.742	NA	NA	hypothetical protein
b3407|CDS|predicted	7.2	1.0	23.700	NA	NA	hypothetical protein
BVU0885|CDS|glycosyltransferase	7.2	1.0	23.700	NA	NA	hypothetical protein
TS28Bac3843|CDS|CDS	7.2	1.0	23.700	NA	NA	hypothetical protein
Msmi741131|CDS|CDS	4.8	0.7	23.562	NA	NA	hypothetical protein
Msmi750546|CDS|CDS	4.8	0.7	23.562	NA	NA	hypothetical protein
TS28Met1065|CDS|CDS	4.8	0.7	23.562	NA	NA	hypothetical protein
TS28Ali1360|CDS|CDS	121.0	17.0	23.538	NA	NA	hypothetical protein
TS28Fae12734|CDS|CDS	78.0	11.0	23.449	NA	NA	hypothetical protein
TS28Clo02774|CDS|CDS	248.0	35.0	23.432	NA	NA	hypothetical protein
TS28Ali1252|CDS|CDS	197.5	28.0	23.326	NA	NA	hypothetical protein
BactD22971|CDS|CDS	2.3	0.3	23.149	NA	NA	hypothetical protein
BT4002|CDS|ATPase,	2.3	0.3	23.149	NA	NA	hypothetical protein
Bsp1162318|CDS|CDS	2.3	0.3	23.149	NA	NA	hypothetical protein
TS29Rum12973|CDS|CDS	2.3	0.3	23.149	NA	NA	hypothetical protein
Msm1119|CDS|hypothetical	4.7	0.7	23.149	NA	NA	hypothetical protein
EFER3766|CDS|RNA	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum05538|CDS|CDS	4.7	0.7	23.149	NA	NA	hypothetical protein
BVU3198|CDS|putative	52.5	7.5	23.149	NA	NA	hypothetical protein
Cbar0165|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
Bste2230|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
PRABACTJOHN2647|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Clo09437|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum11840|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Bova0453|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum20539|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
BactD10240|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
TS28RumUnc1061|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Col0207|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
TS28Bac0696|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
TS28Bac8374|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
TS28Rum15903|CDS|CDS	42.0	6.0	23.149	NA	NA	hypothetical protein
TS28Fae06925|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
Cbar1166|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Rum10230|CDS|CDS	35.0	5.0	23.149	NA	NA	hypothetical protein
EUBREC0767|CDS|hypothetical	3.5	0.5	23.149	NA	NA	hypothetical protein
Bcro0095|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Robe2615|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Pmer0241|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
Dfor2402|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
HPAG10375|CDS|copper-transporting	7.0	1.0	23.149	NA	NA	hypothetical protein
Dfor2465|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Fae08893|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Bac01575|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Fae07113|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
TS28Clo08589|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Ali0717|CDS|CDS	28.0	4.0	23.149	NA	NA	hypothetical protein
Msm0852|CDS|predicted	1.8	0.3	23.149	NA	NA	hypothetical protein
TS28Fae14572|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Ccom1704|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Bdor3591|CDS|CDS	35.0	5.0	23.149	NA	NA	hypothetical protein
HPAG10559|CDS|hypothetical	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum00252|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Bac11216|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Bfin1178|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum14225|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Bac6640|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
BactD22860|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28RumUnc1811|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Cbar1454|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Csym2463|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Bac07953|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
HPAG10031|CDS|ATP-dependent	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Fae09784|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
PRABACTJOHN2234|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Bac05948|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum10339|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum12282|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Bac0258|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
TS28Rum16007|CDS|CDS	35.0	5.0	23.149	NA	NA	hypothetical protein
TS28Fae08102|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
Even1363|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Bova1220|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Rum12904|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Rum11984|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Ccom1113|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Pmer2749|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
TS28Fae03909|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Bste1850|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
FpraM2122218|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Fae22172|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Bac09117|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Rum11154|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Bthe3730729|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein

TS28Clo08495|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Cbar2055|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
EUBREC2729|CDS|hypothetical	3.5	0.5	23.149	NA	NA	hypothetical protein
TS29RumUnc0315|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Fae01396|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Dfor0385|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Eub1926|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Rum15313|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
HPAG10764|CDS|bifunctional	7.0	1.0	23.149	NA	NA	hypothetical protein
Msmi741221|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Fae06161|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
HPAG11409|CDS|putative	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Ali0882|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Dfor1021|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS29Bac09424|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
Even1954|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
TS28Par1461|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Robe1069|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
TS28RumUnc0277|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
HPAG11183|CDS|alanyl-tRNA	7.0	1.0	23.149	NA	NA	hypothetical protein
Bthe3732923|CDS|CDS	7.0	1.0	23.149	NA	NA	hypothetical protein
Msm1056|CDS|6-pyruvoyl-tetrahydropterin	3.5	0.5	23.149	NA	NA	hypothetical protein
Bste1799|CDS|CDS	3.5	0.5	23.149	NA	NA	hypothetical protein
TS28Rum05265|CDS|CDS	14.0	2.0	23.149	NA	NA	hypothetical protein
b0523|CDS|N5-carboxyaminoimidazole	7.0	1.0	23.149	NA	NA	hypothetical protein
BactD11392|CDS|CDS	2.3	0.3	23.149	NA	NA	hypothetical protein
TS29Bac00797|CDS|CDS	2.3	0.3	23.149	NA	NA	hypothetical protein
BVU2570|CDS|hypothetical	38.3	5.5	23.048	NA	NA	hypothetical protein
TS28Rum14625|CDS|CDS	20.8	3.0	22.965	NA	NA	hypothetical protein
TS28Fae21577|CDS|CDS	55.5	8.0	22.942	NA	NA	hypothetical protein
Msm1202|CDS|branched-chain-amino-acid	4.0	0.6	22.865	NA	NA	hypothetical protein
BVU0512|CDS|two-component	10.3	1.5	22.781	NA	NA	hypothetical protein
TS28Fae12331|CDS|CDS	55.0	8.0	22.735	NA	NA	hypothetical protein
Msm1735|CDS|adhesin-like	8.0	1.2	22.676	NA	NA	hypothetical protein
BLD1770|CDS|Putative	2.3	0.3	22.322	NA	NA	hypothetical protein
Bova2144|CDS|CDS	2.3	0.3	22.322	NA	NA	hypothetical protein
BactD14049|CDS|CDS	2.3	0.3	22.322	NA	NA	hypothetical protein
TS28Ali0084|CDS|CDS	54.0	8.0	22.322	NA	NA	hypothetical protein
TS28Rum10451|CDS|CDS	13.5	2.0	22.322	NA	NA	hypothetical protein
TS28Bac0563|CDS|CDS	13.5	2.0	22.322	NA	NA	hypothetical protein
BVU2965|CDS|hypothetical	13.5	2.0	22.322	NA	NA	hypothetical protein
TS29Fae09130|CDS|CDS	6.8	1.0	22.322	NA	NA	hypothetical protein
Bste0897|CDS|CDS	13.5	2.0	22.322	NA	NA	hypothetical protein
BVU3041|CDS|hypothetical	34.8	5.2	22.295	NA	NA	hypothetical protein
Buni0266|CDS|CDS	128.0	19.0	22.278	NA	NA	hypothetical protein
TS28Ali1250|CDS|CDS	37.0	5.5	22.247	NA	NA	hypothetical protein
BVU2712|CDS|hypothetical	47.0	7.0	22.204	NA	NA	hypothetical protein
TS28Clo05823|CDS|CDS	127.0	19.0	22.104	NA	NA	hypothetical protein
Msmi750766|CDS|CDS	13.4	2.0	22.074	NA	NA	hypothetical protein
Msmi740081|CDS|CDS	3.3	0.5	22.046	NA	NA	hypothetical protein
TS28Clo04582|CDS|CDS	20.0	3.0	22.046	NA	NA	hypothetical protein
Buni2847|CDS|CDS	3.3	0.5	22.046	NA	NA	hypothetical protein
Msm0107|CDS|hydrogenase	8.3	1.3	22.046	NA	NA	hypothetical protein
BVU4104|CDS|putative	3.3	0.5	22.046	NA	NA	hypothetical protein
Pmer2076|CDS|CDS	3.3	0.5	22.046	NA	NA	hypothetical protein
HPAG11127|CDS|hypothetical	2.2	0.3	21.826	NA	NA	hypothetical protein
Msm1528|CDS|predicted	16.5	2.5	21.826	NA	NA	hypothetical protein
TS28Met0022|CDS|CDS	16.5	2.5	21.826	NA	NA	hypothetical protein
TS28Ali0122|CDS|CDS	66.0	10.0	21.826	NA	NA	hypothetical protein
TS28Fae04553|CDS|CDS	46.0	7.0	21.731	NA	NA	hypothetical protein
Msm1412|CDS|tungsten	15.1	2.3	21.639	NA	NA	hypothetical protein
Bdor3550|CDS|CDS	16.3	2.5	21.605	NA	NA	hypothetical protein
TS28Clo02076|CDS|CDS	111.0	17.0	21.592	NA	NA	hypothetical protein
Msm0198|CDS|inorganic	3.8	0.6	21.542	NA	NA	hypothetical protein
TS28Fae15725|CDS|CDS	143.2	22.0	21.520	NA	NA	hypothetical protein
BVU3153|CDS|hypothetical	19.5	3.0	21.495	NA	NA	hypothetical protein
Bste2608|CDS|CDS	13.0	2.0	21.495	NA	NA	hypothetical protein
Bdor1207|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein
Bxyl0775|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein
TS28Fae20341|CDS|CDS	13.0	2.0	21.495	NA	NA	hypothetical protein
EUBREC3652|CDS|hypothetical	13.0	2.0	21.495	NA	NA	hypothetical protein
TS29Rum00345|CDS|CDS	3.3	0.5	21.495	NA	NA	hypothetical protein
TS29Bac12204|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein
TS29Rum13310|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein
TS28Clo04463|CDS|CDS	13.0	2.0	21.495	NA	NA	hypothetical protein
b4336|CDS|conserved	6.5	1.0	21.495	NA	NA	hypothetical protein
TS28Par1009|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein
Buni1588|CDS|CDS	26.0	4.0	21.495	NA	NA	hypothetical protein
Bryfor4421|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein

TS28Col0689|CDS|CDS	13.0	2.0	21.495	NA	NA	hypothetical protein
TS28Fae04617|CDS|CDS	13.0	2.0	21.495	NA	NA	hypothetical protein
Dfor0621|CDS|CDS	6.5	1.0	21.495	NA	NA	hypothetical protein
TS29Bac01780|CDS|CDS	4.3	0.7	21.495	NA	NA	hypothetical protein
Buni1961|CDS|CDS	4.3	0.7	21.495	NA	NA	hypothetical protein
BVU2305|CDS|hypothetical	292.0	45.0	21.458	NA	NA	hypothetical protein
TS28Ali1359|CDS|CDS	415.0	64.0	21.443	NA	NA	hypothetical protein
TS29Bac09240|CDS|CDS	18.3	2.8	21.398	NA	NA	hypothetical protein
FpraM2121900|CDS|CDS	19.3	3.0	21.311	NA	NA	hypothetical protein
TS28Fae21570|CDS|CDS	528.0	82.0	21.293	NA	NA	hypothetical protein
Msmi750883|CDS|CDS	7.5	1.2	21.259	NA	NA	hypothetical protein
TS28Fae05702|CDS|CDS	45.0	7.0	21.259	NA	NA	hypothetical protein
Msm1007|CDS|tetrahydromethanopterin	19.3	3.0	21.219	NA	NA	hypothetical protein
TS28Bac7637|CDS|CDS	12.8	2.0	21.219	NA	NA	hypothetical protein
Bdor3258|CDS|CDS	12.8	2.0	21.219	NA	NA	hypothetical protein
Msm1069|CDS|energy-converting	1.6	0.3	21.164	NA	NA	hypothetical protein
TS29Fae08625|CDS|CDS	51.0	8.0	21.082	NA	NA	hypothetical protein
TS29Eub1925|CDS|CDS	44.5	7.0	21.023	NA	NA	hypothetical protein
EUBREC2215|CDS|glucose-1-phosphate	9.5	1.5	20.944	NA	NA	hypothetical protein
Msmi741479|CDS|CDS	6.3	1.0	20.944	NA	NA	hypothetical protein
b0462|CDS|multidrug	6.3	1.0	20.944	NA	NA	hypothetical protein
BVU1160|CDS|arylsulfatase	21.0	3.3	20.834	NA	NA	hypothetical protein
Msm1414|CDS|tungsten	4.4	0.7	20.786	NA	NA	hypothetical protein
Bova3099|CDS|CDS	22.0	3.5	20.786	NA	NA	hypothetical protein
TS29Bac00519|CDS|CDS	6.3	1.0	20.786	NA	NA	hypothetical protein
Msm0559|CDS|pyruvate:ferredoxin	18.8	3.0	20.742	NA	NA	hypothetical protein
b0074|CDS|2-isopropylmalate	12.5	2.0	20.668	NA	NA	hypothetical protein
TS28Clo07297|CDS|CDS	12.5	2.0	20.668	NA	NA	hypothetical protein
Cbar2604|CDS|CDS	12.5	2.0	20.668	NA	NA	hypothetical protein
TS28Fae17952|CDS|CDS	25.0	4.0	20.668	NA	NA	hypothetical protein
BVU0012|CDS|30S	25.0	4.0	20.668	NA	NA	hypothetical protein
b0922|CDS|Involved	6.3	1.0	20.668	NA	NA	hypothetical protein
PRABACTJOHN1062|CDS|CDS	28.0	4.5	20.576	NA	NA	hypothetical protein
BVU3897|CDS|putative	9.3	1.5	20.576	NA	NA	hypothetical protein
BVU3771|CDS|small	43.5	7.0	20.550	NA	NA	hypothetical protein
TS28Ali0569|CDS|CDS	31.0	5.0	20.503	NA	NA	hypothetical protein
BVU1171|CDS|putative	6.2	1.0	20.393	NA	NA	hypothetical protein
TS28Dor1132|CDS|CDS	18.5	3.0	20.393	NA	NA	hypothetical protein
TS28Fae18047|CDS|CDS	18.5	3.0	20.393	NA	NA	hypothetical protein
TS28Fae07504|CDS|CDS	37.0	6.0	20.393	NA	NA	hypothetical protein
TS29Bac01386|CDS|CDS	24.7	4.0	20.393	NA	NA	hypothetical protein
BVU2971|CDS|recombination	8.2	1.3	20.255	NA	NA	hypothetical protein
Bdor3598|CDS|CDS	21.3	3.5	20.157	NA	NA	hypothetical protein
BVU0792|CDS|30S	36.5	6.0	20.117	NA	NA	hypothetical protein
TS28Ali1244|CDS|CDS	175.0	29.0	19.956	NA	NA	hypothetical protein
Msm0881|CDS|porphobilinogen	13.0	2.2	19.892	NA	NA	hypothetical protein
TS29Bac04377|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
BLD1908|CDS|neutral	2.0	0.3	19.842	NA	NA	hypothetical protein
BactD11137|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
Msmi740056|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
BactD11147|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
BactD12681|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
Msmi740374|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
Bxyl3055|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
TS29Met0536|CDS|CDS	2.0	0.3	19.842	NA	NA	hypothetical protein
STER1722|CDS|excinuclease	2.0	0.3	19.842	NA	NA	hypothetical protein
Pmer3147|CDS|CDS	9.0	1.5	19.842	NA	NA	hypothetical protein
Msm1795|CDS|predicted	9.0	1.5	19.842	NA	NA	hypothetical protein
TS28RumUnc1280|CDS|CDS	36.0	6.0	19.842	NA	NA	hypothetical protein
TS28Clo01242|CDS|CDS	102.0	17.0	19.842	NA	NA	hypothetical protein
TS28Met1238|CDS|CDS	7.5	1.3	19.842	NA	NA	hypothetical protein
Rgna2950|CDS|CDS	15.0	2.5	19.842	NA	NA	hypothetical protein
HPAG11097|CDS|pyrroline-5-carboxylate	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Fae05069|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Msm0757|CDS|50S	1.5	0.3	19.842	NA	NA	hypothetical protein
Pmer2710|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28RumUnc0646|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS29Rum11382|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Cbar2144|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bste0234|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Cste1153|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Robe0359|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bste1301|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Fae00458|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Cbar1167|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28Clo06462|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Ehal0743|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Fae12240|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
HPAG11393|CDS|type	6.0	1.0	19.842	NA	NA	hypothetical protein
b0269|CDS|CP4-6	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Fae10328|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Rum05596|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28Clo08471|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
b3024|CDS|conserved	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Bac03632|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Ali1831|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Rum00807|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Bac2287|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Msm0832|CDS|aspartate	13.5	2.3	19.842	NA	NA	hypothetical protein
TS29Rum14185|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28Fae01478|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Rum13033|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein

TS29Bac09926|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Cnex0884|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bcap0861|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Rum06012|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
b0511|CDS|predicted	6.0	1.0	19.842	NA	NA	hypothetical protein
BVU1968|CDS|putative	3.0	0.5	19.842	NA	NA	hypothetical protein
Msm0407|CDS|P-loop	1.5	0.3	19.842	NA	NA	hypothetical protein
TS28Fae03774|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
Acod0503|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Fae05178|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bxyl2615|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
TS29Rum20236|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Fae01701|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
HPAG10950|CDS|cobalt-zinc-cadmium	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Met1413|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28CorUnc036|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS29Fae03005|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS29Rum14148|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Bac08280|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Msm1495|CDS|nuclease,	1.5	0.3	19.842	NA	NA	hypothetical protein
TS28Rum09358|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bdor0720|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
FpraM2120998|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Cbol0452|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Dfor3069|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
b2255|CDS|fused	3.0	0.5	19.842	NA	NA	hypothetical protein
Bste2553|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bste2382|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Clo06666|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Robe3907|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
M23Apeg1252|CDS|ATP	6.0	1.0	19.842	NA	NA	hypothetical protein
EUBREC3137|CDS|hypothetical	3.0	0.5	19.842	NA	NA	hypothetical protein
Csym0962|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Ali0676|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Rtor1223|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28Bac2015|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
Pmer2421|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS29Bac09716|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
PRABACTJOHN2247|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Par1404|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
FpraM2121219|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
TS29Rum07142|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Rum01632|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Fae04583|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Clo08751|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Fae10828|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Bif3147|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
TS29Rum13819|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Ceut1169|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
b4160|CDS|phosphatidylserine	6.0	1.0	19.842	NA	NA	hypothetical protein
b0086|CDS|UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Ali0590|CDS|CDS	21.0	3.5	19.842	NA	NA	hypothetical protein
TS28Par0556|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
TS28Clo08394|CDS|CDS	24.0	4.0	19.842	NA	NA	hypothetical protein
TS29Eub1007|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
TS28Ali1114|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Col1469|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
EUBREC3667|CDS|hypothetical	3.0	0.5	19.842	NA	NA	hypothetical protein
RintL11107|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28Bac2480|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Clo07943|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Clo06123|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bcap2605|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Dfor1979|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
Eeli0695|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
Robe0993|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
TS28Fae01319|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
FpraM2120692|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
Cbar0635|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
BVU0322|CDS|hypothetical	3.0	0.5	19.842	NA	NA	hypothetical protein
Bdor0848|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
HPAG11022|CDS|biotin	6.0	1.0	19.842	NA	NA	hypothetical protein
TS29Clo4878|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
Cbar2670|CDS|CDS	12.0	2.0	19.842	NA	NA	hypothetical protein
TS28Clo02092|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Pmer0371|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
TS28Clo08322|CDS|CDS	54.0	9.0	19.842	NA	NA	hypothetical protein
TS29Fae08351|CDS|CDS	3.0	0.5	19.842	NA	NA	hypothetical protein
Bthe3733475|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
BFych462832|CDS|hypothetical	6.0	1.0	19.842	NA	NA	hypothetical protein
Bdor1198|CDS|CDS	6.0	1.0	19.842	NA	NA	hypothetical protein
Bdor1594|CDS|CDS	39.7	6.7	19.676	NA	NA	hypothetical protein
Msm0219|CDS|putative	7.9	1.3	19.635	NA	NA	hypothetical protein
TS28RumUnc2041|CDS|CDS	65.0	11.0	19.541	NA	NA	hypothetical protein
Bdor3155|CDS|CDS	62.0	10.5	19.527	NA	NA	hypothetical protein
TS28Ali1423|CDS|CDS	106.0	18.0	19.474	NA	NA	hypothetical protein
Msmi750871|CDS|CDS	9.7	1.7	19.312	NA	NA	hypothetical protein
BVU0763|CDS|putative	70.0	12.0	19.290	NA	NA	hypothetical protein
TS28Ali1427|CDS|CDS	35.0	6.0	19.290	NA	NA	hypothetical protein
BVU3585|CDS|glyceraldehyde	34.9	6.0	19.245	NA	NA	hypothetical protein
TS28Clo10250|CDS|CDS	157.0	27.0	19.229	NA	NA	hypothetical protein

TS28Bac2231|CDS|CDS	23.3	4.0	19.222	NA	NA	hypothetical protein
Bcoproc0082|CDS|CDS	1.9	0.3	19.180	NA	NA	hypothetical protein
Bple1063|CDS|CDS	1.9	0.3	19.180	NA	NA	hypothetical protein
Msm1377|CDS|50S	14.5	2.5	19.180	NA	NA	hypothetical protein
Msm1001|CDS|methyl	18.8	3.3	19.163	NA	NA	hypothetical protein
BactD10315|CDS|CDS	1.9	0.3	19.133	NA	NA	hypothetical protein
Rgna2454|CDS|CDS	155.8	27.0	19.086	NA	NA	hypothetical protein
BVU1488|CDS|RNA	121.2	21.0	19.080	NA	NA	hypothetical protein
Pmer0317|CDS|CDS	49.0	8.5	19.063	NA	NA	hypothetical protein
BVU0801|CDS|30S	46.0	8.0	19.015	NA	NA	hypothetical protein
BT1920|CDS|hypothetical	11.5	2.0	19.015	NA	NA	hypothetical protein
TS28Ali1050|CDS|CDS	46.0	8.0	19.015	NA	NA	hypothetical protein
Msm0969|CDS|predicted	5.8	1.0	19.015	NA	NA	hypothetical protein
Msm0870|CDS|molecular	14.4	2.5	18.982	NA	NA	hypothetical protein
Buni0615|CDS|CDS	11.5	2.0	18.956	NA	NA	hypothetical protein
TS28Ali1173|CDS|CDS	20.0	3.5	18.897	NA	NA	hypothetical protein
TS29Fae01548|CDS|CDS	20.0	3.5	18.897	NA	NA	hypothetical protein
Msm1160|CDS|nitrogenase	5.9	1.0	18.882	NA	NA	hypothetical protein
Msm0729|CDS|molybdopterin	2.9	0.5	18.850	NA	NA	hypothetical protein
BVU4086|CDS|hypothetical	45.5	8.0	18.808	NA	NA	hypothetical protein
TS28Bac7924|CDS|CDS	2.8	0.5	18.739	NA	NA	hypothetical protein
b3533|CDS|cellulose	5.7	1.0	18.739	NA	NA	hypothetical protein
Buni0612|CDS|CDS	5.7	1.0	18.739	NA	NA	hypothetical protein
TS28Clo06726|CDS|CDS	17.0	3.0	18.739	NA	NA	hypothetical protein
TS29Bac10948|CDS|CDS	8.5	1.5	18.739	NA	NA	hypothetical protein
TS28Fae03818|CDS|CDS	17.0	3.0	18.739	NA	NA	hypothetical protein
TS28Fae03118|CDS|CDS	17.0	3.0	18.739	NA	NA	hypothetical protein
L129481|CDS|hypothetical	5.7	1.0	18.739	NA	NA	hypothetical protein
Bova1588|CDS|CDS	2.8	0.5	18.739	NA	NA	hypothetical protein
BVU4056|CDS|hypothetical	2.8	0.5	18.739	NA	NA	hypothetical protein
BactD10771|CDS|CDS	2.8	0.5	18.739	NA	NA	hypothetical protein
BVU0826|CDS|tyrosine	141.5	25.0	18.717	NA	NA	hypothetical protein
BFych462831|CDS|hypothetical	6.6	1.2	18.708	NA	NA	hypothetical protein
BVU1945|CDS|hypothetical	50.8	9.0	18.647	NA	NA	hypothetical protein
TS28Bac8247|CDS|CDS	62.0	11.0	18.639	NA	NA	hypothetical protein
Bste2614|CDS|CDS	22.5	4.0	18.602	NA	NA	hypothetical protein
BVU1354|CDS|transcription	44.8	8.0	18.531	NA	NA	hypothetical protein
BVU2904|CDS|putative	4.7	0.8	18.519	NA	NA	hypothetical protein
BactD11817|CDS|CDS	2.8	0.5	18.519	NA	NA	hypothetical protein
Msm1474|CDS|chorismate	2.8	0.5	18.519	NA	NA	hypothetical protein
TS29Bac04870|CDS|CDS	2.8	0.5	18.519	NA	NA	hypothetical protein
TS28Fae06890|CDS|CDS	28.0	5.0	18.519	NA	NA	hypothetical protein
BLD0102|CDS|Membrane	9.5	1.7	18.480	NA	NA	hypothetical protein
BVU3301|CDS|putative	243.5	44.0	18.301	NA	NA	hypothetical protein
BVU1109|CDS|dihydrolipoamide	13.8	2.5	18.298	NA	NA	hypothetical protein
TS28Clo02077|CDS|CDS	116.0	21.0	18.267	NA	NA	hypothetical protein
Msmi751652|CDS|CDS	3.7	0.7	18.188	NA	NA	hypothetical protein
Msmi740158|CDS|CDS	3.7	0.7	18.188	NA	NA	hypothetical protein
TS28Met0053|CDS|CDS	3.7	0.7	18.188	NA	NA	hypothetical protein
Msmi751006|CDS|CDS	3.7	0.7	18.188	NA	NA	hypothetical protein
BVU0795|CDS|50S	27.5	5.0	18.188	NA	NA	hypothetical protein
TS28Dor1751|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
Dlon0756|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS28Fae18480|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS29Bac00254|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS29Fae03223|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
BFych462824|CDS|putative	2.8	0.5	18.188	NA	NA	hypothetical protein
Msm1729|CDS|hypothetical	2.8	0.5	18.188	NA	NA	hypothetical protein
TS29Fae06323|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
HPAG10438|CDS|type	11.0	2.0	18.188	NA	NA	hypothetical protein
Pmer0472|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS28Rum07101|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
Bdor3766|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
Msmi750111|CDS|CDS	2.8	0.5	18.188	NA	NA	hypothetical protein
TS28Fae01301|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
Msm0257|CDS|hypothetical	2.8	0.5	18.188	NA	NA	hypothetical protein
Bste2641|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
Bste1053|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
Eeli0873|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS28Clo08418|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS28Ali2279|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
Bova1767|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
TS29Fae07796|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
TS29Fae04746|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
TS29Fae09428|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
HPAG11502|CDS|ATP-dependent	11.0	2.0	18.188	NA	NA	hypothetical protein
Pmer0107|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
CspL21861|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
TS29Bac11605|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS29Bac05017|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
b2113|CDS|antiporter	5.5	1.0	18.188	NA	NA	hypothetical protein
b1493|CDS|glutamate	5.5	1.0	18.188	NA	NA	hypothetical protein
TS28Col0177|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS28Rum02101|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
TS28Clo07103|CDS|CDS	11.0	2.0	18.188	NA	NA	hypothetical protein
TS29Bac10785|CDS|CDS	5.5	1.0	18.188	NA	NA	hypothetical protein
HPAG10636|CDS|alpha	5.5	1.0	18.188	NA	NA	hypothetical protein
TS28Fae01305|CDS|CDS	22.0	4.0	18.188	NA	NA	hypothetical protein
BVU0191|CDS|ROK	33.0	6.0	18.188	NA	NA	hypothetical protein
TS28Ali1012|CDS|CDS	181.0	33.0	18.138	NA	NA	hypothetical protein
Msm0424|CDS|transcription	8.7	1.6	18.136	NA	NA	hypothetical protein
TS28Rum08672|CDS|CDS	52.0	9.5	18.101	NA	NA	hypothetical protein

BVU2080|CDS|hypothetical	65.5	12.0	18.050	NA	NA	hypothetical protein
Bint0742|CDS|CDS	1.1	0.2	18.038	NA	NA	hypothetical protein
Bdor1465|CDS|CDS	1.1	0.2	18.038	NA	NA	hypothetical protein
Pmer0670|CDS|CDS	1.1	0.2	18.038	NA	NA	hypothetical protein
TS28Bac7061|CDS|CDS	38.2	7.0	18.031	NA	NA	hypothetical protein
BVU3614|CDS|hypothetical	38.2	7.0	18.031	NA	NA	hypothetical protein
BVU3584|CDS|tRNA	10.8	2.0	17.913	NA	NA	hypothetical protein
TS28Ali1246|CDS|CDS	92.0	17.0	17.896	NA	NA	hypothetical protein
TS28Met1117|CDS|CDS	9.0	1.7	17.857	NA	NA	hypothetical protein
TS28Clo05901|CDS|CDS	27.0	5.0	17.857	NA	NA	hypothetical protein
TS28Bac8240|CDS|CDS	81.0	15.0	17.857	NA	NA	hypothetical protein
TS29Bac11276|CDS|CDS	13.5	2.5	17.857	NA	NA	hypothetical protein
TS28Ali0654|CDS|CDS	151.0	28.0	17.834	NA	NA	hypothetical protein
TS28Ali1847|CDS|CDS	248.0	46.0	17.829	NA	NA	hypothetical protein
TS28Ali0436|CDS|CDS	167.0	31.0	17.815	NA	NA	hypothetical protein
Buni0657|CDS|CDS	58.8	11.0	17.687	NA	NA	hypothetical protein
TS28Ali0680|CDS|CDS	181.5	34.0	17.653	NA	NA	hypothetical protein
Bxyl2128|CDS|CDS	2.7	0.5	17.637	NA	NA	hypothetical protein
TS28Rum02142|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
TS28Ali0149|CDS|CDS	32.0	6.0	17.637	NA	NA	hypothetical protein
BL1181|CDS|hypothetical	4.0	0.8	17.637	NA	NA	hypothetical protein
Pmer0471|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
TS29Rum12028|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
TS28Clo02039|CDS|CDS	32.0	6.0	17.637	NA	NA	hypothetical protein
TS28Fae07973|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
TS28Par0638|CDS|CDS	8.0	1.5	17.637	NA	NA	hypothetical protein
Pmer1161|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
TS28Eub5571|CDS|CDS	2.7	0.5	17.637	NA	NA	hypothetical protein
TS28Clo02082|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
Rtor0319|CDS|CDS	16.0	3.0	17.637	NA	NA	hypothetical protein
Bova3371|CDS|CDS	2.7	0.5	17.637	NA	NA	hypothetical protein
Msm1695|CDS|excinuclease	1.3	0.3	17.637	NA	NA	hypothetical protein
BVU3511|CDS|putative	2.4	0.5	17.622	NA	NA	hypothetical protein
BactD11029|CDS|CDS	20.3	3.8	17.541	NA	NA	hypothetical protein
TS28Fae12311|CDS|CDS	37.0	7.0	17.480	NA	NA	hypothetical protein
BVU0803|CDS|50S	52.6	10.0	17.391	NA	NA	hypothetical protein
TS28Ali0950|CDS|CDS	268.0	51.0	17.378	NA	NA	hypothetical protein
Msm0652|CDS|pyruvate	1.8	0.3	17.361	NA	NA	hypothetical protein
TS29Rum21191|CDS|CDS	21.0	4.0	17.361	NA	NA	hypothetical protein
Bdor1384|CDS|CDS	10.5	2.0	17.361	NA	NA	hypothetical protein
Msm0821|CDS|orotate	3.5	0.7	17.361	NA	NA	hypothetical protein
TS28Ali0055|CDS|CDS	26.0	5.0	17.196	NA	NA	hypothetical protein
Bste2573|CDS|CDS	26.0	5.0	17.196	NA	NA	hypothetical protein
Bste3065|CDS|CDS	26.0	5.0	17.196	NA	NA	hypothetical protein
TS28Clo02071|CDS|CDS	26.0	5.0	17.196	NA	NA	hypothetical protein
BT4012|CDS|putative	17.3	3.3	17.196	NA	NA	hypothetical protein
BVU2337|CDS|hypothetical	10.3	2.0	17.086	NA	NA	hypothetical protein
Bdor2769|CDS|CDS	10.3	2.0	17.086	NA	NA	hypothetical protein
BFych462834|CDS|hypothetical	6.0	1.2	17.007	NA	NA	hypothetical protein
Bthe3733477|CDS|CDS	6.0	1.2	17.007	NA	NA	hypothetical protein
BVU2573|CDS|hypothetical	13.7	2.7	16.948	NA	NA	hypothetical protein
TS28Fae22740|CDS|CDS	20.5	4.0	16.948	NA	NA	hypothetical protein
TS28Bac2397|CDS|CDS	7.7	1.5	16.902	NA	NA	hypothetical protein
TS28Ali1675|CDS|CDS	153.0	30.0	16.865	NA	NA	hypothetical protein
TS28Ali0116|CDS|CDS	28.0	5.5	16.835	NA	NA	hypothetical protein
Msm0273|CDS|3-phosphoshikimate	6.8	1.3	16.824	NA	NA	hypothetical protein
BVU2964|CDS|hypothetical	33.0	6.5	16.789	NA	NA	hypothetical protein
Bdor0464|CDS|CDS	15.2	3.0	16.718	NA	NA	hypothetical protein
TS28Fae15749|CDS|CDS	96.0	19.0	16.709	NA	NA	hypothetical protein
TS28Fae05414|CDS|CDS	111.0	22.0	16.685	NA	NA	hypothetical protein
Msm0981|CDS|hypothetical	8.4	1.7	16.667	NA	NA	hypothetical protein
Bdor2812|CDS|CDS	55.2	11.0	16.585	NA	NA	hypothetical protein
BVU0798|CDS|50S	57.6	11.5	16.576	NA	NA	hypothetical protein
BactD13746|CDS|CDS	1.7	0.3	16.535	NA	NA	hypothetical protein
TS28Par2502|CDS|CDS	1.7	0.3	16.535	NA	NA	hypothetical protein
PRABACTJOHN3202|CDS|CDS	1.7	0.3	16.535	NA	NA	hypothetical protein
BDI2136|CDS|hypothetical	1.7	0.3	16.535	NA	NA	hypothetical protein
Bxyl1816|CDS|CDS	1.7	0.3	16.535	NA	NA	hypothetical protein
TS29Rum11723|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS28Eub5700|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS29Bac00382|CDS|CDS	1.7	0.3	16.535	NA	NA	hypothetical protein
BVU2311|CDS|ketoisovalerate	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Dor0410|CDS|CDS	7.5	1.5	16.535	NA	NA	hypothetical protein
TS28Bac5058|CDS|CDS	15.0	3.0	16.535	NA	NA	hypothetical protein
Bova2231|CDS|CDS	30.0	6.0	16.535	NA	NA	hypothetical protein
TS29Rum20344|CDS|CDS	7.5	1.5	16.535	NA	NA	hypothetical protein
Msm0814|CDS|phosphoribosylformylglycinamidine	3.3	0.7	16.535	NA	NA	hypothetical protein
TS29Bac02021|CDS|CDS	3.3	0.7	16.535	NA	NA	hypothetical protein
TS28EryUnc38|CDS|CDS	15.0	3.0	16.535	NA	NA	hypothetical protein
TS28Par1049|CDS|CDS	15.0	3.0	16.535	NA	NA	hypothetical protein
TS28Fae04140|CDS|CDS	30.0	6.0	16.535	NA	NA	hypothetical protein
Eeli0600|CDS|CDS	15.0	3.0	16.535	NA	NA	hypothetical protein
Dlon2094|CDS|CDS	7.5	1.5	16.535	NA	NA	hypothetical protein
BVU4106|CDS|hypothetical	2.5	0.5	16.535	NA	NA	hypothetical protein
TS28Eub1849|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
RintL10526|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
M23Apeg361|CDS|hypothetical	5.0	1.0	16.535	NA	NA	hypothetical protein
Bcat0773|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Ehal2078|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS29Bac00340|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Fae07933|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein

TS29Rum06488|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28RumUnc1298|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
b4021|CDS|(alpha)-aspartyl	5.0	1.0	16.535	NA	NA	hypothetical protein
b0356|CDS|alcohol	5.0	1.0	16.535	NA	NA	hypothetical protein
BL1735|CDS|hypothetical	1.3	0.3	16.535	NA	NA	hypothetical protein
EFER0010|CDS|chaperone	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG11238|CDS|DNA-directed	5.0	1.0	16.535	NA	NA	hypothetical protein
Cbol3622|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Clo2174|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Cspi0219|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
TS29Fae00685|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Fae07785|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG11191|CDS|3'-5'	5.0	1.0	16.535	NA	NA	hypothetical protein
BL1571|CDS|50S	1.3	0.3	16.535	NA	NA	hypothetical protein
Casp4857|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Bac3906|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
Bryfor2144|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG10326|CDS|membrane	5.0	1.0	16.535	NA	NA	hypothetical protein
Cbol4929|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
Pmer1192|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28RumUnc0399|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG10728|CDS|hypothetical	5.0	1.0	16.535	NA	NA	hypothetical protein
Cmet0699|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Bac5925|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Rtor0331|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
Bbre1162|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Bac5221|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
HPAG10442|CDS|hypothetical	5.0	1.0	16.535	NA	NA	hypothetical protein
Msm1539|CDS|sialic	1.3	0.3	16.535	NA	NA	hypothetical protein
TS28Fae11611|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Ali0229|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Par2312|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Bif0372|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Bif2567|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Clo03997|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
TS29Rum15434|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Cbol6475|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
b3426|CDS|sn-glycerol-3-phosphate	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Fae08067|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
Csym3648|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Msm1499|CDS|predicted	2.5	0.5	16.535	NA	NA	hypothetical protein
RintL11285|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Rum03540|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS29Rum19980|CDS|CDS	17.5	3.5	16.535	NA	NA	hypothetical protein
TS28Clo05011|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
TS28Rum13181|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Cbar1101|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
TS28Fae14138|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Svar1806|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Fae00075|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
b2985|CDS|predicted	5.0	1.0	16.535	NA	NA	hypothetical protein
RintL13438|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Bdor0105|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
HPAG10505|CDS|cag	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Fae05896|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS28Bac0025|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG10297|CDS|flagellar	10.0	2.0	16.535	NA	NA	hypothetical protein
b3465|CDS|predicted	5.0	1.0	16.535	NA	NA	hypothetical protein
Bste1906|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
BLD0256|CDS|ABC-type	5.0	1.0	16.535	NA	NA	hypothetical protein
b3807|CDS|frataxin,	5.0	1.0	16.535	NA	NA	hypothetical protein
RintL11580|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG10518|CDS|cag	5.0	1.0	16.535	NA	NA	hypothetical protein
b2895|CDS|flavodoxin	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Bac11661|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Bdor3519|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
TS29Fae09972|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
CspL20959|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Cbar0701|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Eeli1332|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
HPAG10344|CDS|CTP	5.0	1.0	16.535	NA	NA	hypothetical protein
b0560|CDS|DLP12	5.0	1.0	16.535	NA	NA	hypothetical protein
Ccom1706|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
FpraM2120500|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
CspSS20532|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Acol0421|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
RintL10311|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
FpraM2121640|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
TS28Bac4467|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Fae03802|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Hfil3398|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Par1419|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS29Fae04635|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein
TS28Met0229|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Bac1039|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
Rlac0751|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Bac2039|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Rum12358|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Clo07275|CDS|CDS	10.0	2.0	16.535	NA	NA	hypothetical protein
Aput0794|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
BLD1913|CDS|Hypothetical	1.3	0.3	16.535	NA	NA	hypothetical protein
BactD12275|CDS|CDS	2.5	0.5	16.535	NA	NA	hypothetical protein

Msmi741458|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Eub3595|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Col1389|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Bac05372|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS29Clo0774|CDS|CDS	5.0	1.0	16.535	NA	NA	hypothetical protein
TS28Fae00850|CDS|CDS	1.7	0.3	16.535	NA	NA	hypothetical protein
TS28Fae17537|CDS|CDS	74.0	15.0	16.314	NA	NA	hypothetical protein
Msmi741304|CDS|CDS	5.8	1.2	16.298	NA	NA	hypothetical protein
TS28Met0294|CDS|CDS	7.3	1.5	16.167	NA	NA	hypothetical protein
Msm0377|CDS|2-C-methyl-D-erythritol	3.3	0.7	16.121	NA	NA	hypothetical protein
Bdor1836|CDS|CDS	19.5	4.0	16.121	NA	NA	hypothetical protein
Msm0766|CDS|biotin-[acetyl-CoA-carboxylase]	9.8	2.0	16.121	NA	NA	hypothetical protein
TS28Rum14135|CDS|CDS	34.0	7.0	16.062	NA	NA	hypothetical protein
TS28Par0007|CDS|CDS	1.8	0.4	16.026	NA	NA	hypothetical protein
BT4263|CDS|glyceraldehyde	1.2	0.3	16.020	NA	NA	hypothetical protein
Bsp1162550|CDS|CDS	1.2	0.3	16.020	NA	NA	hypothetical protein
Bdor0018|CDS|CDS	9.7	2.0	15.984	NA	NA	hypothetical protein
TS28Rum03031|CDS|CDS	29.0	6.0	15.984	NA	NA	hypothetical protein
TS29Bac02877|CDS|CDS	4.8	1.0	15.984	NA	NA	hypothetical protein
TS28Ali2086|CDS|CDS	48.0	10.0	15.873	NA	NA	hypothetical protein
BVU3609|CDS|ABC	24.0	5.0	15.873	NA	NA	hypothetical protein
BVU2993|CDS|F0F1	26.3	5.5	15.833	NA	NA	hypothetical protein
Msm0322|CDS|predicted	3.8	0.8	15.831	NA	NA	hypothetical protein
TS28Fae10171|CDS|CDS	67.0	14.0	15.826	NA	NA	hypothetical protein
TS28Fae10173|CDS|CDS	43.0	9.0	15.800	NA	NA	hypothetical protein
Msm1454|CDS|predicted	10.3	2.2	15.772	NA	NA	hypothetical protein
TS28Fae17838|CDS|CDS	9.5	2.0	15.708	NA	NA	hypothetical protein
Msmi740339|CDS|CDS	9.5	2.0	15.708	NA	NA	hypothetical protein
TS28Fae10170|CDS|CDS	19.0	4.0	15.708	NA	NA	hypothetical protein
Pmer1229|CDS|CDS	9.5	2.0	15.708	NA	NA	hypothetical protein
Bste2164|CDS|CDS	19.0	4.0	15.708	NA	NA	hypothetical protein
Pmer2645|CDS|CDS	9.5	2.0	15.708	NA	NA	hypothetical protein
TS28Ali1633|CDS|CDS	85.5	18.0	15.708	NA	NA	hypothetical protein
TS28Fae11485|CDS|CDS	19.0	4.0	15.708	NA	NA	hypothetical protein
BVU1943|CDS|hypothetical	52.0	11.0	15.633	NA	NA	hypothetical protein
Aput0299|CDS|CDS	33.0	7.0	15.590	NA	NA	hypothetical protein
TS28Col0633|CDS|CDS	33.0	7.0	15.590	NA	NA	hypothetical protein
BVU3530|CDS|glutamine	23.5	5.0	15.543	NA	NA	hypothetical protein
TS28Bac4616|CDS|CDS	23.5	5.0	15.543	NA	NA	hypothetical protein
TS28Eub5740|CDS|CDS	23.5	5.0	15.543	NA	NA	hypothetical protein
Bova4219|CDS|CDS	2.4	0.5	15.543	NA	NA	hypothetical protein
Bxyl1316|CDS|CDS	20.3	4.3	15.517	NA	NA	hypothetical protein
TS28Ali1771|CDS|CDS	37.5	8.0	15.501	NA	NA	hypothetical protein
TS28Met0821|CDS|CDS	52.9	11.3	15.440	NA	NA	hypothetical protein
Buni3623|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
TS28Bif1446|CDS|CDS	7.0	1.5	15.432	NA	NA	hypothetical protein
Bdor0684|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
TS28Eub8606|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
Msm1471|CDS|acyl-CoA	14.0	3.0	15.432	NA	NA	hypothetical protein
Rumhyd3576|CDS|CDS	28.0	6.0	15.432	NA	NA	hypothetical protein
Bdor4427|CDS|CDS	63.0	13.5	15.432	NA	NA	hypothetical protein
Acol2273|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
TS28Par0392|CDS|CDS	7.0	1.5	15.432	NA	NA	hypothetical protein
HPAG10625|CDS|putative	14.0	3.0	15.432	NA	NA	hypothetical protein
FpraM2122221|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
TS28Ali0075|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
Pmer0570|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
TS28Ali1725|CDS|CDS	14.0	3.0	15.432	NA	NA	hypothetical protein
Bova2171|CDS|CDS	2.3	0.5	15.432	NA	NA	hypothetical protein
TS29Bac12023|CDS|CDS	4.7	1.0	15.432	NA	NA	hypothetical protein
b2942|CDS|methionine	4.7	1.0	15.432	NA	NA	hypothetical protein
TS29Fae04859|CDS|CDS	2.3	0.5	15.432	NA	NA	hypothetical protein
TS29Rum02139|CDS|CDS	2.3	0.5	15.432	NA	NA	hypothetical protein
FpraM2120878|CDS|CDS	5.8	1.3	15.344	NA	NA	hypothetical protein
TS28Ali2376|CDS|CDS	88.0	19.0	15.316	NA	NA	hypothetical protein
Acac0859|CDS|CDS	0.9	0.2	15.295	NA	NA	hypothetical protein
TS28Rum15902|CDS|CDS	69.0	15.0	15.212	NA	NA	hypothetical protein
Bdor1963|CDS|CDS	11.5	2.5	15.212	NA	NA	hypothetical protein
Buni3559|CDS|CDS	4.6	1.0	15.157	NA	NA	hypothetical protein
TS28Bac2481|CDS|CDS	4.6	1.0	15.157	NA	NA	hypothetical protein
TS28Bac6559|CDS|CDS	40.3	8.8	15.100	NA	NA	hypothetical protein
TS28RumUnc1683|CDS|CDS	105.0	23.0	15.097	NA	NA	hypothetical protein
Bdor0190|CDS|CDS	13.7	3.0	15.065	NA	NA	hypothetical protein
TS29Fae03931|CDS|CDS	18.2	4.0	15.019	NA	NA	hypothetical protein
BVU4120|CDS|glucosamine-6-phosphate	28.7	6.3	14.968	NA	NA	hypothetical protein
Msm1020|CDS|Fe-S	1.5	0.3	14.881	NA	NA	hypothetical protein
TS29Bac10053|CDS|CDS	3.0	0.7	14.881	NA	NA	hypothetical protein
TS29Fae03933|CDS|CDS	3.0	0.7	14.881	NA	NA	hypothetical protein
Msm0972|CDS|tRNA-dihydrouridine	1.5	0.3	14.881	NA	NA	hypothetical protein
Msm0428|CDS|integrase-recombinase	1.5	0.3	14.881	NA	NA	hypothetical protein
Buni0453|CDS|CDS	1.5	0.3	14.881	NA	NA	hypothetical protein
Msm1785|CDS|hypothetical	1.5	0.3	14.881	NA	NA	hypothetical protein
Msm0054|CDS|2'-5'	1.5	0.3	14.881	NA	NA	hypothetical protein
CspM6212207|CDS|CDS	6.0	1.3	14.881	NA	NA	hypothetical protein
Bdor0123|CDS|CDS	19.5	4.3	14.881	NA	NA	hypothetical protein
TS29Fae10158|CDS|CDS	4.5	1.0	14.881	NA	NA	hypothetical protein
TS28Rum11142|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Fae01274|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Rum15412|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
Cbar0708|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Fae00281|CDS|CDS	4.5	1.0	14.881	NA	NA	hypothetical protein
CspSS22348|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein

TS28Fae00774|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
b2761|CDS|conserved	4.5	1.0	14.881	NA	NA	hypothetical protein
Bste2587|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Rum09372|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
HPAG11388|CDS|hypothetical	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Bac02133|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
b2067|CDS|predicted	4.5	1.0	14.881	NA	NA	hypothetical protein
Ccom1871|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
b3519|CDS|cytoplasmic	4.5	1.0	14.881	NA	NA	hypothetical protein
TS29Fae01399|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
HPAG11469|CDS|iron(III)	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Fae01599|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS29Rum03632|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
Pmer0604|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS28Par2125|CDS|CDS	4.5	1.0	14.881	NA	NA	hypothetical protein
TS28Fae16047|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS28Rum02284|CDS|CDS	2.3	0.5	14.881	NA	NA	hypothetical protein
BDI2375|CDS|50S	9.0	2.0	14.881	NA	NA	hypothetical protein
TS28Ali1262|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
TS28Clo05407|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
BVU1469|CDS|hypothetical	22.5	5.0	14.881	NA	NA	hypothetical protein
TS29Fae08913|CDS|CDS	4.5	1.0	14.881	NA	NA	hypothetical protein
b3588|CDS|aldehyde	4.5	1.0	14.881	NA	NA	hypothetical protein
Buni3577|CDS|CDS	11.3	2.5	14.881	NA	NA	hypothetical protein
b2456|CDS|predicted	4.5	1.0	14.881	NA	NA	hypothetical protein
HPAG11013|CDS|alpha	4.5	1.0	14.881	NA	NA	hypothetical protein
TS28Par2060|CDS|CDS	4.5	1.0	14.881	NA	NA	hypothetical protein
TS28Clo07192|CDS|CDS	18.0	4.0	14.881	NA	NA	hypothetical protein
Rumhyd3570|CDS|CDS	9.0	2.0	14.881	NA	NA	hypothetical protein
b3955|CDS|conserved	4.5	1.0	14.881	NA	NA	hypothetical protein
TS28Eub5220|CDS|CDS	217.5	48.5	14.830	NA	NA	hypothetical protein
TS28Ali2286|CDS|CDS	215.0	48.0	14.812	NA	NA	hypothetical protein
TS28Bac7403|CDS|CDS	38.0	8.5	14.784	NA	NA	hypothetical protein
TS28Ali1840|CDS|CDS	58.0	13.0	14.754	NA	NA	hypothetical protein
Msm0530|CDS|predicted	8.9	2.0	14.743	NA	NA	hypothetical protein
TS29Fae06615|CDS|CDS	93.5	21.0	14.724	NA	NA	hypothetical protein
BVU1887|CDS|hypothetical	40.0	9.0	14.697	NA	NA	hypothetical protein
TS29Bac01847|CDS|CDS	13.3	3.0	14.697	NA	NA	hypothetical protein
Msm0516|CDS|corrinoid	5.9	1.3	14.675	NA	NA	hypothetical protein
TS28Fae13772|CDS|CDS	24.3	5.5	14.581	NA	NA	hypothetical protein
Msm0558|CDS|pyruvate:ferredoxin	7.3	1.7	14.551	NA	NA	hypothetical protein
BVU4141|CDS|sialate	3.7	0.8	14.551	NA	NA	hypothetical protein
Robe0842|CDS|CDS	11.0	2.5	14.551	NA	NA	hypothetical protein
TS28RumUnc0011|CDS|CDS	22.0	5.0	14.551	NA	NA	hypothetical protein
TS28Clo07962|CDS|CDS	22.0	5.0	14.551	NA	NA	hypothetical protein
Bova1547|CDS|CDS	2.2	0.5	14.551	NA	NA	hypothetical protein
BVU3048|CDS|putative	11.0	2.5	14.551	NA	NA	hypothetical protein
TS28Par1962|CDS|CDS	11.0	2.5	14.551	NA	NA	hypothetical protein
Msmi750667|CDS|CDS	6.6	1.5	14.514	NA	NA	hypothetical protein
BVU2737|CDS|serine	175.5	40.0	14.509	NA	NA	hypothetical protein
BVU2304|CDS|hypothetical	144.5	33.0	14.480	NA	NA	hypothetical protein
Msm1122|CDS|coenzyme	18.2	4.2	14.471	NA	NA	hypothetical protein
TS28Fae20467|CDS|CDS	305.0	70.0	14.409	NA	NA	hypothetical protein
Msm1284|CDS|pyruvate	2.2	0.5	14.330	NA	NA	hypothetical protein
Bdor3136|CDS|CDS	21.7	5.0	14.330	NA	NA	hypothetical protein
BVU3054|CDS|transcriptional	8.7	2.0	14.330	NA	NA	hypothetical protein
Msm1480|CDS|predicted	8.7	2.0	14.330	NA	NA	hypothetical protein
HPAG11210|CDS|NADH	13.0	3.0	14.330	NA	NA	hypothetical protein
TS29Clo4979|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
Rtor0412|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
BVU3234|CDS|Na(+)-translocating	6.5	1.5	14.330	NA	NA	hypothetical protein
Pmer2965|CDS|CDS	6.5	1.5	14.330	NA	NA	hypothetical protein
Bxyl3032|CDS|CDS	6.5	1.5	14.330	NA	NA	hypothetical protein
TS28Clo02037|CDS|CDS	52.0	12.0	14.330	NA	NA	hypothetical protein
TS29Fae01271|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
TS29Bac12187|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
TS28Ali0196|CDS|CDS	39.0	9.0	14.330	NA	NA	hypothetical protein
Bdor4047|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
TS28Clo02047|CDS|CDS	26.0	6.0	14.330	NA	NA	hypothetical protein
TS29Bac02389|CDS|CDS	6.5	1.5	14.330	NA	NA	hypothetical protein
TS28Fae06331|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
TS28Clo02816|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
TS28Rum10815|CDS|CDS	13.0	3.0	14.330	NA	NA	hypothetical protein
TS29Rum05543|CDS|CDS	4.3	1.0	14.330	NA	NA	hypothetical protein
b0660|CDS|predicted	4.3	1.0	14.330	NA	NA	hypothetical protein
TS28Met1235|CDS|CDS	2.2	0.5	14.330	NA	NA	hypothetical protein
Msm1085|CDS|aquaporin,	2.9	0.7	14.302	NA	NA	hypothetical protein
Msmi740637|CDS|CDS	5.8	1.3	14.261	NA	NA	hypothetical protein
TS28Fae10754|CDS|CDS	32.3	7.5	14.257	NA	NA	hypothetical protein
TS29Fae09687|CDS|CDS	32.3	7.5	14.257	NA	NA	hypothetical protein
BVU2254|CDS|hypothetical	118.5	27.5	14.250	NA	NA	hypothetical protein
TS29Fae06988|CDS|CDS	21.5	5.0	14.220	NA	NA	hypothetical protein
Msm0156|CDS|aspartyl/glutamyl-tRNA	2.2	0.5	14.220	NA	NA	hypothetical protein
BVU0051|CDS|hypothetical	72.3	16.8	14.210	NA	NA	hypothetical protein
TS28Bac5355|CDS|CDS	30.0	7.0	14.173	NA	NA	hypothetical protein
Msm1561|CDS|hypothetical	11.8	2.8	14.150	NA	NA	hypothetical protein
BVU0517|CDS|dihydropteroate	5.7	1.3	14.054	NA	NA	hypothetical protein
Msm1232|CDS|signal	5.7	1.3	14.054	NA	NA	hypothetical protein
Msm0325|CDS|hypothetical	4.3	1.0	14.054	NA	NA	hypothetical protein
TS29Fae02120|CDS|CDS	8.5	2.0	14.054	NA	NA	hypothetical protein
TS28Bac5799|CDS|CDS	8.5	2.0	14.054	NA	NA	hypothetical protein
BactD14017|CDS|CDS	4.3	1.0	14.054	NA	NA	hypothetical protein

TS28Bac7626|CDS|CDS	8.5	2.0	14.054	NA	NA	hypothetical protein
Msm0966|CDS|predicted	4.3	1.0	14.054	NA	NA	hypothetical protein
TS28Clo06556|CDS|CDS	17.0	4.0	14.054	NA	NA	hypothetical protein
TS28Clo07006|CDS|CDS	17.0	4.0	14.054	NA	NA	hypothetical protein
BactD12151|CDS|CDS	4.3	1.0	14.054	NA	NA	hypothetical protein
TS28Ali0628|CDS|CDS	17.0	4.0	14.054	NA	NA	hypothetical protein
TS28Ali1053|CDS|CDS	34.0	8.0	14.054	NA	NA	hypothetical protein
TS29Rum00095|CDS|CDS	8.5	2.0	14.054	NA	NA	hypothetical protein
TS28Ali0288|CDS|CDS	266.0	63.0	13.963	NA	NA	hypothetical protein
BVU0790|CDS|50S	67.2	16.0	13.896	NA	NA	hypothetical protein
Msm0848|CDS|predicted	3.5	0.8	13.889	NA	NA	hypothetical protein
Msm1478|CDS|phenylalanyl-tRNA	10.5	2.5	13.889	NA	NA	hypothetical protein
TS28Rum03425|CDS|CDS	10.5	2.5	13.889	NA	NA	hypothetical protein
TS28Bac1064|CDS|CDS	21.0	5.0	13.889	NA	NA	hypothetical protein
TS28Bac5486|CDS|CDS	29.3	7.0	13.858	NA	NA	hypothetical protein
TS28Eub2090|CDS|CDS	20.9	5.0	13.801	NA	NA	hypothetical protein
TS28Fae10167|CDS|CDS	8.3	2.0	13.779	NA	NA	hypothetical protein
TS29Fae03168|CDS|CDS	12.5	3.0	13.779	NA	NA	hypothetical protein
TS28Par0360|CDS|CDS	12.5	3.0	13.779	NA	NA	hypothetical protein
BVU2795|CDS|6-phosphogluconate	25.0	6.0	13.779	NA	NA	hypothetical protein
FpraM2120394|CDS|CDS	2.1	0.5	13.779	NA	NA	hypothetical protein
BVU2242|CDS|putative	12.5	3.0	13.779	NA	NA	hypothetical protein
Msm0849|CDS|molybdenum	3.8	0.9	13.709	NA	NA	hypothetical protein
TS28Clo02045|CDS|CDS	29.0	7.0	13.700	NA	NA	hypothetical protein
Dfor0620|CDS|CDS	14.5	3.5	13.700	NA	NA	hypothetical protein
TS28Eub4865|CDS|CDS	124.2	30.0	13.687	NA	NA	hypothetical protein
TS28Ali2331|CDS|CDS	155.0	37.5	13.669	NA	NA	hypothetical protein
Pmer3010|CDS|CDS	41.3	10.0	13.669	NA	NA	hypothetical protein
Msm0075|CDS|DNA	5.5	1.3	13.641	NA	NA	hypothetical protein
Msm1037|CDS|proteasome,	2.8	0.7	13.641	NA	NA	hypothetical protein
Msmi750586|CDS|CDS	2.8	0.7	13.641	NA	NA	hypothetical protein
Bxyl1553|CDS|CDS	5.5	1.3	13.641	NA	NA	hypothetical protein
TS29Bac00399|CDS|CDS	5.5	1.3	13.641	NA	NA	hypothetical protein
CspM6211317|CDS|CDS	13.7	3.3	13.558	NA	NA	hypothetical protein
Cnex1177|CDS|CDS	4.1	1.0	13.528	NA	NA	hypothetical protein
TS29Fae10123|CDS|CDS	24.5	6.0	13.503	NA	NA	hypothetical protein
Msmi751678|CDS|CDS	10.2	2.5	13.448	NA	NA	hypothetical protein
TS28Fae01246|CDS|CDS	65.0	16.0	13.434	NA	NA	hypothetical protein
TS29Eub0058|CDS|CDS	32.5	8.0	13.434	NA	NA	hypothetical protein
TS28Clo02042|CDS|CDS	69.0	17.0	13.422	NA	NA	hypothetical protein
TS28Ali1426|CDS|CDS	52.5	13.0	13.355	NA	NA	hypothetical protein
BVU0013|CDS|30S	64.5	16.0	13.338	NA	NA	hypothetical protein
TS28Ali1358|CDS|CDS	197.0	49.0	13.295	NA	NA	hypothetical protein
FpraM2120354|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
STER1942|CDS|anaerobic	6.7	1.7	13.228	NA	NA	hypothetical protein
BL0615|CDS|alkyl	1.3	0.3	13.228	NA	NA	hypothetical protein
TS29Rum05541|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
TS28Clo03934|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28Ali1027|CDS|CDS	52.0	13.0	13.228	NA	NA	hypothetical protein
Bdor0496|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28Fae07864|CDS|CDS	20.0	5.0	13.228	NA	NA	hypothetical protein
TS28Fae03912|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28Clo02083|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28Clo07921|CDS|CDS	20.0	5.0	13.228	NA	NA	hypothetical protein
TS28Fae10851|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
Bste1800|CDS|CDS	6.0	1.5	13.228	NA	NA	hypothetical protein
Bthe3733487|CDS|CDS	6.0	1.5	13.228	NA	NA	hypothetical protein
Bdor0286|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
BactD13831|CDS|CDS	6.0	1.5	13.228	NA	NA	hypothetical protein
TS29Fae06140|CDS|CDS	6.0	1.5	13.228	NA	NA	hypothetical protein
TS28Clo09581|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28Clo05714|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28RumUnc1569|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
TS28Ali2393|CDS|CDS	12.0	3.0	13.228	NA	NA	hypothetical protein
Cbar2741|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum08845|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10807|CDS|excinuclease	4.0	1.0	13.228	NA	NA	hypothetical protein
CspM6211664|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Bac06166|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
Ehal1545|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Dfor0358|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Svar0140|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bdor2574|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Bac5689|CDS|CDS	16.0	4.0	13.228	NA	NA	hypothetical protein
Msm1048|CDS|phosphopantothenoylcysteine	1.0	0.3	13.228	NA	NA	hypothetical protein
CspSS21914|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Bac02429|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Clo09424|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
BVU3877|CDS|hypothetical	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum13848|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Par0861|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Fae04484|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
EUBREC2217|CDS|homoserine	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Par2021|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Bac1168|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BactD20559|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Eub1214|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Cbol4050|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae14836|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Bac7821|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Msm1543|CDS|hypothetical	1.0	0.3	13.228	NA	NA	hypothetical protein
TS28Ali1438|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein

TS29Fae05935|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Robe2378|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
b4130|CDS|predicted	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum17254|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Ccom0430|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
b3958|CDS|N-acetyl-gamma-glutamylphosphate	2.0	0.5	13.228	NA	NA	hypothetical protein
Rtor0930|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10528|CDS|transcription	4.0	1.0	13.228	NA	NA	hypothetical protein
Csci0744|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BactD10157|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
Bxyl1605|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Rum14905|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Msm0661|CDS|30S	1.0	0.3	13.228	NA	NA	hypothetical protein
Dlon0951|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae15722|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS29Rum13482|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10951|CDS|cobalt-zinc-cadmium	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Eub0441|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Msmi750006|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
TS28CloUnc085|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Fae19769|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
FpraM2122646|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Fae19788|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Ali1304|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Bac01238|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
HPAG11075|CDS|F0F1	4.0	1.0	13.228	NA	NA	hypothetical protein
Bova2602|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Bthe7331635|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
Cbar0278|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG11351|CDS|hypothetical	4.0	1.0	13.228	NA	NA	hypothetical protein
Bthe7331630|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
Rbro0611|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Fae03042|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Cspi1679|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
FpraM2121275|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
HPAG10819|CDS|hypothetical	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10063|CDS|hypothetical	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Bac00022|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bdor3923|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Bac3703|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Clo04876|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Eub0683|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
EUBREC1612|CDS|unspecific	2.0	0.5	13.228	NA	NA	hypothetical protein
Acod0937|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BactD10457|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Cbar2423|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Fae04461|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae00154|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
HPAG10866|CDS|cysteinyl-tRNA	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10527|CDS|glutamate	4.0	1.0	13.228	NA	NA	hypothetical protein
Bdor2760|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Hfil1034|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Bac0284|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Clo04648|CDS|CDS	16.0	4.0	13.228	NA	NA	hypothetical protein
TS29Bac04550|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
EUBREC1870|CDS|DNA	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Bac5987|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae22056|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Msm0344|CDS|hypothetical	1.0	0.3	13.228	NA	NA	hypothetical protein
FpraM2120641|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Bdor0836|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum11626|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Par1876|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Bif0719|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BVU2417|CDS|naphthoate	8.0	2.0	13.228	NA	NA	hypothetical protein
BactD10535|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
CspM6210520|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Par0874|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Aput2122|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum13291|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Fae00819|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Bdor0799|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Bfin1852|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Par0261|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
BVU0261|CDS|hypothetical	8.0	2.0	13.228	NA	NA	hypothetical protein
BactD10160|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
TS28Col1158|CDS|CDS	16.0	4.0	13.228	NA	NA	hypothetical protein
Robe1610|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
CspSS22098|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
FpraM2122510|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bint0431|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
TS28Bac8326|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bfra31123676|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BLD1592|CDS|NTP	1.0	0.3	13.228	NA	NA	hypothetical protein
EUBREC1648|CDS|glutamate	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Rum08446|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Rum15686|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BWH25658|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
L0277|CDS|DNA	4.0	1.0	13.228	NA	NA	hypothetical protein
Begg1204|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
HPAG10840|CDS|phosphoheptose	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10347|CDS|flagellar	4.0	1.0	13.228	NA	NA	hypothetical protein

Acol0903|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae07282|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Rum01490|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Aput1043|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
BactD20912|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Fae03013|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bova3305|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Bac5336|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Ali2349|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
M23Apeg869|CDS|SSU	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Eub2564|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bdor0225|CDS|CDS	16.0	4.0	13.228	NA	NA	hypothetical protein
Bdor3858|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Bac1156|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum13937|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Msm0779|CDS|predicted	1.0	0.3	13.228	NA	NA	hypothetical protein
BactD12679|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Fae00530|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Ccom1985|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae05114|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
BVU3855|CDS|putative	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae14915|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Ehal1724|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Bac02966|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS28Fae13488|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Eub1935|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
HPAG10024|CDS|type	4.0	1.0	13.228	NA	NA	hypothetical protein
Bxyl4376|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
Msmi750110|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
Begg1865|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Pmer2373|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Dlon2195|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
TS29Rum14917|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS28Bac7744|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Fae05047|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Fae08291|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum18577|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum13085|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Hfil3435|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS29Rum14482|CDS|CDS	8.0	2.0	13.228	NA	NA	hypothetical protein
Bthe3734423|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
Bthe3735760|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
TS28Rum02945|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Msm1075|CDS|putative	1.0	0.3	13.228	NA	NA	hypothetical protein
Acol1322|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Msmi740740|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
TS29Bac04680|CDS|CDS	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Bac11462|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
Bthe3734418|CDS|CDS	1.0	0.3	13.228	NA	NA	hypothetical protein
CspL21890|CDS|CDS	5.3	1.3	13.228	NA	NA	hypothetical protein
TS29Rum06242|CDS|CDS	4.0	1.0	13.228	NA	NA	hypothetical protein
TS28Bac6131|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
BactD11099|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
TS29Rum12818|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
str1997|CDS|30S	1.3	0.3	13.228	NA	NA	hypothetical protein
stu1997|CDS|30S	1.3	0.3	13.228	NA	NA	hypothetical protein
Bova0103|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
Msmi740189|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
Buni0317|CDS|CDS	1.3	0.3	13.228	NA	NA	hypothetical protein
STER1973|CDS|30S	1.3	0.3	13.228	NA	NA	hypothetical protein
BVU1351|CDS|protein	2.0	0.5	13.228	NA	NA	hypothetical protein
TS29Fae00065|CDS|CDS	27.8	7.0	13.118	NA	NA	hypothetical protein
Pmer2301|CDS|CDS	39.5	10.0	13.062	NA	NA	hypothetical protein
BVU2888|CDS|putative	11.8	3.0	13.044	NA	NA	hypothetical protein
BVU2668|CDS|hypothetical	59.0	15.0	13.007	NA	NA	hypothetical protein
BVU0794|CDS|50S	15.7	4.0	12.952	NA	NA	hypothetical protein
TS28Ali1091|CDS|CDS	47.0	12.0	12.952	NA	NA	hypothetical protein
TS28Ali0581|CDS|CDS	78.0	20.0	12.897	NA	NA	hypothetical protein
BVU0865|CDS|hypothetical	19.5	5.0	12.897	NA	NA	hypothetical protein
TS28Eub8039|CDS|CDS	56.5	14.5	12.886	NA	NA	hypothetical protein
BVU0817|CDS|50S	44.7	11.5	12.865	NA	NA	hypothetical protein
BVU4062|CDS|Holliday	5.8	1.5	12.860	NA	NA	hypothetical protein
BactD13478|CDS|CDS	23.3	6.0	12.860	NA	NA	hypothetical protein
BVU4109|CDS|glucose-6-phosphate	15.5	4.0	12.814	NA	NA	hypothetical protein
TS29Bac11641|CDS|CDS	9.7	2.5	12.787	NA	NA	hypothetical protein
Msm0795|CDS|heterodisulfide	13.5	3.5	12.787	NA	NA	hypothetical protein
Bova3102|CDS|CDS	23.2	6.0	12.768	NA	NA	hypothetical protein
Msm0382|CDS|hypothetical	2.3	0.6	12.755	NA	NA	hypothetical protein
Msmi740154|CDS|CDS	2.3	0.6	12.755	NA	NA	hypothetical protein
TS29Bac09836|CDS|CDS	4.5	1.2	12.755	NA	NA	hypothetical protein
BactD11680|CDS|CDS	4.5	1.2	12.755	NA	NA	hypothetical protein
EUBREC0736|CDS|electron	28.8	7.5	12.713	NA	NA	hypothetical protein
TS28Ali1057|CDS|CDS	96.0	25.0	12.699	NA	NA	hypothetical protein
TS28Fae21972|CDS|CDS	56.3	14.7	12.683	NA	NA	hypothetical protein
TS28Ali1935|CDS|CDS	161.0	42.0	12.677	NA	NA	hypothetical protein
Ccom1703|CDS|CDS	23.0	6.0	12.677	NA	NA	hypothetical protein
BVU1353|CDS|hypothetical	23.0	6.0	12.677	NA	NA	hypothetical protein
Bdor1989|CDS|CDS	23.0	6.0	12.677	NA	NA	hypothetical protein
TS29Rum20035|CDS|CDS	23.0	6.0	12.677	NA	NA	hypothetical protein
TS28RumUnc1462|CDS|CDS	23.0	6.0	12.677	NA	NA	hypothetical protein
TS29Bac03080|CDS|CDS	3.8	1.0	12.677	NA	NA	hypothetical protein
Bxyl0906|CDS|CDS	3.8	1.0	12.677	NA	NA	hypothetical protein

Bcro1215|CDS|CDS	3.8	1.0	12.677	NA	NA	hypothetical protein
BactD11218|CDS|CDS	3.8	1.0	12.677	NA	NA	hypothetical protein
TS29Bac12101|CDS|CDS	3.8	1.0	12.677	NA	NA	hypothetical protein
BVU3815|CDS|endopeptidase	119.5	31.3	12.612	NA	NA	hypothetical protein
BVU2745|CDS|putative	38.0	10.0	12.566	NA	NA	hypothetical protein
TS28Fae13014|CDS|CDS	57.0	15.0	12.566	NA	NA	hypothetical protein
TS29Rum17049|CDS|CDS	9.5	2.5	12.566	NA	NA	hypothetical protein
TS28Rum15068|CDS|CDS	9.5	2.5	12.566	NA	NA	hypothetical protein
TS28Rum06856|CDS|CDS	9.5	2.5	12.566	NA	NA	hypothetical protein
TS28Bac8354|CDS|CDS	19.0	5.0	12.566	NA	NA	hypothetical protein
TS28Clo02090|CDS|CDS	19.0	5.0	12.566	NA	NA	hypothetical protein
TS28Rum00347|CDS|CDS	34.0	9.0	12.493	NA	NA	hypothetical protein
TS28Fae03758|CDS|CDS	7.5	2.0	12.456	NA	NA	hypothetical protein
BVU1404|CDS|S-adenosyl-methyltransferase	13.2	3.5	12.440	NA	NA	hypothetical protein
Buni3230|CDS|CDS	5.0	1.3	12.401	NA	NA	hypothetical protein
Msm0854|CDS|hypothetical	1.3	0.3	12.401	NA	NA	hypothetical protein
Msm1564|CDS|predicted	1.3	0.3	12.401	NA	NA	hypothetical protein
Msmi750297|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
Msmi750742|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
Msm0064|CDS|hypothetical	1.3	0.3	12.401	NA	NA	hypothetical protein
Bpse1841|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
STER1546|CDS|cation	1.3	0.3	12.401	NA	NA	hypothetical protein
Msmi740353|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
TS28Bif5273|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
TS29Bif0036|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
Msm0712|CDS|hypothetical	1.3	0.3	12.401	NA	NA	hypothetical protein
Msm1697|CDS|hypothetical	1.3	0.3	12.401	NA	NA	hypothetical protein
Bfra31123867|CDS|CDS	2.5	0.7	12.401	NA	NA	hypothetical protein
Msmi750398|CDS|CDS	1.3	0.3	12.401	NA	NA	hypothetical protein
Bste1198|CDS|CDS	15.0	4.0	12.401	NA	NA	hypothetical protein
TS28RumUnc0628|CDS|CDS	30.0	8.0	12.401	NA	NA	hypothetical protein
Aput2153|CDS|CDS	7.5	2.0	12.401	NA	NA	hypothetical protein
TS28Clo02339|CDS|CDS	15.0	4.0	12.401	NA	NA	hypothetical protein
TS28Clo02607|CDS|CDS	15.0	4.0	12.401	NA	NA	hypothetical protein
Bdor2704|CDS|CDS	7.5	2.0	12.401	NA	NA	hypothetical protein
TS28Fae10484|CDS|CDS	15.0	4.0	12.401	NA	NA	hypothetical protein
Bste1678|CDS|CDS	15.0	4.0	12.401	NA	NA	hypothetical protein
Aput0646|CDS|CDS	0.6	0.2	12.381	NA	NA	hypothetical protein
Msm1404|CDS|formate	24.5	6.6	12.353	NA	NA	hypothetical protein
TS28Rum11527|CDS|CDS	1.9	0.5	12.346	NA	NA	hypothetical protein
Msm0677|CDS|aspartate	2.8	0.8	12.346	NA	NA	hypothetical protein
BVU1987|CDS|hypothetical	9.3	2.5	12.346	NA	NA	hypothetical protein
Msmi750093|CDS|CDS	10.3	2.8	12.326	NA	NA	hypothetical protein
FpraM2120971|CDS|CDS	13.0	3.5	12.283	NA	NA	hypothetical protein
TS28Clo02064|CDS|CDS	137.0	37.0	12.245	NA	NA	hypothetical protein
Msm1286|CDS|3-octaprenyl-4-hydroxybenzoate	1.2	0.3	12.236	NA	NA	hypothetical protein
TS28Ali0452|CDS|CDS	48.0	13.0	12.210	NA	NA	hypothetical protein
TS28Ali1227|CDS|CDS	81.0	22.0	12.176	NA	NA	hypothetical protein
Msm0765|CDS|pyruvate	7.7	2.1	12.170	NA	NA	hypothetical protein
BVU3440|CDS|hypothetical	3.7	1.0	12.125	NA	NA	hypothetical protein
Cspi0974|CDS|CDS	3.7	1.0	12.125	NA	NA	hypothetical protein
Msmi750728|CDS|CDS	0.9	0.3	12.125	NA	NA	hypothetical protein
TS29Bac11215|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
Dlon0618|CDS|CDS	5.5	1.5	12.125	NA	NA	hypothetical protein
Bste2550|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
Rtor1585|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS28Bac1125|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS28Bac6257|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS29Rum20803|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
FpraM2120995|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
Acol3854|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS28RumUnc1175|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS29Rum01328|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS29Rum13036|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS29Fae08172|CDS|CDS	5.5	1.5	12.125	NA	NA	hypothetical protein
M23Apeg48|CDS|Pyruvate,phosphate	11.0	3.0	12.125	NA	NA	hypothetical protein
TS28Fae04521|CDS|CDS	22.0	6.0	12.125	NA	NA	hypothetical protein
Bdor0160|CDS|CDS	5.5	1.5	12.125	NA	NA	hypothetical protein
TS29Rum15040|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS29Eub0873|CDS|CDS	22.0	6.0	12.125	NA	NA	hypothetical protein
TS28Fae09935|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS28Par2261|CDS|CDS	11.0	3.0	12.125	NA	NA	hypothetical protein
TS28Rum13928|CDS|CDS	7.3	2.0	12.125	NA	NA	hypothetical protein
BL1160|CDS|peptide	3.7	1.0	12.125	NA	NA	hypothetical protein
TS28Fae21066|CDS|CDS	21.9	6.0	12.052	NA	NA	hypothetical protein
BVU2367|CDS|putative	65.5	18.0	12.034	NA	NA	hypothetical protein
TS29Bac10371|CDS|CDS	13.3	3.7	12.025	NA	NA	hypothetical protein
BWH21673|CDS|CDS	4.8	1.3	11.988	NA	NA	hypothetical protein
BFnctc1734|CDS|hypothetical	4.8	1.3	11.988	NA	NA	hypothetical protein
TS28Rum01944|CDS|CDS	58.0	16.0	11.988	NA	NA	hypothetical protein
TS29Bac09289|CDS|CDS	14.5	4.0	11.988	NA	NA	hypothetical protein
Msm0506|CDS|5-aminoimidazole-4-carboxamide-1-beta-D-ribofuranosyl	12.7	3.5	11.968	NA	NA	hypothetical protein
TS28Met0529|CDS|CDS	79.4	22.0	11.930	NA	NA	hypothetical protein
HPAG10119|CDS|hypothetical	1.2	0.3	11.905	NA	NA	hypothetical protein
Bxyl4378|CDS|CDS	3.0	0.8	11.905	NA	NA	hypothetical protein
TS28Ali0326|CDS|CDS	36.0	10.0	11.905	NA	NA	hypothetical protein
TS28Col0872|CDS|CDS	18.0	5.0	11.905	NA	NA	hypothetical protein
TS28Clo06585|CDS|CDS	18.0	5.0	11.905	NA	NA	hypothetical protein
Msm0704|CDS|translation	4.5	1.3	11.905	NA	NA	hypothetical protein
TS28Clo02048|CDS|CDS	108.0	30.0	11.905	NA	NA	hypothetical protein
Msm0919|CDS|triosephosphate	0.9	0.3	11.905	NA	NA	hypothetical protein

<table>
<tr><td>Buni0291|CDS|CDS</td><td>3.0</td><td>0.8</td><td>11.905</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Bac1538|CDS|CDS</td><td>3.0</td><td>0.8</td><td>11.905</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac11275|CDS|CDS</td><td>13.8</td><td>3.8</td><td>11.891</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BVU2319|CDS|xylulose</td><td>7.2</td><td>2.0</td><td>11.850</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BVU1927|CDS|aminoacyl-histidine</td><td>12.5</td><td>3.5</td><td>11.810</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Rum13035|CDS|CDS</td><td>25.0</td><td>7.0</td><td>11.810</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Met0241|CDS|CDS</td><td>8.3</td><td>2.3</td><td>11.810</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BLD1015|CDS|hypothetical</td><td>2.1</td><td>0.6</td><td>11.810</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>FpraM2120511|CDS|CDS</td><td>3.0</td><td>0.8</td><td>11.773</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BVU2612|CDS|preprotein</td><td>32.0</td><td>9.0</td><td>11.758</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae14026|CDS|CDS</td><td>145.5</td><td>41.0</td><td>11.736</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BVU1157|CDS|putative</td><td>56.3</td><td>16.0</td><td>11.643</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Aput0648|CDS|CDS</td><td>0.5</td><td>0.2</td><td>11.594</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BVU2340|CDS|hypothetical</td><td>59.5</td><td>17.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Rum07220|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BactD23789|CDS|CDS</td><td>1.8</td><td>0.5</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>b3038|CDS|predicted</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Eub4356|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bdor0502|CDS|CDS</td><td>21.0</td><td>6.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Rum01499|CDS|CDS</td><td>14.0</td><td>4.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bste0766|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Par2433|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Msm1055|CDS|coenzyme</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Clo02431|CDS|CDS</td><td>14.0</td><td>4.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Clo02072|CDS|CDS</td><td>14.0</td><td>4.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Pmer2612|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Cbar0305|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Fae05910|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Clo08419|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bpse0864|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Clo07310|CDS|CDS</td><td>21.0</td><td>6.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac10054|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Ali1230|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Rum07214|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Clo06590|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Rum06945|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae10797|CDS|CDS</td><td>10.5</td><td>3.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Csci3403|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bxyl3820|CDS|CDS</td><td>1.8</td><td>0.5</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>b3247|CDS|ribonuclease</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bste3163|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Par1622|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BactD23409|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Bac7667|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Pmer1296|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>b2319|CDS|predicted</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BDI3889|CDS|conserved</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Msm0883|CDS|orotate</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>ShigspD91340|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac07957|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Cbar0569|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Pmer3064|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>EUBREC2228|CDS|RecA</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae04866|CDS|CDS</td><td>14.0</td><td>4.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>BVU0543|CDS|putative</td><td>56.0</td><td>16.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Msmi741494|CDS|CDS</td><td>1.8</td><td>0.5</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>ShigspD92449|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Fae05171|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Met1224|CDS|CDS</td><td>1.8</td><td>0.5</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Rtor2091|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Fae00175|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>b1268|CDS|predicted</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Ali0014|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>EUBREC3100|CDS|mrp</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bcap2089|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Bif1396|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae01893|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae08306|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Eeli1338|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac06322|CDS|CDS</td><td>1.8</td><td>0.5</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Msm0686|CDS|acetolactate</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Dfor0628|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac10900|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>EUBREC1905|CDS|DnaJ</td><td>10.5</td><td>3.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bste2231|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae19886|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Rum13721|CDS|CDS</td><td>14.0</td><td>4.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>HPAG11529|CDS|undecaprenyl</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Even0032|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac07809|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bbre1603|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Bxyl0626|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Par0598|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Buni3484|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Msmi741490|CDS|CDS</td><td>1.8</td><td>0.5</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Bac7738|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>Dfor1505|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Bac6422|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Par0725|CDS|CDS</td><td>3.5</td><td>1.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac04313|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS29Bac04216|CDS|CDS</td><td>14.0</td><td>4.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
<tr><td>TS28Fae19390|CDS|CDS</td><td>7.0</td><td>2.0</td><td>11.574</td><td>NA</td><td>NA</td><td>hypothetical protein</td></tr>
</table>

Acol1288|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
TS28Rum04826|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
TS28Ali1378|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
TS28Rum16145|CDS|CDS	3.5	1.0	11.574	NA	NA	hypothetical protein
RintL12691|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
Cbar1947|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
TS28Par2008|CDS|CDS	3.5	1.0	11.574	NA	NA	hypothetical protein
Msm0659|CDS|hypothetical	1.8	0.5	11.574	NA	NA	hypothetical protein
TS28Fae15131|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
TS29Rum05175|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
TS28Col0173|CDS|CDS	7.0	2.0	11.574	NA	NA	hypothetical protein
Bxyl4218|CDS|CDS	3.5	1.0	11.574	NA	NA	hypothetical protein
BT1103|CDS|RNA	1.8	0.5	11.574	NA	NA	hypothetical protein
BVU0251|CDS|glutamate	70.7	20.5	11.410	NA	NA	hypothetical protein
BactD12781|CDS|CDS	6.9	2.0	11.397	NA	NA	hypothetical protein
Msm1625|CDS|thiol:fumarate	4.6	1.3	11.368	NA	NA	hypothetical protein
Buni0658|CDS|CDS	10.3	3.0	11.358	NA	NA	hypothetical protein
Msmi740223|CDS|CDS	2.0	0.6	11.338	NA	NA	hypothetical protein
Msmi751456|CDS|CDS	2.0	0.6	11.338	NA	NA	hypothetical protein
BVU3241|CDS|phosphoserine	37.7	11.0	11.324	NA	NA	hypothetical protein
BVU0016|CDS|two-component	133.5	39.0	11.320	NA	NA	hypothetical protein
BVU3907|CDS|hypothetical	32.5	9.5	11.313	NA	NA	hypothetical protein
TS28Col0352|CDS|CDS	54.7	16.0	11.299	NA	NA	hypothetical protein
Bste1338|CDS|CDS	51.0	15.0	11.244	NA	NA	hypothetical protein
EUBREC3019|CDS|hypothetical	17.0	5.0	11.244	NA	NA	hypothetical protein
TS28Fae13589|CDS|CDS	17.0	5.0	11.244	NA	NA	hypothetical protein
BVU0988|CDS|2-amino-3-ketobutyrate	59.5	17.5	11.244	NA	NA	hypothetical protein
Msm1529|CDS|putative	8.5	2.5	11.244	NA	NA	hypothetical protein
BVU0981|CDS|2-amino-3-ketobutyrate	59.5	17.5	11.244	NA	NA	hypothetical protein
TS28Fae06397|CDS|CDS	17.0	5.0	11.244	NA	NA	hypothetical protein
BFych462845|CDS|hypothetical	10.7	3.2	11.209	NA	NA	hypothetical protein
TS28Ali0298|CDS|CDS	88.0	26.0	11.193	NA	NA	hypothetical protein
TS28Rum10997|CDS|CDS	27.0	8.0	11.161	NA	NA	hypothetical protein
TS28Fae19847|CDS|CDS	6.8	2.0	11.161	NA	NA	hypothetical protein
TS28Clo08465|CDS|CDS	27.0	8.0	11.161	NA	NA	hypothetical protein
TS28Par0404|CDS|CDS	13.5	4.0	11.161	NA	NA	hypothetical protein
Msm0707|CDS|predicted	4.2	1.3	11.111	NA	NA	hypothetical protein
TS28Ali1354|CDS|CDS	84.0	25.0	11.111	NA	NA	hypothetical protein
TS28Bac6680|CDS|CDS	70.5	21.0	11.102	NA	NA	hypothetical protein
BVU0799|CDS|30S	66.5	19.8	11.091	NA	NA	hypothetical protein
Msmi740013|CDS|CDS	8.9	2.7	11.058	NA	NA	hypothetical protein
Msmi741320|CDS|CDS	1.7	0.5	11.023	NA	NA	hypothetical protein
Bxyl0905|CDS|CDS	1.7	0.5	11.023	NA	NA	hypothetical protein
Msmi751577|CDS|CDS	3.3	1.0	11.023	NA	NA	hypothetical protein
Bint2002|CDS|CDS	3.3	1.0	11.023	NA	NA	hypothetical protein
Pmer3221|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
TS28Fae00145|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
BactD13115|CDS|CDS	1.7	0.5	11.023	NA	NA	hypothetical protein
TS28Rum13199|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
TS28Rum13115|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS28RumUnc1425|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
Bxyl1368|CDS|CDS	1.7	0.5	11.023	NA	NA	hypothetical protein
Even1782|CDS|CDS	20.0	6.0	11.023	NA	NA	hypothetical protein
FpraM2120422|CDS|CDS	1.7	0.5	11.023	NA	NA	hypothetical protein
BVU2994|CDS|ATP	10.0	3.0	11.023	NA	NA	hypothetical protein
TS29Bif3258|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS28Fae10978|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
CspM6210548|CDS|CDS	3.3	1.0	11.023	NA	NA	hypothetical protein
TS29Rum03114|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
stu0164|CDS|ABC	1.7	0.5	11.023	NA	NA	hypothetical protein
BactD10434|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
b2996|CDS|hydrogenase	3.3	1.0	11.023	NA	NA	hypothetical protein
CspSS21448|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS29Bac07908|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
BLD0921|CDS|MalE-type	10.0	3.0	11.023	NA	NA	hypothetical protein
TS28Rum13096|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
Bste2906|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS28Rum06350|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
TS29Par836|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
Eeli1384|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
TS29Fae03142|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS28Bac8124|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
TS28Ali1145|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
Msm1781|CDS|hypothetical	6.7	2.0	11.023	NA	NA	hypothetical protein
Bdor1537|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS28Bif4659|CDS|CDS	5.0	1.5	11.023	NA	NA	hypothetical protein
TS28Ali0094|CDS|CDS	40.0	12.0	11.023	NA	NA	hypothetical protein
TS28Clo02517|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
str0164|CDS|ABC	1.7	0.5	11.023	NA	NA	hypothetical protein
Aput0975|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
Aput0549|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
Bdor1552|CDS|CDS	30.0	9.0	11.023	NA	NA	hypothetical protein
TS28Bac6889|CDS|CDS	10.0	3.0	11.023	NA	NA	hypothetical protein
BVU2268|CDS|hypothetical	11.7	3.5	11.023	NA	NA	hypothetical protein
EFER3760|CDS|thiamin	3.3	1.0	11.023	NA	NA	hypothetical protein
TS29Eub2143|CDS|CDS	3.3	1.0	11.023	NA	NA	hypothetical protein
BactD22959|CDS|CDS	3.3	1.0	11.023	NA	NA	hypothetical protein
TS28Clo00339|CDS|CDS	3.3	1.0	11.023	NA	NA	hypothetical protein
Bado0890|CDS|CDS	1.7	0.5	11.023	NA	NA	hypothetical protein
STER1622|CDS|pyruvate	1.7	0.5	11.023	NA	NA	hypothetical protein
Msm0620|CDS|50S	3.1	0.9	11.003	NA	NA	hypothetical protein
TS28Met1808|CDS|CDS	3.1	0.9	11.003	NA	NA	hypothetical protein

Msm1337|CDS|serine	6.7	2.0	10.996	NA	NA	hypothetical protein
Bdor3601|CDS|CDS	22.2	6.7	10.996	NA	NA	hypothetical protein
EUBREC0477|CDS|galactose/glucose-binding	18.3	5.5	10.973	NA	NA	hypothetical protein
TS28Ali2375|CDS|CDS	63.0	19.0	10.965	NA	NA	hypothetical protein
BVU2537|CDS|chorismate	54.7	16.5	10.956	NA	NA	hypothetical protein
Msm1152|CDS|hypothetical	4.4	1.3	10.954	NA	NA	hypothetical protein
Bdor3069|CDS|CDS	21.5	6.5	10.938	NA	NA	hypothetical protein
Bthe3733474|CDS|CDS	6.6	2.0	10.913	NA	NA	hypothetical protein
Bcoprop2838|CDS|CDS	6.6	2.0	10.913	NA	NA	hypothetical protein
TS29Fae06535|CDS|CDS	3.3	1.0	10.913	NA	NA	hypothetical protein
Robe1900|CDS|CDS	61.0	18.5	10.904	NA	NA	hypothetical protein
BL1799|CDS|hypothetical	3.8	1.2	10.866	NA	NA	hypothetical protein
Bste1394|CDS|CDS	16.4	5.0	10.847	NA	NA	hypothetical protein
TS29Bac11470|CDS|CDS	4.9	1.5	10.839	NA	NA	hypothetical protein
BactD13580|CDS|CDS	4.9	1.5	10.839	NA	NA	hypothetical protein
Bple1077|CDS|CDS	3.9	1.2	10.839	NA	NA	hypothetical protein
BWH21661|CDS|CDS	3.9	1.2	10.839	NA	NA	hypothetical protein
Bcoproc0096|CDS|CDS	3.9	1.2	10.839	NA	NA	hypothetical protein
Bcoproc0192|CDS|CDS	3.9	1.2	10.839	NA	NA	hypothetical protein
BVU2329|CDS|chaperone	24.5	7.5	10.803	NA	NA	hypothetical protein
TS28Met1053|CDS|CDS	9.3	2.8	10.796	NA	NA	hypothetical protein
BactD23268|CDS|CDS	9.8	3.0	10.748	NA	NA	hypothetical protein
TS28Rum03768|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
TS28Bac8382|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
TS28Fae12196|CDS|CDS	3.3	1.0	10.748	NA	NA	hypothetical protein
Ehal1458|CDS|CDS	13.0	4.0	10.748	NA	NA	hypothetical protein
TS29Fae01275|CDS|CDS	13.0	4.0	10.748	NA	NA	hypothetical protein
BVU3860|CDS|glycosyltransferase	6.5	2.0	10.748	NA	NA	hypothetical protein
TS28Clo05849|CDS|CDS	13.0	4.0	10.748	NA	NA	hypothetical protein
Bova3645|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
Ehal1995|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
BVU3635|CDS|50S	6.5	2.0	10.748	NA	NA	hypothetical protein
Bdor2130|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
M23Apeg881|CDS|Translation	6.5	2.0	10.748	NA	NA	hypothetical protein
TS28Bac7712|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
Bdor2614|CDS|CDS	6.5	2.0	10.748	NA	NA	hypothetical protein
TS29Rum01213|CDS|CDS	13.0	4.0	10.748	NA	NA	hypothetical protein
Msm1713|CDS|predicted	1.1	0.3	10.748	NA	NA	hypothetical protein
Msmi740739|CDS|CDS	6.8	2.1	10.714	NA	NA	hypothetical protein
Bova0264|CDS|CDS	4.9	1.5	10.692	NA	NA	hypothetical protein
BactD23742|CDS|CDS	4.9	1.5	10.692	NA	NA	hypothetical protein
TS28Bac8216|CDS|CDS	32.3	10.0	10.692	NA	NA	hypothetical protein
Msm0997|CDS|dihydroorotase,	7.0	2.2	10.684	NA	NA	hypothetical protein
TS28Bac6866|CDS|CDS	54.3	16.8	10.674	NA	NA	hypothetical protein
Bdor3225|CDS|CDS	64.5	20.0	10.665	NA	NA	hypothetical protein
TS28Rum03202|CDS|CDS	6.4	2.0	10.610	NA	NA	hypothetical protein
Msm0561|CDS|formate	6.4	2.0	10.610	NA	NA	hypothetical protein
TS28Par2305|CDS|CDS	8.0	2.5	10.582	NA	NA	hypothetical protein
Msm0307|CDS|sugar	1.6	0.5	10.582	NA	NA	hypothetical protein
BactD21983|CDS|CDS	8.0	2.5	10.582	NA	NA	hypothetical protein
BFych462788|CDS|tyrosine	0.8	0.3	10.582	NA	NA	hypothetical protein
Bova2652|CDS|CDS	8.0	2.5	10.582	NA	NA	hypothetical protein
TS28Par2453|CDS|CDS	8.0	2.5	10.582	NA	NA	hypothetical protein
TS28Bif0948|CDS|CDS	2.7	0.8	10.582	NA	NA	hypothetical protein
Bpse1839|CDS|CDS	2.7	0.8	10.582	NA	NA	hypothetical protein
Msm0102|CDS|methionine	5.3	1.7	10.582	NA	NA	hypothetical protein
Msmi751507|CDS|CDS	4.3	1.3	10.541	NA	NA	hypothetical protein
TS29Bac03564|CDS|CDS	4.3	1.3	10.541	NA	NA	hypothetical protein
Bova2164|CDS|CDS	4.3	1.3	10.541	NA	NA	hypothetical protein
Bxyl2122|CDS|CDS	4.3	1.3	10.541	NA	NA	hypothetical protein
TS28Ali1642|CDS|CDS	51.0	16.0	10.541	NA	NA	hypothetical protein
Rgna0966|CDS|CDS	3.7	1.2	10.528	NA	NA	hypothetical protein
BVU2762|CDS|hypothetical	17.5	5.5	10.522	NA	NA	hypothetical protein
TS28Ali2243|CDS|CDS	35.0	11.0	10.522	NA	NA	hypothetical protein
Msm1626|CDS|predicted	1.9	0.6	10.488	NA	NA	hypothetical protein
Msm1174|CDS|heat	3.2	1.0	10.472	NA	NA	hypothetical protein
b3902|CDS|rhamnulose-1-phosphate	3.2	1.0	10.472	NA	NA	hypothetical protein
TS28Fae00848|CDS|CDS	9.5	3.0	10.472	NA	NA	hypothetical protein
TS28Par2283|CDS|CDS	9.5	3.0	10.472	NA	NA	hypothetical protein
TS28Dor0805|CDS|CDS	38.0	12.0	10.472	NA	NA	hypothetical protein
TS28Bac0256|CDS|CDS	9.5	3.0	10.472	NA	NA	hypothetical protein
Pmer0600|CDS|CDS	19.0	6.0	10.472	NA	NA	hypothetical protein
TS28Clo08427|CDS|CDS	19.0	6.0	10.472	NA	NA	hypothetical protein
L0368|CDS|elongation	3.2	1.0	10.472	NA	NA	hypothetical protein
TS28Rum14110|CDS|CDS	19.0	6.0	10.472	NA	NA	hypothetical protein
Msm0427|CDS|DNA	6.3	2.0	10.472	NA	NA	hypothetical protein
TS28Clo03127|CDS|CDS	98.0	31.0	10.454	NA	NA	hypothetical protein
Msmi751277|CDS|CDS	3.7	1.2	10.440	NA	NA	hypothetical protein
TS28Ali0766|CDS|CDS	101.0	32.0	10.438	NA	NA	hypothetical protein
BVU2086|CDS|hypothetical	53.5	17.0	10.407	NA	NA	hypothetical protein
TS28Clo09194|CDS|CDS	44.0	14.0	10.393	NA	NA	hypothetical protein
TS28Ali0894|CDS|CDS	22.0	7.0	10.393	NA	NA	hypothetical protein
BVU2608|CDS|myo-inositol-1-phosphate	15.7	5.0	10.362	NA	NA	hypothetical protein
BVU1163|CDS|putative	23.5	7.5	10.362	NA	NA	hypothetical protein
TS29Rum08907|CDS|CDS	7.8	2.5	10.362	NA	NA	hypothetical protein
BVU3880|CDS|aspartate	28.2	9.0	10.349	NA	NA	hypothetical protein
BVU1767|CDS|glycoside	4.2	1.3	10.334	NA	NA	hypothetical protein
TS28Rum12603|CDS|CDS	25.0	8.0	10.334	NA	NA	hypothetical protein
TS28Par1118|CDS|CDS	12.5	4.0	10.334	NA	NA	hypothetical protein
TS29Bac09496|CDS|CDS	10.9	3.5	10.330	NA	NA	hypothetical protein
TS28Met0874|CDS|CDS	40.5	13.0	10.302	NA	NA	hypothetical protein
BVU0384|CDS|3-oxoacyl-[acyl-carrier	18.7	6.0	10.288	NA	NA	hypothetical protein

Bdor0470|CDS|CDS	14.0	4.5	10.288	NA	NA	hypothetical protein
TS28Ali0428|CDS|CDS	90.0	29.0	10.263	NA	NA	hypothetical protein
FpraM2120623|CDS|CDS	28.9	9.3	10.246	NA	NA	hypothetical protein
Msm0313|CDS|[NiFe]-hydrogenase-3-type	5.0	1.6	10.228	NA	NA	hypothetical protein
BVU4084|CDS|hypothetical	37.0	12.0	10.196	NA	NA	hypothetical protein
TS28Clo00072|CDS|CDS	40.0	13.0	10.175	NA	NA	hypothetical protein
BVU2313|CDS|2-ketoisovalerate	44.5	14.5	10.149	NA	NA	hypothetical protein
BVU3634|CDS|50S	27.5	9.0	10.105	NA	NA	hypothetical protein
TS29Fae08595|CDS|CDS	36.5	12.0	10.059	NA	NA	hypothetical protein
BVU1319|CDS|phosphate	13.7	4.5	10.043	NA	NA	hypothetical protein
TS29Eub2152|CDS|CDS	0.5	16.6	0.100	NA	NA	hypothetical protein
Clep1858|CDS|CDS	3.0	99.5	0.100	NA	NA	hypothetical protein
Bint2023|CDS|CDS	0.3	11.1	0.099	NA	NA	hypothetical protein
TS28Bac4061|CDS|CDS	3.0	100.0	0.099	NA	NA	hypothetical protein
EUBREC2012|CDS|hypothetical	5.5	183.3	0.099	NA	NA	hypothetical protein
EUBREC1182|CDS|hypothetical	5.5	183.3	0.099	NA	NA	hypothetical protein
BVU2880|CDS|formate	1.0	33.5	0.099	NA	NA	hypothetical protein
FpraM2120295|CDS|CDS	2.0	67.0	0.099	NA	NA	hypothetical protein
BVU0340|CDS|putative	1.0	33.5	0.099	NA	NA	hypothetical protein
EUBREC3573|CDS|peptidase,	0.3	11.2	0.099	NA	NA	hypothetical protein
TS28Eub7929|CDS|CDS	2.5	84.0	0.098	NA	NA	hypothetical protein
BVU2229|CDS|glycoside	1.0	33.7	0.098	NA	NA	hypothetical protein
TS28Clo00931|CDS|CDS	3.0	101.0	0.098	NA	NA	hypothetical protein
EUBREC0465|CDS|sensor	1.5	50.5	0.098	NA	NA	hypothetical protein
TS28Fae19036|CDS|CDS	1.5	50.5	0.098	NA	NA	hypothetical protein
EUBREC2543|CDS|glutamine	2.0	67.5	0.098	NA	NA	hypothetical protein
Robe2661|CDS|CDS	1.0	33.8	0.098	NA	NA	hypothetical protein
BL1707|CDS|hypothetical	0.3	8.5	0.097	NA	NA	hypothetical protein
TS28Fae17383|CDS|CDS	0.5	17.0	0.097	NA	NA	hypothetical protein
BVU3044|CDS|hypothetical	0.5	17.0	0.097	NA	NA	hypothetical protein
TS29Rum18921|CDS|CDS	2.0	68.0	0.097	NA	NA	hypothetical protein
TS29Fae00076|CDS|CDS	1.0	34.0	0.097	NA	NA	hypothetical protein
TS29Fae03980|CDS|CDS	0.5	17.0	0.097	NA	NA	hypothetical protein
TS28Bac6304|CDS|CDS	1.0	34.0	0.097	NA	NA	hypothetical protein
TS28Fae11970|CDS|CDS	0.5	17.0	0.097	NA	NA	hypothetical protein
TS29Fae05304|CDS|CDS	0.5	17.0	0.097	NA	NA	hypothetical protein
TS29Fae01831|CDS|CDS	0.3	8.5	0.097	NA	NA	hypothetical protein
EUBREC1965|CDS|YjeF-like	1.0	34.0	0.097	NA	NA	hypothetical protein
TS28Clo01072|CDS|CDS	12.0	410.0	0.097	NA	NA	hypothetical protein
Bfra31120119|CDS|CDS	0.4	13.2	0.097	NA	NA	hypothetical protein
PRABACTJOHN1627|CDS|CDS	0.4	13.2	0.097	NA	NA	hypothetical protein
Bste0891|CDS|CDS	0.4	13.2	0.097	NA	NA	hypothetical protein
Cbol3992|CDS|CDS	0.4	13.8	0.096	NA	NA	hypothetical protein
TS28Bac0395|CDS|CDS	2.7	92.0	0.096	NA	NA	hypothetical protein
TS28Eub0880|CDS|CDS	2.0	69.0	0.096	NA	NA	hypothetical protein
TS28Eub6143|CDS|CDS	2.0	69.0	0.096	NA	NA	hypothetical protein
TS28Fae17554|CDS|CDS	0.3	11.5	0.096	NA	NA	hypothetical protein
TS29Bac09962|CDS|CDS	1.2	41.5	0.096	NA	NA	hypothetical protein
FpraM2122486|CDS|CDS	1.2	41.9	0.095	NA	NA	hypothetical protein
BVU1274|CDS|aminopeptidase	1.5	52.3	0.095	NA	NA	hypothetical protein
Ccom1638|CDS|CDS	0.3	9.0	0.095	NA	NA	hypothetical protein
BFnctc3865|CDS|fusion	0.1	5.0	0.094	NA	NA	hypothetical protein
TS28Clo00741|CDS|CDS	3.0	105.0	0.094	NA	NA	hypothetical protein
TS29Fae08072|CDS|CDS	0.5	17.5	0.094	NA	NA	hypothetical protein
TS28Fae14830|CDS|CDS	0.5	17.5	0.094	NA	NA	hypothetical protein
TS29Rum15490|CDS|CDS	0.5	17.5	0.094	NA	NA	hypothetical protein
EUBREC3434|CDS|DNA/RNA	2.0	70.0	0.094	NA	NA	hypothetical protein
TS28Rum14592|CDS|CDS	0.5	17.5	0.094	NA	NA	hypothetical protein
Bste1778|CDS|CDS	0.5	17.5	0.094	NA	NA	hypothetical protein
TS28Col0454|CDS|CDS	1.0	35.0	0.094	NA	NA	hypothetical protein
BVU2245|CDS|hypothetical	0.5	17.5	0.094	NA	NA	hypothetical protein
TS29Bac08027|CDS|CDS	0.5	17.5	0.094	NA	NA	hypothetical protein
TS29Bac08012|CDS|CDS	0.7	23.5	0.094	NA	NA	hypothetical protein
Bste1789|CDS|CDS	0.7	23.5	0.094	NA	NA	hypothetical protein
TS28Clo00999|CDS|CDS	4.0	141.0	0.094	NA	NA	hypothetical protein
TS28Bac5136|CDS|CDS	0.7	23.5	0.094	NA	NA	hypothetical protein
TS28Eub4255|CDS|CDS	3.0	106.0	0.094	NA	NA	hypothetical protein
Cnex2281|CDS|CDS	0.3	10.1	0.093	NA	NA	hypothetical protein
Rbro1727|CDS|CDS	0.3	10.1	0.093	NA	NA	hypothetical protein
Ceut2207|CDS|CDS	0.3	10.1	0.093	NA	NA	hypothetical protein
Dfor2026|CDS|CDS	0.3	10.1	0.093	NA	NA	hypothetical protein
TS29Rum01264|CDS|CDS	0.3	10.1	0.093	NA	NA	hypothetical protein
TS28Rum13917|CDS|CDS	1.0	35.5	0.093	NA	NA	hypothetical protein
TS28Eub6745|CDS|CDS	2.0	71.0	0.093	NA	NA	hypothetical protein
FpraM2121174|CDS|CDS	1.0	35.5	0.093	NA	NA	hypothetical protein
TS28Bac8472|CDS|CDS	1.0	35.5	0.093	NA	NA	hypothetical protein
BLD0787|CDS|Cation	0.3	8.9	0.093	NA	NA	hypothetical protein
TS28Fae21303|CDS|CDS	1.0	36.0	0.092	NA	NA	hypothetical protein
TS28Clo00992|CDS|CDS	1.0	36.0	0.092	NA	NA	hypothetical protein
TS28Fae16975|CDS|CDS	1.0	36.0	0.092	NA	NA	hypothetical protein
TS28Fae12953|CDS|CDS	0.5	18.0	0.092	NA	NA	hypothetical protein
TS28Ali0960|CDS|CDS	1.0	36.0	0.092	NA	NA	hypothetical protein
TS28Bac7592|CDS|CDS	0.5	18.0	0.092	NA	NA	hypothetical protein
BVU2387|CDS|putative	0.5	18.0	0.092	NA	NA	hypothetical protein
Bdor4008|CDS|CDS	1.5	54.0	0.092	NA	NA	hypothetical protein
TS28Fae17291|CDS|CDS	0.5	18.0	0.092	NA	NA	hypothetical protein
FpraM2120961|CDS|CDS	0.5	18.0	0.092	NA	NA	hypothetical protein
TS28Ali2208|CDS|CDS	1.0	36.0	0.092	NA	NA	hypothetical protein
TS28Clo01681|CDS|CDS	2.0	72.0	0.092	NA	NA	hypothetical protein
TS28Bac8335|CDS|CDS	0.3	12.0	0.092	NA	NA	hypothetical protein
TS28Clo01828|CDS|CDS	0.3	12.0	0.092	NA	NA	hypothetical protein
FpraM2120898|CDS|CDS	5.0	180.5	0.092	NA	NA	hypothetical protein

TS28Clo01074|CDS|CDS	6.0	217.0	0.091	NA	NA	hypothetical protein
BVU2574|CDS|valyl-tRNA	1.5	54.3	0.091	NA	NA	hypothetical protein
EUBREC2996|CDS|alginate	1.0	36.5	0.091	NA	NA	hypothetical protein
Hfil2137|CDS|CDS	0.2	7.3	0.090	NA	NA	hypothetical protein
Dlon2156|CDS|CDS	0.7	24.7	0.089	NA	NA	hypothetical protein
TS28Fae08745|CDS|CDS	1.0	37.0	0.089	NA	NA	hypothetical protein
TS28Fae22548|CDS|CDS	0.5	18.5	0.089	NA	NA	hypothetical protein
RintL10789|CDS|CDS	0.5	18.5	0.089	NA	NA	hypothetical protein
TS28Eub7903|CDS|CDS	1.0	37.0	0.089	NA	NA	hypothetical protein
BVU1253|CDS|putative	0.5	18.5	0.089	NA	NA	hypothetical protein
BVU1130|CDS|multiple	1.0	37.0	0.089	NA	NA	hypothetical protein
TS28Eub6997|CDS|CDS	1.0	37.0	0.089	NA	NA	hypothetical protein
TS28Clo01578|CDS|CDS	3.0	111.0	0.089	NA	NA	hypothetical protein
BFych460108|CDS|hypothetical	0.7	24.7	0.089	NA	NA	hypothetical protein
EUBREC1095|CDS|hypothetical	3.5	130.0	0.089	NA	NA	hypothetical protein
TS29Fae09750|CDS|CDS	2.0	74.5	0.089	NA	NA	hypothetical protein
TS29Fae07130|CDS|CDS	0.8	28.0	0.089	NA	NA	hypothetical protein
TS28Fae16906|CDS|CDS	0.7	25.0	0.088	NA	NA	hypothetical protein
TS28Clo00445|CDS|CDS	1.0	37.5	0.088	NA	NA	hypothetical protein
Bdor0336|CDS|CDS	0.3	12.5	0.088	NA	NA	hypothetical protein
BVU3633|CDS|HPr(Ser)	0.3	12.5	0.088	NA	NA	hypothetical protein
CspSS21812|CDS|CDS	0.9	32.0	0.088	NA	NA	hypothetical protein
TS28Eub6783|CDS|CDS	1.5	56.5	0.088	NA	NA	hypothetical protein
TS28Bac7122|CDS|CDS	1.0	37.7	0.088	NA	NA	hypothetical protein
TS28Fae22192|CDS|CDS	2.0	76.0	0.087	NA	NA	hypothetical protein
EUBREC1119|CDS|glycine	1.0	38.0	0.087	NA	NA	hypothetical protein
TS28Rum02391|CDS|CDS	1.0	38.0	0.087	NA	NA	hypothetical protein
TS28Eub4655|CDS|CDS	1.0	38.0	0.087	NA	NA	hypothetical protein
EUBREC2391|CDS|hypothetical	1.0	38.0	0.087	NA	NA	hypothetical protein
EUBREC2602|CDS|hypothetical	1.0	38.0	0.087	NA	NA	hypothetical protein
BVU1011|CDS|3-oxoacyl-[acyl-carrier	0.5	19.0	0.087	NA	NA	hypothetical protein
TS28Bac5238|CDS|CDS	0.5	19.0	0.087	NA	NA	hypothetical protein
BVU1256|CDS|hypothetical	0.5	19.0	0.087	NA	NA	hypothetical protein
TS29Bac06574|CDS|CDS	1.0	38.0	0.087	NA	NA	hypothetical protein
TS28Clo00878|CDS|CDS	2.0	76.0	0.087	NA	NA	hypothetical protein
EUBREC3500|CDS|hypothetical	1.0	38.2	0.087	NA	NA	hypothetical protein
TS29Fae09519|CDS|CDS	1.5	57.5	0.086	NA	NA	hypothetical protein
TS28Eub8336|CDS|CDS	1.5	57.5	0.086	NA	NA	hypothetical protein
TS28Bac6904|CDS|CDS	1.0	38.5	0.086	NA	NA	hypothetical protein
FpraM2120591|CDS|CDS	2.0	77.0	0.086	NA	NA	hypothetical protein
TS28Eub8527|CDS|CDS	1.0	38.5	0.086	NA	NA	hypothetical protein
TS28Clo01077|CDS|CDS	2.0	77.0	0.086	NA	NA	hypothetical protein
BVU3651|CDS|tRNA	1.0	38.5	0.086	NA	NA	hypothetical protein
TS28Fae11127|CDS|CDS	1.3	51.5	0.086	NA	NA	hypothetical protein
BL0724|CDS|threonyl-tRNA	0.2	6.5	0.085	NA	NA	hypothetical protein
FpraM2120610|CDS|CDS	0.5	19.5	0.085	NA	NA	hypothetical protein
TS28Ali2018|CDS|CDS	1.0	39.0	0.085	NA	NA	hypothetical protein
TS29Fae06141|CDS|CDS	0.5	19.5	0.085	NA	NA	hypothetical protein
TS28Eub4169|CDS|CDS	0.5	19.5	0.085	NA	NA	hypothetical protein
BVU2935|CDS|hypothetical	1.0	39.0	0.085	NA	NA	hypothetical protein
TS28Bac6294|CDS|CDS	5.0	195.0	0.085	NA	NA	hypothetical protein
TS28Fae20102|CDS|CDS	1.0	39.0	0.085	NA	NA	hypothetical protein
EUBREC0433|CDS|50S	0.5	19.5	0.085	NA	NA	hypothetical protein
TS28Clo00874|CDS|CDS	2.0	78.0	0.085	NA	NA	hypothetical protein
TS28Fae10688|CDS|CDS	0.5	19.5	0.085	NA	NA	hypothetical protein
TS28Bac6511|CDS|CDS	0.3	13.0	0.085	NA	NA	hypothetical protein
TS28Rum06775|CDS|CDS	0.3	13.0	0.085	NA	NA	hypothetical protein
TS28Bac5945|CDS|CDS	3.0	117.8	0.084	NA	NA	hypothetical protein
BVU1757|CDS|NADH	1.0	39.3	0.084	NA	NA	hypothetical protein
TS28Clo01570|CDS|CDS	3.0	118.0	0.084	NA	NA	hypothetical protein
TS28Clo01017|CDS|CDS	2.0	79.0	0.084	NA	NA	hypothetical protein
TS28Clo00902|CDS|CDS	2.0	79.0	0.084	NA	NA	hypothetical protein
EUBREC0308|CDS|cysteine	1.0	39.5	0.084	NA	NA	hypothetical protein
EUBREC3563|CDS|hypothetical	1.0	39.9	0.083	NA	NA	hypothetical protein
BFnctc1739|CDS|hypothetical	0.4	14.7	0.083	NA	NA	hypothetical protein
TS28Clo00759|CDS|CDS	1.0	40.0	0.083	NA	NA	hypothetical protein
TS28Eub8893|CDS|CDS	2.0	80.0	0.083	NA	NA	hypothetical protein
TS29Fae10148|CDS|CDS	2.0	80.0	0.083	NA	NA	hypothetical protein
TS28Clo01047|CDS|CDS	2.0	80.0	0.083	NA	NA	hypothetical protein
TS28Rum02014|CDS|CDS	0.5	20.0	0.083	NA	NA	hypothetical protein
TS28Eub6732|CDS|CDS	1.0	40.0	0.083	NA	NA	hypothetical protein
TS28Met1423|CDS|CDS	0.5	20.0	0.083	NA	NA	hypothetical protein
TS28Clo01136|CDS|CDS	1.0	40.0	0.083	NA	NA	hypothetical protein
TS28Eub4043|CDS|CDS	1.0	40.0	0.083	NA	NA	hypothetical protein
TS28Clo00460|CDS|CDS	1.0	40.0	0.083	NA	NA	hypothetical protein
TS28Clo02444|CDS|CDS	0.5	20.0	0.083	NA	NA	hypothetical protein
TS28Rum12055|CDS|CDS	0.5	20.0	0.083	NA	NA	hypothetical protein
BWH22235|CDS|CDS	0.4	14.8	0.082	NA	NA	hypothetical protein
EUBREC0002|CDS|DNA	1.0	40.5	0.082	NA	NA	hypothetical protein
TS28Eub8902|CDS|CDS	1.0	40.5	0.082	NA	NA	hypothetical protein
FpraM2120220|CDS|CDS	1.0	40.5	0.082	NA	NA	hypothetical protein
BVU0082|CDS|putative	1.0	40.5	0.082	NA	NA	hypothetical protein
TS28Clo01070|CDS|CDS	3.0	122.0	0.081	NA	NA	hypothetical protein
BVU2881|CDS|hypothetical	0.7	29.1	0.081	NA	NA	hypothetical protein
BVU1691|CDS|hypothetical	0.7	29.1	0.081	NA	NA	hypothetical protein
BL1757|CDS|hypothetical	1.0	40.8	0.081	NA	NA	hypothetical protein
TS28Clo01082|CDS|CDS	1.0	41.0	0.081	NA	NA	hypothetical protein
BVU2796|CDS|glucose-6-phosphate	1.0	41.0	0.081	NA	NA	hypothetical protein
BVU2556|CDS|acetohydroxyacid	0.5	20.5	0.081	NA	NA	hypothetical protein
EUBREC1453|CDS|putative	2.0	82.0	0.081	NA	NA	hypothetical protein
TS28Ali1207|CDS|CDS	1.0	41.0	0.081	NA	NA	hypothetical protein
TS29Fae08113|CDS|CDS	1.0	41.3	0.080	NA	NA	hypothetical protein

TS28Clo00764|CDS|CDS	3.0	124.0	0.080	NA	NA	hypothetical protein
BVU1565|CDS|conserved	0.3	10.3	0.080	NA	NA	hypothetical protein
TS28Bac7839|CDS|CDS	2.3	96.5	0.080	NA	NA	hypothetical protein
TS28Eub7436|CDS|CDS	1.0	41.5	0.080	NA	NA	hypothetical protein
TS28Bac1117|CDS|CDS	1.0	41.5	0.080	NA	NA	hypothetical protein
TS28Bac6293|CDS|CDS	4.0	166.0	0.080	NA	NA	hypothetical protein
TS28Clo00697|CDS|CDS	10.0	416.0	0.079	NA	NA	hypothetical protein
Rgna2288|CDS|CDS	2.2	91.7	0.079	NA	NA	hypothetical protein
Dfor0547|CDS|CDS	0.2	7.0	0.079	NA	NA	hypothetical protein
EUBREC0552|CDS|NLP/P60	0.5	21.0	0.079	NA	NA	hypothetical protein
EUBREC1838|CDS|metal	1.0	42.0	0.079	NA	NA	hypothetical protein
EUBREC3645|CDS|hypothetical	1.0	42.0	0.079	NA	NA	hypothetical protein
TS29Fae02179|CDS|CDS	0.5	21.0	0.079	NA	NA	hypothetical protein
TS28Fae16966|CDS|CDS	1.0	42.0	0.079	NA	NA	hypothetical protein
EUBREC0251|CDS|hypothetical	0.5	21.0	0.079	NA	NA	hypothetical protein
TS28Fae17816|CDS|CDS	0.5	21.0	0.079	NA	NA	hypothetical protein
TS28Clo00700|CDS|CDS	1.0	42.0	0.079	NA	NA	hypothetical protein
EUBREC3644|CDS|hypothetical	1.0	42.0	0.079	NA	NA	hypothetical protein
TS29Fae00811|CDS|CDS	0.5	21.0	0.079	NA	NA	hypothetical protein
Robe2900|CDS|CDS	0.5	21.0	0.079	NA	NA	hypothetical protein
BWH22245|CDS|CDS	0.3	10.5	0.079	NA	NA	hypothetical protein
EUBREC1766|CDS|putative	1.0	42.0	0.079	NA	NA	hypothetical protein
TS28Fae18334|CDS|CDS	0.3	14.0	0.079	NA	NA	hypothetical protein
Begg3361|CDS|CDS	0.1	2.1	0.079	NA	NA	hypothetical protein
TS28Eub3950|CDS|CDS	1.7	70.1	0.079	NA	NA	hypothetical protein
TS29Rum18282|CDS|CDS	0.9	36.0	0.078	NA	NA	hypothetical protein
RintL10352|CDS|CDS	1.8	74.0	0.078	NA	NA	hypothetical protein
Rbro0048|CDS|CDS	1.8	74.0	0.078	NA	NA	hypothetical protein
BWH22270|CDS|CDS	0.4	15.6	0.078	NA	NA	hypothetical protein
BVU3095|CDS|TonB-dependent	1.0	42.5	0.078	NA	NA	hypothetical protein
TS28Dor3147|CDS|CDS	1.0	42.5	0.078	NA	NA	hypothetical protein
Rbro0066|CDS|CDS	1.0	42.7	0.078	NA	NA	hypothetical protein
TS28Clo10465|CDS|CDS	1.0	42.7	0.078	NA	NA	hypothetical protein
TS28Eub5978|CDS|CDS	1.5	64.0	0.078	NA	NA	hypothetical protein
TS28Clo01592|CDS|CDS	1.0	43.0	0.077	NA	NA	hypothetical protein
TS28Eub7583|CDS|CDS	1.0	43.0	0.077	NA	NA	hypothetical protein
TS29Rum18619|CDS|CDS	0.5	21.5	0.077	NA	NA	hypothetical protein
TS28Eub8337|CDS|CDS	0.5	21.5	0.077	NA	NA	hypothetical protein
TS29Bac02045|CDS|CDS	0.5	21.5	0.077	NA	NA	hypothetical protein
TS28Clo01463|CDS|CDS	1.0	43.0	0.077	NA	NA	hypothetical protein
TS29Fae09566|CDS|CDS	0.5	21.5	0.077	NA	NA	hypothetical protein
Dfor2615|CDS|CDS	0.6	25.8	0.077	NA	NA	hypothetical protein
EUBREC0814|CDS|hypothetical	1.0	43.2	0.077	NA	NA	hypothetical protein
EUBREC2680|CDS|hypothetical	1.0	43.2	0.077	NA	NA	hypothetical protein
TS28Clo02095|CDS|CDS	1.0	43.5	0.076	NA	NA	hypothetical protein
TS28Met0193|CDS|CDS	0.3	14.6	0.076	NA	NA	hypothetical protein
EUBREC1221|CDS|NADH	2.0	89.0	0.076	NA	NA	hypothetical protein
TS28Fae21214|CDS|CDS	3.0	131.5	0.075	NA	NA	hypothetical protein
Bcro1276|CDS|CDS	2.0	88.0	0.075	NA	NA	hypothetical protein
BVU2928|CDS|hypothetical	0.5	22.0	0.075	NA	NA	hypothetical protein
TS28Fae16382|CDS|CDS	0.5	22.0	0.075	NA	NA	hypothetical protein
TS28Clo00824|CDS|CDS	3.0	132.0	0.075	NA	NA	hypothetical protein
TS28Fae14948|CDS|CDS	0.5	22.0	0.075	NA	NA	hypothetical protein
TS29Rum18587|CDS|CDS	0.5	22.0	0.075	NA	NA	hypothetical protein
TS28Fae21581|CDS|CDS	1.0	44.0	0.075	NA	NA	hypothetical protein
TS28Ali1393|CDS|CDS	1.0	44.0	0.075	NA	NA	hypothetical protein
TS28Clo01525|CDS|CDS	1.0	44.0	0.075	NA	NA	hypothetical protein
TS28Fae22354|CDS|CDS	0.5	22.0	0.075	NA	NA	hypothetical protein
TS29Fae06611|CDS|CDS	1.0	44.0	0.075	NA	NA	hypothetical protein
TS28Clo01622|CDS|CDS	2.0	88.5	0.075	NA	NA	hypothetical protein
TS28Clo00762|CDS|CDS	2.0	88.5	0.075	NA	NA	hypothetical protein
Buni1905|CDS|CDS	0.5	22.2	0.075	NA	NA	hypothetical protein
Even0433|CDS|CDS	1.0	44.5	0.074	NA	NA	hypothetical protein
TS28Eub4351|CDS|CDS	4.0	178.0	0.074	NA	NA	hypothetical protein
FpraM2121613|CDS|CDS	1.3	55.8	0.074	NA	NA	hypothetical protein
EUBREC0331|CDS|transketolase	0.8	33.5	0.074	NA	NA	hypothetical protein
BL0529|CDS|alpha-1,4-glucosidase;	0.3	11.2	0.074	NA	NA	hypothetical protein
BVU2644|CDS|hypothetical	1.0	45.0	0.073	NA	NA	hypothetical protein
EUBREC1887|CDS|two-component	0.5	22.5	0.073	NA	NA	hypothetical protein
TS28Eub5932|CDS|CDS	1.0	45.0	0.073	NA	NA	hypothetical protein
TS28Fae05485|CDS|CDS	1.0	45.0	0.073	NA	NA	hypothetical protein
TS28Eub4271|CDS|CDS	1.0	45.0	0.073	NA	NA	hypothetical protein
EUBREC2325|CDS|ABC	2.0	90.0	0.073	NA	NA	hypothetical protein
TS28Fae11740|CDS|CDS	1.0	45.0	0.073	NA	NA	hypothetical protein
BVU0144|CDS|aspartate	0.3	15.0	0.073	NA	NA	hypothetical protein
EUBREC2968|CDS|cation-transporting	1.5	68.0	0.073	NA	NA	hypothetical protein
EUBREC1410|CDS|hypothetical	0.5	22.7	0.073	NA	NA	hypothetical protein
Buni1620|CDS|CDS	0.5	23.0	0.072	NA	NA	hypothetical protein
TS29Fae02488|CDS|CDS	0.5	23.0	0.072	NA	NA	hypothetical protein
BVU1672|CDS|transcriptional	0.5	23.0	0.072	NA	NA	hypothetical protein
TS28Clo01534|CDS|CDS	2.0	92.0	0.072	NA	NA	hypothetical protein
TS28Rum14107|CDS|CDS	1.0	46.0	0.072	NA	NA	hypothetical protein
TS28Clo00591|CDS|CDS	2.0	92.0	0.072	NA	NA	hypothetical protein
TS28Met1710|CDS|CDS	0.5	23.0	0.072	NA	NA	hypothetical protein
TS28Clo00664|CDS|CDS	0.5	23.0	0.072	NA	NA	hypothetical protein
TS28Eub0817|CDS|CDS	0.5	23.0	0.072	NA	NA	hypothetical protein
FpraM2120797|CDS|CDS	1.0	46.0	0.072	NA	NA	hypothetical protein
TS28Clo01865|CDS|CDS	0.5	23.0	0.072	NA	NA	hypothetical protein
FpraM2120067|CDS|CDS	1.0	46.0	0.072	NA	NA	hypothetical protein
EUBREC0430|CDS|50S	0.5	23.0	0.072	NA	NA	hypothetical protein
TS28Eub0391|CDS|CDS	2.0	92.0	0.072	NA	NA	hypothetical protein
BL1637|CDS|hypothetical	0.3	15.3	0.072	NA	NA	hypothetical protein

TS29Clo4938|CDS|CDS	7.0	325.5	0.071	NA	NA	hypothetical protein
TS28Rum02094|CDS|CDS	2.0	93.0	0.071	NA	NA	hypothetical protein
BVU1098|CDS|hypothetical	0.5	23.5	0.070	NA	NA	hypothetical protein
Bdor4009|CDS|CDS	1.0	47.0	0.070	NA	NA	hypothetical protein
FpraM2121408|CDS|CDS	0.5	23.5	0.070	NA	NA	hypothetical protein
TS28Fae18390|CDS|CDS	1.0	47.0	0.070	NA	NA	hypothetical protein
Bint1992|CDS|CDS	1.0	47.0	0.070	NA	NA	hypothetical protein
TS28Fae16526|CDS|CDS	1.0	47.0	0.070	NA	NA	hypothetical protein
PRABACTJOHN1626|CDS|CDS	0.1	3.6	0.070	NA	NA	hypothetical protein
TS28Eub6361|CDS|CDS	1.0	47.4	0.070	NA	NA	hypothetical protein
TS29Rum21229|CDS|CDS	1.0	47.4	0.070	NA	NA	hypothetical protein
Robe0210|CDS|CDS	1.2	55.5	0.070	NA	NA	hypothetical protein
Dfor2556|CDS|CDS	0.2	11.0	0.069	NA	NA	hypothetical protein
Cbar1013|CDS|CDS	0.3	13.7	0.069	NA	NA	hypothetical protein
TS28Bif4317|CDS|CDS	1.0	47.8	0.069	NA	NA	hypothetical protein
TS29Fae05832|CDS|CDS	0.7	32.0	0.069	NA	NA	hypothetical protein
BWH22260|CDS|CDS	0.3	12.0	0.069	NA	NA	hypothetical protein
EUBREC1172|CDS|DNA	1.0	48.0	0.069	NA	NA	hypothetical protein
EUBREC1949|CDS|UDP-glucose	0.5	24.0	0.069	NA	NA	hypothetical protein
BWH25656|CDS|CDS	0.2	9.6	0.069	NA	NA	hypothetical protein
Bint0429|CDS|CDS	0.2	9.6	0.069	NA	NA	hypothetical protein
TS29Bac08050|CDS|CDS	1.0	48.0	0.069	NA	NA	hypothetical protein
BactD10023|CDS|CDS	0.2	9.6	0.069	NA	NA	hypothetical protein
TS29Bac08025|CDS|CDS	1.0	48.0	0.069	NA	NA	hypothetical protein
Bthe3735758|CDS|CDS	0.2	9.6	0.069	NA	NA	hypothetical protein
TS29Bac07259|CDS|CDS	0.2	9.6	0.069	NA	NA	hypothetical protein
BVU2011|CDS|hypothetical	0.5	24.0	0.069	NA	NA	hypothetical protein
TS29Fae00028|CDS|CDS	1.0	48.0	0.069	NA	NA	hypothetical protein
TS28Rum10925|CDS|CDS	1.0	48.0	0.069	NA	NA	hypothetical protein
BVU0159|CDS|hypothetical	1.7	80.5	0.068	NA	NA	hypothetical protein
TS29Fae06508|CDS|CDS	1.0	48.5	0.068	NA	NA	hypothetical protein
TS28Clo00949|CDS|CDS	2.0	97.0	0.068	NA	NA	hypothetical protein
EUBREC3341|CDS|hypothetical	1.0	48.5	0.068	NA	NA	hypothetical protein
TS29Rum17917|CDS|CDS	0.4	19.5	0.068	NA	NA	hypothetical protein
TS28Bac7169|CDS|CDS	0.7	32.5	0.068	NA	NA	hypothetical protein
TS29Eub0209|CDS|CDS	0.5	24.5	0.067	NA	NA	hypothetical protein
TS28Bac0071|CDS|CDS	1.0	49.0	0.067	NA	NA	hypothetical protein
TS28Fae07407|CDS|CDS	0.5	24.5	0.067	NA	NA	hypothetical protein
TS28Eub6443|CDS|CDS	1.0	49.0	0.067	NA	NA	hypothetical protein
TS28Fae12527|CDS|CDS	1.0	49.0	0.067	NA	NA	hypothetical protein
BLD1516|CDS|SalY-type	0.3	16.4	0.067	NA	NA	hypothetical protein
TS28Bac6946|CDS|CDS	2.0	99.0	0.067	NA	NA	hypothetical protein
TS28Clo00683|CDS|CDS	2.0	99.0	0.067	NA	NA	hypothetical protein
EUBREC0214|CDS|hypothetical	1.3	66.0	0.067	NA	NA	hypothetical protein
BVU2051|CDS|cofactor-independent	0.3	16.5	0.067	NA	NA	hypothetical protein
TS28Fae22430|CDS|CDS	0.7	33.3	0.066	NA	NA	hypothetical protein
TS28Fae00197|CDS|CDS	0.5	25.0	0.066	NA	NA	hypothetical protein
TS28Rum16284|CDS|CDS	1.0	50.0	0.066	NA	NA	hypothetical protein
TS28Eub5044|CDS|CDS	1.0	50.0	0.066	NA	NA	hypothetical protein
EUBREC2884|CDS|sugar	2.0	100.5	0.066	NA	NA	hypothetical protein
TS28Eub6500|CDS|CDS	1.0	50.5	0.065	NA	NA	hypothetical protein
EUBREC1412|CDS|glucuronide	1.0	50.8	0.065	NA	NA	hypothetical protein
Cmet1600|CDS|CDS	0.2	8.5	0.065	NA	NA	hypothetical protein
TS28Clo01010|CDS|CDS	1.0	51.0	0.065	NA	NA	hypothetical protein
TS28Eub7284|CDS|CDS	1.0	51.0	0.065	NA	NA	hypothetical protein
TS29Rum11749|CDS|CDS	0.3	17.0	0.065	NA	NA	hypothetical protein
TS28Rum11489|CDS|CDS	0.3	17.0	0.065	NA	NA	hypothetical protein
Bdor1706|CDS|CDS	1.0	51.2	0.065	NA	NA	hypothetical protein
Bste0823|CDS|CDS	0.2	11.1	0.065	NA	NA	hypothetical protein
Bste0014|CDS|CDS	0.2	11.1	0.065	NA	NA	hypothetical protein
TS28Clo01765|CDS|CDS	4.0	205.5	0.064	NA	NA	hypothetical protein
TS28Rum13599|CDS|CDS	1.0	51.5	0.064	NA	NA	hypothetical protein
BVU2193|CDS|TonB-dependent	1.0	51.5	0.064	NA	NA	hypothetical protein
TS28Rum14265|CDS|CDS	2.0	103.0	0.064	NA	NA	hypothetical protein
TS29Fae06530|CDS|CDS	0.5	25.8	0.064	NA	NA	hypothetical protein
BLD1743|CDS|Translation	0.5	26.0	0.064	NA	NA	hypothetical protein
TS28Eub5549|CDS|CDS	0.5	26.0	0.064	NA	NA	hypothetical protein
TS28Eub8390|CDS|CDS	4.0	208.5	0.063	NA	NA	hypothetical protein
TS28Eub8473|CDS|CDS	0.7	35.0	0.063	NA	NA	hypothetical protein
Ceut0015|CDS|CDS	0.4	21.0	0.063	NA	NA	hypothetical protein
TS28Fae18989|CDS|CDS	0.3	17.5	0.063	NA	NA	hypothetical protein
Dfor3094|CDS|CDS	0.7	36.6	0.063	NA	NA	hypothetical protein
Ccom2068|CDS|CDS	0.7	36.6	0.063	NA	NA	hypothetical protein
TS28Bif3723|CDS|CDS	1.3	70.2	0.063	NA	NA	hypothetical protein
EUBREC2580|CDS|valyl-tRNA	3.0	158.0	0.063	NA	NA	hypothetical protein
TS28Ali1768|CDS|CDS	0.5	26.5	0.062	NA	NA	hypothetical protein
EUBREC2250|CDS|UDP-N-acetylmuramoylalanine-D-glutamate	0.5	26.5	0.062	NA	NA	hypothetical protein
TS29Fae06618|CDS|CDS	0.5	26.5	0.062	NA	NA	hypothetical protein
TS28Bac0075|CDS|CDS	1.0	53.0	0.062	NA	NA	hypothetical protein
TS28Met0525|CDS|CDS	0.3	17.8	0.062	NA	NA	hypothetical protein
TS28Clo01654|CDS|CDS	3.0	160.0	0.062	NA	NA	hypothetical protein
TS28Fae12737|CDS|CDS	2.0	107.0	0.062	NA	NA	hypothetical protein
TS28Clo00447|CDS|CDS	3.0	161.0	0.062	NA	NA	hypothetical protein
TS28Met1428|CDS|CDS	0.8	40.3	0.061	NA	NA	hypothetical protein
RintL10087|CDS|CDS	0.3	15.4	0.061	NA	NA	hypothetical protein
Csci3164|CDS|CDS	0.3	15.4	0.061	NA	NA	hypothetical protein
TS29Fae07277|CDS|CDS	0.5	27.0	0.061	NA	NA	hypothetical protein
BVU4189|CDS|TonB-dependent	0.5	27.0	0.061	NA	NA	hypothetical protein
BVU2307|CDS|putative	0.5	27.0	0.061	NA	NA	hypothetical protein
TS28Rum13641|CDS|CDS	0.5	27.0	0.061	NA	NA	hypothetical protein
EUBREC1878|CDS|3-isopropylmalate	0.5	27.0	0.061	NA	NA	hypothetical protein

FpraM2120773|CDS|CDS	0.3	18.0	0.061	NA	NA	hypothetical protein
BVU0548|CDS|hypothetical	0.3	18.0	0.061	NA	NA	hypothetical protein
TS29Rum19624|CDS|CDS	1.0	54.3	0.061	NA	NA	hypothetical protein
TS28Clo00448|CDS|CDS	2.0	109.0	0.061	NA	NA	hypothetical protein
TS29Rum00383|CDS|CDS	2.5	136.5	0.061	NA	NA	hypothetical protein
TS28Eub4277|CDS|CDS	1.0	55.0	0.060	NA	NA	hypothetical protein
TS28Ali0566|CDS|CDS	1.0	55.0	0.060	NA	NA	hypothetical protein
BVU2915|CDS|polysaccharide	1.0	55.0	0.060	NA	NA	hypothetical protein
BVU0892|CDS|glycosyltransferase	0.5	27.5	0.060	NA	NA	hypothetical protein
Robe2898|CDS|CDS	1.0	55.0	0.060	NA	NA	hypothetical protein
BLD0861|CDS|Phosphoribosylformylglycinamidine	0.3	18.4	0.060	NA	NA	hypothetical protein
EUBREC0046|CDS|hypothetical	2.0	111.0	0.060	NA	NA	hypothetical protein
TS28Clo00667|CDS|CDS	2.0	111.0	0.060	NA	NA	hypothetical protein
TS29Fae06763|CDS|CDS	0.3	14.0	0.059	NA	NA	hypothetical protein
Robe3851|CDS|CDS	0.5	28.0	0.059	NA	NA	hypothetical protein
TS28Eub7859|CDS|CDS	0.5	28.0	0.059	NA	NA	hypothetical protein
TS28Clo00941|CDS|CDS	1.0	56.0	0.059	NA	NA	hypothetical protein
TS28Fae18280|CDS|CDS	0.5	28.0	0.059	NA	NA	hypothetical protein
TS28Clo00896|CDS|CDS	2.0	112.0	0.059	NA	NA	hypothetical protein
TS28Fae16649|CDS|CDS	0.5	28.0	0.059	NA	NA	hypothetical protein
TS29Rum16988|CDS|CDS	1.0	56.0	0.059	NA	NA	hypothetical protein
TS28Bac6295|CDS|CDS	3.0	169.0	0.059	NA	NA	hypothetical protein
Dfor3093|CDS|CDS	2.0	113.0	0.059	NA	NA	hypothetical protein
Rtor0960|CDS|CDS	0.3	17.5	0.058	NA	NA	hypothetical protein
Robe0055|CDS|CDS	0.3	14.2	0.058	NA	NA	hypothetical protein
CspSS21646|CDS|CDS	1.1	61.0	0.058	NA	NA	hypothetical protein
TS28Clo01056|CDS|CDS	1.0	57.0	0.058	NA	NA	hypothetical protein
TS29Rum11599|CDS|CDS	1.0	57.0	0.058	NA	NA	hypothetical protein
BVU1419|CDS|RNA	0.3	19.0	0.058	NA	NA	hypothetical protein
Msm1534|CDS|adhesin-like	0.7	38.3	0.058	NA	NA	hypothetical protein
Bdor1741|CDS|CDS	0.3	19.2	0.058	NA	NA	hypothetical protein
TS29Bac08638|CDS|CDS	0.4	21.2	0.057	NA	NA	hypothetical protein
EUBREC3385|CDS|hypothetical	2.0	115.5	0.057	NA	NA	hypothetical protein
EUBREC1492|CDS|3-dehydroquinate	1.0	58.0	0.057	NA	NA	hypothetical protein
TS28Par2472|CDS|CDS	1.0	58.0	0.057	NA	NA	hypothetical protein
TS28Fae14509|CDS|CDS	1.0	58.0	0.057	NA	NA	hypothetical protein
TS28Fae05387|CDS|CDS	1.0	58.0	0.057	NA	NA	hypothetical protein
Ebif0556|CDS|CDS	0.7	39.0	0.057	NA	NA	hypothetical protein
CspM6211849|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
Rbro1723|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
Acol2781|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
Dfor2033|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
TS28Clo00184|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
Acac2252|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
Cnex2286|CDS|CDS	0.3	18.1	0.056	NA	NA	hypothetical protein
BLD0034|CDS|truncated	0.8	45.9	0.056	NA	NA	hypothetical protein
TS28Fae05287|CDS|CDS	0.2	9.8	0.056	NA	NA	hypothetical protein
TS29Fae09069|CDS|CDS	0.5	29.5	0.056	NA	NA	hypothetical protein
TS29Fae01773|CDS|CDS	0.5	29.5	0.056	NA	NA	hypothetical protein
BVU1268|CDS|glycoside	1.0	59.0	0.056	NA	NA	hypothetical protein
TS28Clo00480|CDS|CDS	3.0	178.0	0.056	NA	NA	hypothetical protein
EUBREC1173|CDS|hypothetical	2.0	119.0	0.056	NA	NA	hypothetical protein
TS28Bac1201|CDS|CDS	0.3	19.8	0.056	NA	NA	hypothetical protein
TS28Clo10837|CDS|CDS	0.7	40.0	0.055	NA	NA	hypothetical protein
TS29Dor2086|CDS|CDS	1.0	60.0	0.055	NA	NA	hypothetical protein
TS29Bac07992|CDS|CDS	1.5	90.0	0.055	NA	NA	hypothetical protein
TS29Fae06583|CDS|CDS	0.5	30.0	0.055	NA	NA	hypothetical protein
TS29Bac08057|CDS|CDS	3.0	181.2	0.055	NA	NA	hypothetical protein
Rumhyd1704|CDS|CDS	1.0	61.8	0.055	NA	NA	hypothetical protein
TS28Dor2258|CDS|CDS	6.0	364.0	0.055	NA	NA	hypothetical protein
BL1411|CDS|cell	0.3	15.3	0.054	NA	NA	hypothetical protein
TS28Fae18222|CDS|CDS	1.0	61.0	0.054	NA	NA	hypothetical protein
EUBREC3685|CDS|hypothetical	2.5	152.5	0.054	NA	NA	hypothetical protein
TS28Clo01065|CDS|CDS	1.0	61.0	0.054	NA	NA	hypothetical protein
Dlon2013|CDS|CDS	0.6	36.8	0.054	NA	NA	hypothetical protein
EUBREC3570|CDS|DNA	1.0	58.4	0.054	NA	NA	hypothetical protein
Ceut2234|CDS|CDS	0.3	20.5	0.054	NA	NA	hypothetical protein
TS28Dor0606|CDS|CDS	0.3	20.5	0.054	NA	NA	hypothetical protein
Bcoproc0600|CDS|CDS	0.4	22.6	0.054	NA	NA	hypothetical protein
Bple1110|CDS|CDS	0.4	22.6	0.054	NA	NA	hypothetical protein
FpraM2121552|CDS|CDS	0.8	51.5	0.054	NA	NA	hypothetical protein
TS28Fae21222|CDS|CDS	2.0	124.0	0.053	NA	NA	hypothetical protein
Rtor0962|CDS|CDS	0.1	9.0	0.052	NA	NA	hypothetical protein
TS28Clo01372|CDS|CDS	1.0	63.0	0.052	NA	NA	hypothetical protein
Acol1939|CDS|CDS	0.3	21.0	0.052	NA	NA	hypothetical protein
Cbol4015|CDS|CDS	0.2	12.7	0.052	NA	NA	hypothetical protein
TS28Bif5373|CDS|CDS	0.3	15.8	0.052	NA	NA	hypothetical protein
TS28Fae08466|CDS|CDS	1.0	64.0	0.052	NA	NA	hypothetical protein
TS29Fae03678|CDS|CDS	0.3	16.0	0.052	NA	NA	hypothetical protein
Bint2007|CDS|CDS	0.3	16.0	0.052	NA	NA	hypothetical protein
Rtor0322|CDS|CDS	0.3	20.0	0.051	NA	NA	hypothetical protein
TS29Dor2225|CDS|CDS	0.5	32.5	0.051	NA	NA	hypothetical protein
TS28Bac8044|CDS|CDS	0.5	32.5	0.051	NA	NA	hypothetical protein
TS28Dor2627|CDS|CDS	0.5	32.5	0.051	NA	NA	hypothetical protein
TS29Fae06075|CDS|CDS	0.4	26.0	0.051	NA	NA	hypothetical protein
TS28Eub1526|CDS|CDS	2.0	130.5	0.051	NA	NA	hypothetical protein
Rbro0068|CDS|CDS	2.5	163.5	0.051	NA	NA	hypothetical protein
TS28Fae12986|CDS|CDS	0.5	33.0	0.050	NA	NA	hypothetical protein
TS29Fae09070|CDS|CDS	1.0	66.0	0.050	NA	NA	hypothetical protein
TS28Clo01384|CDS|CDS	1.0	66.0	0.050	NA	NA	hypothetical protein
TS28Eub6436|CDS|CDS	1.5	99.5	0.050	NA	NA	hypothetical protein

RintL11240|CDS|CDS	0.3	20.4	0.050	NA	NA	hypothetical protein
EUBREC0458|CDS|transcription-repair	1.5	100.0	0.050	NA	NA	hypothetical protein
TS28Clo01370|CDS|CDS	1.0	67.0	0.049	NA	NA	hypothetical protein
TS29Fae07181|CDS|CDS	1.0	67.0	0.049	NA	NA	hypothetical protein
BVU1555|CDS|putative	0.2	13.6	0.049	NA	NA	hypothetical protein
TS28Fae08953|CDS|CDS	1.0	68.0	0.049	NA	NA	hypothetical protein
TS28Clo01235|CDS|CDS	1.0	68.0	0.049	NA	NA	hypothetical protein
EUBREC1977|CDS|hypothetical	1.0	68.0	0.049	NA	NA	hypothetical protein
BVU0679|CDS|putative	0.2	13.6	0.049	NA	NA	hypothetical protein
Cbol3997|CDS|CDS	0.3	17.0	0.049	NA	NA	hypothetical protein
Cbar1002|CDS|CDS	1.0	68.2	0.049	NA	NA	hypothetical protein
TS29RumUnc1290|CDS|CDS	2.5	171.0	0.048	NA	NA	hypothetical protein
TS28Clo00982|CDS|CDS	1.0	68.5	0.048	NA	NA	hypothetical protein
BVU2622|CDS|putative	0.1	3.4	0.048	NA	NA	hypothetical protein
BVU1425|CDS|putative	0.1	3.4	0.048	NA	NA	hypothetical protein
TS28Clo10832|CDS|CDS	0.5	34.5	0.048	NA	NA	hypothetical protein
TS28Eub0795|CDS|CDS	0.5	34.5	0.048	NA	NA	hypothetical protein
TS29Rum13608|CDS|CDS	0.5	35.0	0.047	NA	NA	hypothetical protein
TS28Clo01058|CDS|CDS	1.0	71.0	0.047	NA	NA	hypothetical protein
TS28Bac5143|CDS|CDS	1.0	71.0	0.047	NA	NA	hypothetical protein
EUBREC1053|CDS|isoleucyl-tRNA	0.5	35.5	0.047	NA	NA	hypothetical protein
Rbro0328|CDS|CDS	0.3	23.7	0.047	NA	NA	hypothetical protein
Bpse0931|CDS|CDS	0.6	42.7	0.047	NA	NA	hypothetical protein
TS28Clo00918|CDS|CDS	2.0	142.5	0.046	NA	NA	hypothetical protein
TS28Bac1206|CDS|CDS	0.8	53.8	0.046	NA	NA	hypothetical protein
TS28Clo01133|CDS|CDS	2.0	144.0	0.046	NA	NA	hypothetical protein
TS28Rum08536|CDS|CDS	0.3	18.0	0.046	NA	NA	hypothetical protein
EUBREC2171|CDS|putative	1.0	72.0	0.046	NA	NA	hypothetical protein
TS28Bac5647|CDS|CDS	0.5	36.0	0.046	NA	NA	hypothetical protein
TS28Clo01725|CDS|CDS	3.0	217.0	0.046	NA	NA	hypothetical protein
Ccom1805|CDS|CDS	0.2	14.5	0.046	NA	NA	hypothetical protein
EUBREC0381|CDS|ribosomal	0.4	26.5	0.046	NA	NA	hypothetical protein
FpraM2121398|CDS|CDS	1.0	73.0	0.045	NA	NA	hypothetical protein
TS28Dor1842|CDS|CDS	1.0	74.0	0.045	NA	NA	hypothetical protein
TS28Bac7301|CDS|CDS	1.0	74.0	0.045	NA	NA	hypothetical protein
TS28Eub4340|CDS|CDS	1.0	74.0	0.045	NA	NA	hypothetical protein
TS29Fae08071|CDS|CDS	0.5	37.0	0.045	NA	NA	hypothetical protein
EUBREC3482|CDS|phosphatidylglycerophosphate	0.5	40.2	0.045	NA	NA	hypothetical protein
TS28Bac7857|CDS|CDS	1.0	74.2	0.045	NA	NA	hypothetical protein
TS28Clo00907|CDS|CDS	2.0	149.0	0.044	NA	NA	hypothetical protein
TS28Clo00883|CDS|CDS	2.0	149.0	0.044	NA	NA	hypothetical protein
BVU1198|CDS|hypothetical	0.5	37.5	0.044	NA	NA	hypothetical protein
TS28Eub4093|CDS|CDS	1.0	75.0	0.044	NA	NA	hypothetical protein
TS28Clo00488|CDS|CDS	1.0	75.0	0.044	NA	NA	hypothetical protein
TS28Bif4932|CDS|CDS	0.3	19.1	0.043	NA	NA	hypothetical protein
TS28Clo01036|CDS|CDS	2.0	153.0	0.043	NA	NA	hypothetical protein
TS28Bif2996|CDS|CDS	0.6	46.7	0.043	NA	NA	hypothetical protein
TS28Clo01126|CDS|CDS	1.0	78.0	0.042	NA	NA	hypothetical protein
TS28Clo01501|CDS|CDS	1.0	78.0	0.042	NA	NA	hypothetical protein
BVU1141|CDS|hypothetical	0.3	26.2	0.042	NA	NA	hypothetical protein
EUBREC1134|CDS|putative	1.0	79.0	0.042	NA	NA	hypothetical protein
TS28Eub3890|CDS|CDS	0.5	39.5	0.042	NA	NA	hypothetical protein
TS28Eub8377|CDS|CDS	3.5	276.5	0.042	NA	NA	hypothetical protein
TS28Bif2711|CDS|CDS	2.0	158.5	0.042	NA	NA	hypothetical protein
EUBREC3564|CDS|possible	2.0	158.5	0.042	NA	NA	hypothetical protein
TS28Dor2650|CDS|CDS	1.0	79.3	0.042	NA	NA	hypothetical protein
TS28Clo10371|CDS|CDS	0.3	20.1	0.041	NA	NA	hypothetical protein
TS28Dor2993|CDS|CDS	1.0	80.5	0.041	NA	NA	hypothetical protein
TS28Met0493|CDS|CDS	0.3	27.0	0.041	NA	NA	hypothetical protein
FpraM2122627|CDS|CDS	0.3	27.0	0.041	NA	NA	hypothetical protein
TS28Clo00497|CDS|CDS	2.0	162.5	0.041	NA	NA	hypothetical protein
TS29Fae08867|CDS|CDS	1.3	101.7	0.041	NA	NA	hypothetical protein
TS28Clo00782|CDS|CDS	4.0	326.0	0.041	NA	NA	hypothetical protein
TS28Eub4083|CDS|CDS	0.5	41.0	0.040	NA	NA	hypothetical protein
TS28Bif5176|CDS|CDS	0.3	20.5	0.040	NA	NA	hypothetical protein
TS28Fae21314|CDS|CDS	0.5	41.3	0.040	NA	NA	hypothetical protein
TS28Clo01767|CDS|CDS	1.0	83.0	0.040	NA	NA	hypothetical protein
TS28Fae01105|CDS|CDS	1.0	83.0	0.040	NA	NA	hypothetical protein
TS28Clo00679|CDS|CDS	1.0	83.0	0.040	NA	NA	hypothetical protein
TS28Clo01038|CDS|CDS	2.0	166.0	0.040	NA	NA	hypothetical protein
TS28Bac6292|CDS|CDS	2.0	166.0	0.040	NA	NA	hypothetical protein
TS28Clo01231|CDS|CDS	1.0	83.0	0.040	NA	NA	hypothetical protein
BL1470|CDS|hypothetical	1.5	125.8	0.039	NA	NA	hypothetical protein
TS28Fae22189|CDS|CDS	0.5	42.0	0.039	NA	NA	hypothetical protein
TS29Fae06459|CDS|CDS	0.5	42.0	0.039	NA	NA	hypothetical protein
BVU3827|CDS|putative	0.3	28.0	0.039	NA	NA	hypothetical protein
TS29Rum18681|CDS|CDS	0.6	50.7	0.039	NA	NA	hypothetical protein
EUBREC3015|CDS|hypothetical	1.0	84.5	0.039	NA	NA	hypothetical protein
TS28Clo00751|CDS|CDS	1.0	85.0	0.039	NA	NA	hypothetical protein
Csci3153|CDS|CDS	0.3	26.3	0.039	NA	NA	hypothetical protein
TS28Met1332|CDS|CDS	0.5	42.8	0.039	NA	NA	hypothetical protein
TS28Clo00922|CDS|CDS	1.0	86.0	0.038	NA	NA	hypothetical protein
BVU1365|CDS|glycoside	1.0	86.0	0.038	NA	NA	hypothetical protein
EUBREC1029|CDS|long-chain-fatty-acid	1.0	86.0	0.038	NA	NA	hypothetical protein
BVU3467|CDS|DNA	0.3	28.8	0.038	NA	NA	hypothetical protein
TS28Rum02259|CDS|CDS	2.0	173.5	0.038	NA	NA	hypothetical protein
TS28Eub4687|CDS|CDS	0.5	43.5	0.038	NA	NA	hypothetical protein
TS28Fae22126|CDS|CDS	1.0	87.5	0.038	NA	NA	hypothetical protein
TS28Bac6333|CDS|CDS	1.0	88.0	0.038	NA	NA	hypothetical protein
EUBREC0033|CDS|serine/threonine	1.0	88.5	0.037	NA	NA	hypothetical protein
BVU3523|CDS|putative	0.7	59.0	0.037	NA	NA	hypothetical protein
Cnex1095|CDS|CDS	0.8	71.0	0.037	NA	NA	hypothetical protein

EUBREC2964|CDS|glycogen	0.5	44.5	0.037	NA	NA	hypothetical protein
BFnctc4052|CDS|putative	0.3	29.7	0.037	NA	NA	hypothetical protein
TS28Bac1205|CDS|CDS	0.8	67.3	0.037	NA	NA	hypothetical protein
TS28Fae22125|CDS|CDS	0.5	45.0	0.037	NA	NA	hypothetical protein
EUBREC2203|CDS|stage	1.0	90.0	0.037	NA	NA	hypothetical protein
FpraM2121214|CDS|CDS	0.3	22.5	0.037	NA	NA	hypothetical protein
CspM6210574|CDS|CDS	0.5	49.3	0.036	NA	NA	hypothetical protein
TS28Clo00858|CDS|CDS	1.0	91.0	0.036	NA	NA	hypothetical protein
TS28Eub3931|CDS|CDS	0.5	45.5	0.036	NA	NA	hypothetical protein
TS28Fae19000|CDS|CDS	0.3	23.0	0.036	NA	NA	hypothetical protein
TS28Clo01351|CDS|CDS	1.0	94.0	0.035	NA	NA	hypothetical protein
TS28Fae16430|CDS|CDS	0.5	47.0	0.035	NA	NA	hypothetical protein
TS28Fae22693|CDS|CDS	1.5	141.0	0.035	NA	NA	hypothetical protein
TS29Fae03003|CDS|CDS	1.0	96.0	0.034	NA	NA	hypothetical protein
TS29Rum13270|CDS|CDS	0.7	64.5	0.034	NA	NA	hypothetical protein
TS28Clo00787|CDS|CDS	1.0	97.0	0.034	NA	NA	hypothetical protein
TS28Clo00568|CDS|CDS	1.0	97.0	0.034	NA	NA	hypothetical protein
TS28Clo01659|CDS|CDS	1.0	97.0	0.034	NA	NA	hypothetical protein
BVU1858|CDS|glutaryl-7-ACA	0.3	32.5	0.034	NA	NA	hypothetical protein
TS28Eub7968|CDS|CDS	0.7	65.3	0.034	NA	NA	hypothetical protein
EUBREC1241|CDS|hypothetical	1.0	99.0	0.033	NA	NA	hypothetical protein
Cnex0003|CDS|CDS	0.1	9.0	0.033	NA	NA	hypothetical protein
TS29Eub2196|CDS|CDS	0.5	49.8	0.033	NA	NA	hypothetical protein
TS28Eub8935|CDS|CDS	0.5	50.0	0.033	NA	NA	hypothetical protein
TS29Fae03174|CDS|CDS	0.3	25.0	0.033	NA	NA	hypothetical protein
TS28Fae11974|CDS|CDS	1.0	100.5	0.033	NA	NA	hypothetical protein
TS28Clo00670|CDS|CDS	1.0	101.0	0.033	NA	NA	hypothetical protein
TS28Clo00800|CDS|CDS	2.0	202.0	0.033	NA	NA	hypothetical protein
TS28Clo01557|CDS|CDS	2.0	204.0	0.032	NA	NA	hypothetical protein
TS28Clo01671|CDS|CDS	1.0	103.0	0.032	NA	NA	hypothetical protein
TS28Clo00437|CDS|CDS	1.0	103.0	0.032	NA	NA	hypothetical protein
TS28Fae13655|CDS|CDS	1.0	103.0	0.032	NA	NA	hypothetical protein
TS28Clo01025|CDS|CDS	1.0	103.5	0.032	NA	NA	hypothetical protein
TS28Clo10839|CDS|CDS	0.5	46.8	0.032	NA	NA	hypothetical protein
FpraM2122280|CDS|CDS	0.2	21.0	0.031	NA	NA	hypothetical protein
BVU2323|CDS|Na+/glucose	0.5	52.5	0.031	NA	NA	hypothetical protein
TS28Bac7919|CDS|CDS	0.5	53.0	0.031	NA	NA	hypothetical protein
TS28Clo01210|CDS|CDS	1.0	106.5	0.031	NA	NA	hypothetical protein
Cnex2347|CDS|CDS	0.2	17.8	0.031	NA	NA	hypothetical protein
EUBREC1583|CDS|ferrous	1.0	108.0	0.031	NA	NA	hypothetical protein
TS29Fae04113|CDS|CDS	0.5	54.2	0.031	NA	NA	hypothetical protein
TS28Eub8554|CDS|CDS	0.5	54.5	0.030	NA	NA	hypothetical protein
EUBREC2148|CDS|DNA	1.0	110.0	0.030	NA	NA	hypothetical protein
TS28Bac6246|CDS|CDS	0.3	36.7	0.030	NA	NA	hypothetical protein
RintL10500|CDS|CDS	0.2	25.6	0.030	NA	NA	hypothetical protein
TS28Clo00544|CDS|CDS	1.0	111.0	0.030	NA	NA	hypothetical protein
TS28Clo00904|CDS|CDS	1.0	111.0	0.030	NA	NA	hypothetical protein
TS28Clo01613|CDS|CDS	1.0	111.0	0.030	NA	NA	hypothetical protein
TS28Fae01810|CDS|CDS	1.0	111.0	0.030	NA	NA	hypothetical protein
TS28Met1431|CDS|CDS	0.3	37.3	0.030	NA	NA	hypothetical protein
EUBREC3489|CDS|citrate	0.3	37.3	0.030	NA	NA	hypothetical protein
Bcoproc1108|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
BFych460145|CDS|hypothetical	0.1	8.6	0.030	NA	NA	hypothetical protein
Bfra31120121|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
Bste0893|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
BWH20426|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
Bple3091|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
TS28Ali0488|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
Begg2729|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
BactD10619|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
Bdor4450|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
Bint0769|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
Pmer0644|CDS|CDS	0.1	8.6	0.030	NA	NA	hypothetical protein
TS28Fae11464|CDS|CDS	0.7	75.5	0.029	NA	NA	hypothetical protein
Ceut2216|CDS|CDS	0.3	34.9	0.029	NA	NA	hypothetical protein
TS28Fae17681|CDS|CDS	0.5	57.0	0.029	NA	NA	hypothetical protein
Dfor3099|CDS|CDS	1.8	211.1	0.029	NA	NA	hypothetical protein
TS29Fae09818|CDS|CDS	0.5	58.5	0.028	NA	NA	hypothetical protein
TS28Clo00832|CDS|CDS	1.0	118.0	0.028	NA	NA	hypothetical protein
Bcap2523|CDS|CDS	0.1	14.8	0.028	NA	NA	hypothetical protein
BVU0493|CDS|putative	0.5	59.5	0.028	NA	NA	hypothetical protein
CspL22633|CDS|CDS	0.2	27.5	0.028	NA	NA	hypothetical protein
TS29Fae06839|CDS|CDS	0.5	60.0	0.028	NA	NA	hypothetical protein
EUBREC1011|CDS|arylsulfatase	0.5	60.0	0.028	NA	NA	hypothetical protein
TS28Clo10627|CDS|CDS	0.3	37.2	0.027	NA	NA	hypothetical protein
TS28Clo01502|CDS|CDS	1.0	122.0	0.027	NA	NA	hypothetical protein
TS28Fae19761|CDS|CDS	0.3	31.0	0.027	NA	NA	hypothetical protein
TS28Clo01178|CDS|CDS	1.0	125.0	0.026	NA	NA	hypothetical protein
TS29RumUnc1369|CDS|CDS	0.5	62.5	0.026	NA	NA	hypothetical protein
Bsp1161254|CDS|CDS	0.3	42.0	0.026	NA	NA	hypothetical protein
EUBREC0024|CDS|hypothetical	0.5	64.0	0.026	NA	NA	hypothetical protein
BVU1240|CDS|succinate	0.5	64.0	0.026	NA	NA	hypothetical protein
TS29Fae00933|CDS|CDS	0.5	66.0	0.025	NA	NA	hypothetical protein
TS28Clo00558|CDS|CDS	1.0	133.0	0.025	NA	NA	hypothetical protein
BFych460147|CDS|hypothetical	0.1	19.0	0.025	NA	NA	hypothetical protein
TS28Clo00870|CDS|CDS	2.0	267.0	0.025	NA	NA	hypothetical protein
EUBREC0655|CDS|type	0.5	68.5	0.024	NA	NA	hypothetical protein
TS28Fae22121|CDS|CDS	0.5	69.0	0.024	NA	NA	hypothetical protein
TS29Rum19572|CDS|CDS	0.3	46.0	0.024	NA	NA	hypothetical protein
TS28Bac6628|CDS|CDS	0.3	46.3	0.024	NA	NA	hypothetical protein
Rlac0829|CDS|CDS	0.5	70.0	0.024	NA	NA	hypothetical protein
FpraM2121437|CDS|CDS	0.5	71.0	0.023	NA	NA	hypothetical protein

BWH22274|CDS|CDS	0.3	47.5	0.023	NA	NA	hypothetical protein
TS28Bac7818|CDS|CDS	0.5	72.5	0.023	NA	NA	hypothetical protein
Cbol3090|CDS|CDS	0.3	46.4	0.022	NA	NA	hypothetical protein
BL1199|CDS|fibronectin	0.3	38.2	0.022	NA	NA	hypothetical protein
TS28Clo01083|CDS|CDS	3.0	459.0	0.022	NA	NA	hypothetical protein
TS28Bac4701|CDS|CDS	0.3	38.3	0.022	NA	NA	hypothetical protein
EUBREC2239|CDS|arginyl-tRNA	0.5	78.0	0.021	NA	NA	hypothetical protein
Buni2461|CDS|CDS	0.2	26.7	0.021	NA	NA	hypothetical protein
TS29Clo4936|CDS|CDS	1.0	163.5	0.020	NA	NA	hypothetical protein
TS29Bif3127|CDS|CDS	0.3	41.0	0.020	NA	NA	hypothetical protein
BVU0853|CDS|hypothetical	0.4	59.1	0.020	NA	NA	hypothetical protein
TS29RumUnc1298|CDS|CDS	1.0	170.8	0.019	NA	NA	hypothetical protein
TS28Eub0316|CDS|CDS	1.0	171.0	0.019	NA	NA	hypothetical protein
RintL13987|CDS|CDS	0.4	65.8	0.018	NA	NA	hypothetical protein
EUBREC0667|CDS|putative	0.7	121.0	0.018	NA	NA	hypothetical protein
TS29LacUnc129|CDS|CDS	0.1	22.8	0.018	NA	NA	hypothetical protein
Even1751|CDS|CDS	0.1	12.2	0.018	NA	NA	hypothetical protein
Robe3843|CDS|CDS	0.4	68.8	0.018	NA	NA	hypothetical protein
TS28Eub8453|CDS|CDS	0.3	62.7	0.018	NA	NA	hypothetical protein
TS28Clo01724|CDS|CDS	1.0	190.0	0.017	NA	NA	hypothetical protein
TS28Dor2647|CDS|CDS	0.7	128.0	0.017	NA	NA	hypothetical protein
EUBREC1072|CDS|hypothetical	0.8	160.0	0.017	NA	NA	hypothetical protein
Ccom1795|CDS|CDS	0.4	74.7	0.016	NA	NA	hypothetical protein
EUBREC0006|CDS|DNA	0.5	105.0	0.016	NA	NA	hypothetical protein
Cnex1457|CDS|CDS	0.3	70.0	0.016	NA	NA	hypothetical protein
TS28Eub0701|CDS|CDS	0.3	52.8	0.016	NA	NA	hypothetical protein
Ebif1241|CDS|CDS	0.2	42.5	0.016	NA	NA	hypothetical protein
Ccom0029|CDS|CDS	0.1	15.2	0.015	NA	NA	hypothetical protein
TS29Fae06006|CDS|CDS	0.1	15.9	0.014	NA	NA	hypothetical protein
EUBREC3569|CDS|hypothetical	0.2	48.1	0.014	NA	NA	hypothetical protein
FpraM2121402|CDS|CDS	0.5	131.2	0.013	NA	NA	hypothetical protein
Robe3842|CDS|CDS	0.2	62.4	0.011	NA	NA	hypothetical protein
Cbar1018|CDS|CDS	0.7	241.0	0.009	NA	NA	hypothetical protein
Rgna2287|CDS|CDS	0.2	88.7	0.007	NA	NA	hypothetical protein
Bste3181|CDS|CDS	0.1	23.3	0.007	NA	NA	hypothetical protein
Ccom1796|CDS|CDS	0.2	97.3	0.007	NA	NA	hypothetical protein
CspSS22982|CDS|CDS	0.2	86.2	0.006	NA	NA	hypothetical protein
CspSS22981|CDS|CDS	0.2	141.0	0.005	NA	NA	hypothetical protein
EUBREC3483|CDS|hypothetical	0.1	53.7	0.004	NA	NA	hypothetical protein

Table S12: Genes with high or low relative expression in the TS29 fecal meta-transcriptome.

Gene	cDNA sequences	DNA sequences	Ratio	COG categories	COGs	COG Annotations
TS29Bif3929|CDS|CDS	0.4	23.2	0.1	A	COG1949	Oligoribonuclease (3'->5' exoribonuclease)
TS28Bif0658|CDS|CDS	0.4	23.2	0.1	A	COG1949	Oligoribonuclease (3'->5' exoribonuclease)
BL1723|CDS|oligoribonuclease	0.4	23.2	0.1	A	COG1949	Oligoribonuclease (3'->5' exoribonuclease)
Msmi750160|CDS|CDS	9.5	0.5	86.3	B	COG2036	Histones H3 and H4
Bsp1160960|CDS|CDS	22.0	0.2	600.0	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Bthe3734721|CDS|CDS	21.4	0.2	583.0	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Bthe7331302|CDS|CDS	20.9	0.2	568.1	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Bthe7330297|CDS|CDS	98.1	1.1	411.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Bthe3731370|CDS|CDS	98.1	1.1	411.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Bsp1162970|CDS|CDS	63.6	0.8	384.8	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS29Bac01465|CDS|CDS	81.0	1.0	367.7	C	COG1773|COG1853|COG2025|COG1592	Rubredoxin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Electron transfer flavoprotein, alpha subunit|Rubrerythrin
Bova1491|CDS|CDS	6.3	0.2	143.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Buni2102|CDS|CDS	10.3	0.3	140.7	C	COG0055	F0F1-type ATP synthase, beta subunit
BactD23071|CDS|CDS	5.1	0.2	115.0	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Eub5382|CDS|CDS	11.5	0.5	104.4	C	COG1454	Alcohol dehydrogenase, class IV
BactD11821|CDS|CDS	10.9	0.5	99.3	C	COG0711	F0F1-type ATP synthase, subunit b
TS28Met1185|CDS|CDS	10.9	0.5	99.3	C	COG3383|COG0243	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
BT2414|CDS|ferredoxin	20.3	1.0	91.9	C	COG1145|COG5015	Ferredoxin|Uncharacterized conserved protein
Bxyl0243|CDS|CDS	12.9	0.7	88.1	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Rum11777|CDS|CDS	8.0	0.5	72.6	C	COG0224	F0F1-type ATP synthase, gamma subunit
TS28Fae15025|CDS|CDS	7.5	0.5	68.1	C	COG1592	Rubrerythrin
TS28Fae12704|CDS|CDS	29.5	2.0	66.9	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
Buni0328|CDS|CDS	19.0	1.3	64.7	C	COG0039	Malate/lactate dehydrogenases
TS28Clo03297|CDS|CDS	7.0	0.5	63.6	C	COG1592	Rubrerythrin
Msmi740998|CDS|CDS	3.5	0.3	62.6	C	COG0479|COG2048	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit|Heterodisulfide reductase, subunit B
TS29Rum10999|CDS|CDS	25.0	2.0	56.7	C	COG2086	Electron transfer flavoprotein, beta subunit
Bxyl3870|CDS|CDS	6.2	0.5	56.0	C	COG1592	Rubrerythrin
BactD14279|CDS|CDS	6.2	0.5	55.8	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi740377|CDS|CDS	5.5	0.5	55.5	C	COG3383|COG0243|COG1029	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing|Formylmethanofuran dehydrogenase subunit B
FpraM2120466|CDS|CDS	6.0	0.5	54.5	C	COG0224	F0F1-type ATP synthase, gamma subunit
TS29Met0433|CDS|CDS	23.1	2.0	52.3	C	COG0680	Ni,Fe-hydrogenase maturation factor
TS28Rum11773|CDS|CDS	5.7	0.5	51.8	C	COG0711	F0F1-type ATP synthase, subunit b
Aput0333|CDS|CDS	21.5	2.0	48.8	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi740380|CDS|CDS	4.8	0.5	48.4	C	COG1145	Ferredoxin
Bthe3734372|CDS|CDS	10.6	1.0	48.0	C	COG1882	Pyruvate-formate lyase
Bhan2746|CDS|CDS	10.5	1.0	47.7	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Bova1292|CDS|CDS	41.0	4.0	46.5	C	COG1145	Ferredoxin
TS28Met0338|CDS|CDS	10.0	1.0	45.4	C	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
TS28Rum15623|CDS|CDS	19.2	2.0	43.5	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
Pmer2049|CDS|CDS	3.1	0.3	41.6	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28Clo07501|CDS|CDS	9.0	1.0	40.9	C	COG0778	Nitroreductase
Cbol3480|CDS|CDS	9.0	1.0	40.9	C	COG0355	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)
Bfin3327|CDS|CDS	13.3	1.5	40.4	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Rumhyd2691|CDS|CDS	8.7	1.0	39.3	C	COG1456	CO dehydrogenase/acetyl-CoA synthase gamma subunit (corrinoid Fe-S protein)
Rlac1178|CDS|CDS	8.6	1.0	39.1	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS29Met0501|CDS|CDS	1.7	0.2	37.5	C	COG1035|COG1145	Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin
Buni2911|CDS|CDS	12.2	1.5	36.8	C	COG1951|COG1838	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain|Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain
TS28Fae22603|CDS|CDS	36.2	4.5	36.6	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Rtor1001|CDS|CDS	28.0	3.5	36.3	C	COG1454	Alcohol dehydrogenase, class IV
Msmi751594|CDS|CDS	1.6	0.2	36.3	C	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E
BFych464350|CDS|rubredoxin	8.0	1.0	36.3	C	COG1773	Rubredoxin

Svar2374|CDS|CDS	8.0	1.0	36.2	C	COG2086|COG2025	Electron transfer flavoprotein, beta subunit|Electron transfer flavoprotein, alpha subunit
TS28Fae08859|CDS|CDS	23.7	3.0	35.8	C	COG1592	Rubrerythrin
Eeli1407|CDS|CDS	7.9	1.0	35.7	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Bfin2282|CDS|CDS	1.9	0.3	34.8	C	COG0039	Malate/lactate dehydrogenases
Svar1559|CDS|CDS	3.8	0.5	34.8	C	COG1882	Pyruvate-formate lyase
TS28Met0352|CDS|CDS	10.0	1.3	34.0	C	COG3259|COG0374	Coenzyme F420-reducing hydrogenase, alpha subunit|Ni,Fe-hydrogenase I large subunit
TS28Fae18580|CDS|CDS	30.0	4.0	34.0	C	COG2025|COG2086	Electron transfer flavoprotein, alpha subunit|Electron transfer flavoprotein, beta subunit
TS28Fae12038|CDS|CDS	7.5	1.0	34.0	C	COG2878	Predicted NADH:ubiquinone oxidoreductase, subunit RnfB
TS28Fae15052|CDS|CDS	18.5	2.5	33.6	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS28Rum13674|CDS|CDS	75.3	10.5	32.5	C	COG1151	6Fe-6S prismane cluster-containing protein
TS29Bac10233|CDS|CDS	2.3	0.3	31.8	C	COG1454	Alcohol dehydrogenase, class IV
Bxyl4312|CDS|CDS	1.8	0.3	31.8	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Cste1580|CDS|CDS	7.0	1.0	31.8	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Cint819|CDS|CDS	7.0	1.0	31.8	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi740445|CDS|CDS	12.7	1.8	31.4	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
Cbol4815|CDS|CDS	20.5	3.0	31.0	C	COG0554	Glycerol kinase
TS28Clo06647|CDS|CDS	23.7	3.5	30.7	C	COG1882	Pyruvate-formate lyase
TS29Clo4495|CDS|CDS	27.0	4.0	30.6	C	COG0277	FAD/FMN-containing dehydrogenases
TS28Fae20658|CDS|CDS	33.2	5.0	30.1	C	COG1592	Rubrerythrin
Msmi750889|CDS|CDS	14.3	2.2	30.0	C	COG0374|COG3259	Ni,Fe-hydrogenase I large subunit|Coenzyme F420-reducing hydrogenase, alpha subunit
TS28Met1193|CDS|CDS	5.0	0.8	29.0	C	COG3383|COG0243|COG1029	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing|Formylmethanofuran dehydrogenase subunit B
Buni3129|CDS|CDS	2.0	0.3	27.2	C	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
Bxyl0686|CDS|CDS	2.0	0.3	27.2	C	COG1294	Cytochrome bd-type quinol oxidase, subunit 2
TS28Bac7205|CDS|CDS	2.0	0.3	27.2	C	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
BactD21003|CDS|CDS	6.0	1.0	27.2	C	COG0372	Citrate synthase
TS28Clo04378|CDS|CDS	6.0	1.0	27.2	C	COG1032	Fe-S oxidoreductase
TS28Rum03156|CDS|CDS	3.0	0.5	27.2	C	COG1614	CO dehydrogenase/acetyl-CoA synthase beta subunit
Msmi741088|CDS|CDS	1.5	0.3	27.2	C	COG1151	6Fe-6S prismane cluster-containing protein
TS28Rum13667|CDS|CDS	3.0	0.5	27.2	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS29Rum09446|CDS|CDS	6.0	1.0	27.2	C	COG0636	F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K
Ehal0970|CDS|CDS	15.0	2.5	27.2	C	COG0554	Glycerol kinase
Rumhyd1742|CDS|CDS	6.0	1.0	27.2	C	COG4231	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits
Caer2168|CDS|CDS	3.0	0.5	27.2	C	COG0711	F0F1-type ATP synthase, subunit b
ShigspD92089|CDS|CDS	6.0	1.0	27.2	C	COG1012	NAD-dependent aldehyde dehydrogenases
TS28Bac1044|CDS|CDS	8.0	1.3	27.2	C	COG0039	Malate/lactate dehydrogenases
Bxyl1299|CDS|CDS	1.2	0.2	27.1	C	COG2086	Electron transfer flavoprotein, beta subunit
Rtor0314|CDS|CDS	11.5	2.0	26.1	C	COG1592	Rubrerythrin
Buni1043|CDS|CDS	11.5	2.0	26.1	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
TS28Bac6799|CDS|CDS	18.5	3.3	25.2	C	COG0055	F0F1-type ATP synthase, beta subunit
Acac3064|CDS|CDS	5.5	1.0	25.0	C	COG1592	Rubrerythrin
TS28Bac0410|CDS|CDS	3.7	0.7	25.0	C	COG3808	Inorganic pyrophosphatase
Msmi740795|CDS|CDS	2.8	0.5	25.0	C	COG1145	Ferredoxin
Cbol1760|CDS|CDS	11.0	2.0	25.0	C	COG0372	Citrate synthase
TS29Met0432|CDS|CDS	21.8	4.0	24.7	C	COG3259|COG0374	Coenzyme F420-reducing hydrogenase, alpha subunit|Ni,Fe-hydrogenase I large subunit
TS29Rum08442|CDS|CDS	16.0	3.0	24.2	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
TS28Bac2658|CDS|CDS	12.4	2.3	24.2	C	COG0056	F0F1-type ATP synthase, alpha subunit
Buni2099|CDS|CDS	12.4	2.3	24.2	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS29Met0212|CDS|CDS	1.1	0.2	23.8	C	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E
Msmi751230|CDS|CDS	13.0	2.5	23.7	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
Begg1665|CDS|CDS	5.2	1.0	23.6	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Rumhyd1810|CDS|CDS	15.5	3.0	23.5	C	COG1894|COG4656	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
Bcap2157|CDS|CDS	10.3	2.0	23.3	C	COG4624|COG3383|COG1034|COG0243	Iron only hydrogenase large subunit, C-terminal domain|Uncharacterized anaerobic dehydrogenase|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Anaerobic dehydrogenases, typically selenocysteine-containing
CspL21837|CDS|CDS	1.7	0.3	22.7	C	COG2033	Desulfoferrodoxin
TS29Clo3088|CDS|CDS	10.0	2.0	22.7	C	COG1319	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs
Cbol0145|CDS|CDS	5.0	1.0	22.7	C	COG1014|COG1146|COG4231	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Ferredoxin|Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits
Cspi1525|CDS|CDS	5.0	1.0	22.7	C	COG4624|COG3383|COG1034|COG0243	Iron only hydrogenase large subunit, C-terminal domain|Uncharacterized anaerobic dehydrogenase|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Anaerobic dehydrogenases, typically selenocysteine-containing
TS28Rum16120|CDS|CDS	2.5	0.5	22.7	C	COG1145	Ferredoxin
Aput0085|CDS|CDS	5.0	1.0	22.7	C	COG2878	Predicted NADH:ubiquinone oxidoreductase, subunit RnfB
TS28Rum04448|CDS|CDS	2.5	0.5	22.7	C	COG0538	Isocitrate dehydrogenases

Chyl2945|CDS|CDS	5.0	1.0	22.7	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
Dlon2331|CDS|CDS	5.0	1.0	22.7	C	COG0822	NifU homolog involved in Fe-S cluster formation
Rtor1059|CDS|CDS	2.5	0.5	22.7	C	COG1145	Ferredoxin
Csym1861|CDS|CDS	5.0	1.0	22.7	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
ShigspD90775|CDS|CDS	4.9	1.0	22.3	C	COG2055	Malate/L-lactate dehydrogenases
TS28Clo10641|CDS|CDS	129.0	26.5	22.1	C	COG1882	Pyruvate-formate lyase
Clep2055|CDS|CDS	9.5	2.0	21.6	C	COG1894|COG3411	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin
Msmi751592|CDS|CDS	6.8	1.5	21.3	C	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I
BactD10568|CDS|CDS	2.3	0.5	21.2	C	COG0074	Succinyl-CoA synthetase, alpha subunit
Aput0035|CDS|CDS	23.0	5.0	20.9	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi751292|CDS|CDS	11.3	2.5	20.5	C	COG3383|COG0243	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
Msmi740385|CDS|CDS	11.3	2.5	20.5	C	COG3383|COG0243	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
Bova3369|CDS|CDS	1.5	0.3	20.4	C	COG1883	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
Bxyl4311|CDS|CDS	1.5	0.3	20.4	C	COG1883	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
TS29Bac09081|CDS|CDS	1.5	0.3	20.4	C	COG1048	Aconitase A
Bxyl3889|CDS|CDS	2.3	0.5	20.4	C	COG1032	Fe-S oxidoreductase
Bcel4637|CDS|CDS	2.2	0.5	20.3	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28Rum11189|CDS|CDS	46.3	10.5	20.0	C	COG0280|COG0857	Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
Msmi740097|CDS|CDS	2.4	0.5	20.0	C	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E
TS28Met1780|CDS|CDS	2.4	0.5	20.0	C	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E
Bxyl1082|CDS|CDS	2.2	0.5	19.7	C	COG1048	Aconitase A
TS28Rum04663|CDS|CDS	4.3	1.0	19.7	C	COG0056	F0F1-type ATP synthase, alpha subunit
Msmi751299|CDS|CDS	4.3	1.0	19.5	C	COG1153	Formylmethanofuran dehydrogenase subunit D
TS28Rum15925|CDS|CDS	23.3	5.5	19.2	C	COG1894|COG1905	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|NADH:ubiquinone oxidoreductase 24 kD subunit
TS28Rum02367|CDS|CDS	56.1	13.5	18.9	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
Buni1798|CDS|CDS	18.3	4.5	18.5	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
TS28Met1385|CDS|CDS	4.1	1.0	18.4	C	COG0680	Ni,Fe-hydrogenase maturation factor
TS29Rum19013|CDS|CDS	64.5	16.0	18.3	C	COG2069	CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe-S protein)
TS29Bac00722|CDS|CDS	20.0	5.0	18.2	C	COG0711	F0F1-type ATP synthase, subunit b
Msmi740376|CDS|CDS	8.8	2.2	18.2	C	COG1229	Formylmethanofuran dehydrogenase subunit A
Msmi740096|CDS|CDS	1.0	0.3	18.2	C	COG0636	F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K
Rumhyd0090|CDS|CDS	4.0	1.0	18.2	C	COG1951	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain
TS28Clo05768|CDS|CDS	6.0	1.5	18.2	C	COG1894|COG1905	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|NADH:ubiquinone oxidoreductase 24 kD subunit
TS29Dor0921|CDS|CDS	48.0	12.0	18.2	C	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family
TS29Met0565|CDS|CDS	4.0	1.0	18.2	C	COG3260	Ni,Fe-hydrogenase III small subunit
Acac0816|CDS|CDS	16.0	4.0	18.2	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
DpigGOR10762|CDS|CDS	4.0	1.0	18.2	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
Buni1807|CDS|CDS	8.0	2.0	18.2	C	COG2869	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrC
TS28Fae00076|CDS|CDS	4.0	1.0	18.2	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Cbol0419|CDS|CDS	4.0	1.0	18.2	C	COG2221	Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits
TS28Rum02230|CDS|CDS	5.3	1.3	18.2	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
Bova2870|CDS|CDS	1.3	0.3	18.2	C	COG1979|COG1454	Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family|Alcohol dehydrogenase, class IV
TS28Met1016|CDS|CDS	2.0	0.5	17.7	C	COG1927	Coenzyme F420-dependent N(5),N(10)-methenyltetrahydromethanopterin dehydrogenase
Msmi751092|CDS|CDS	2.0	0.5	17.7	C	COG1927	Coenzyme F420-dependent N(5),N(10)-methenyltetrahydromethanopterin dehydrogenase
Msmi740582|CDS|CDS	2.0	0.5	17.7	C	COG1927	Coenzyme F420-dependent N(5),N(10)-methenyltetrahydromethanopterin dehydrogenase
TS28Met1194|CDS|CDS	8.6	2.2	17.6	C	COG1229	Formylmethanofuran dehydrogenase subunit A
BactD21416|CDS|CDS	1.3	0.3	17.5	C	COG1014|COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
Msmi751494|CDS|CDS	11.5	3.0	17.4	C	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
Bova2002|CDS|CDS	4.1	1.1	17.2	C	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit
TS28Fae08713|CDS|CDS	22.7	6.0	17.2	C	COG2086	Electron transfer flavoprotein, beta subunit
TS28Clo09282|CDS|CDS	15.0	4.0	17.0	C	COG3288|COG1282	NAD/NADP transhydrogenase alpha subunit|NAD/NADP transhydrogenase beta subunit
TS29Bac02967|CDS|CDS	6.9	1.9	16.8	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
Msmi751300|CDS|CDS	5.3	1.5	16.7	C	COG3383|COG0243|COG1029	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing|Formylmethanofuran dehydrogenase subunit B
TS28Rum14310|CDS|CDS	5.5	1.5	16.6	C	COG0371	Glycerol dehydrogenase and related enzymes
Bcap2399|CDS|CDS	7.3	2.0	16.6	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
FpraM2122074|CDS|CDS	7.3	2.0	16.6	C	COG2086|COG2025	Electron transfer flavoprotein, beta subunit|Electron transfer flavoprotein, alpha subunit
Buni3135|CDS|CDS	21.9	6.0	16.6	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Met1186|CDS|CDS	6.4	1.8	16.3	C	COG1908|COG1035|COG1145	Coenzyme F420-reducing hydrogenase, delta subunit|Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin
Buni1040|CDS|CDS	8.9	2.5	16.2	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS29Rum13364|CDS|CDS	177.5	50.0	16.1	C	COG2069	CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe-S protein)
Svar2525|CDS|CDS	1.2	0.3	15.9	C	COG0822	NifU homolog involved in Fe-S cluster formation

TS28Rum01872|CDS|CDS	3.5	1.0	15.9	C	COG2080|COG3427	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Uncharacterized conserved protein
TS28Eub8528|CDS|CDS	3.5	1.0	15.9	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Chyl3388|CDS|CDS	3.5	1.0	15.9	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi740794|CDS|CDS	13.3	3.8	15.8	C	COG0374|COG3259	Ni,Fe-hydrogenase I large subunit|Coenzyme F420-reducing hydrogenase, alpha subunit
TS28Fae16152|CDS|CDS	17.3	5.0	15.7	C	COG1454	Alcohol dehydrogenase, class IV
TS28Met1782|CDS|CDS	7.0	2.0	15.6	C	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I
Bbre0811|CDS|CDS	3.4	1.0	15.4	C	COG1882	Pyruvate-formate lyase
TS28Met0473|CDS|CDS	14.0	4.2	15.3	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
TS29Bac04864|CDS|CDS	13.4	4.0	15.3	C	COG0711	F0F1-type ATP synthase, subunit b
Rbro0916|CDS|CDS	15.0	4.5	15.1	C	COG1454	Alcohol dehydrogenase, class IV
TS28Fae21291|CDS|CDS	5.0	1.5	15.1	C	COG2033	Desulfoferrodoxin
TS28Clo04623|CDS|CDS	5.0	1.5	15.1	C	COG1454|COG1979	Alcohol dehydrogenase, class IV|Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family
Dfor2667|CDS|CDS	10.0	3.0	15.1	C	COG1592	Rubrerythrin
Aput0086|CDS|CDS	10.0	3.0	15.1	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
TS28Rum11774|CDS|CDS	16.5	5.0	15.0	C	COG0712	F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein)
Bxyl1943|CDS|CDS	4.1	1.3	14.9	C	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit
TS29Bac07742|CDS|CDS	8.2	2.5	14.8	C	COG1592	Rubrerythrin
TS28Col0763|CDS|CDS	6.5	2.0	14.8	C	COG0822	NifU homolog involved in Fe-S cluster formation
TS29Bac08258|CDS|CDS	26.0	8.0	14.8	C	COG1592	Rubrerythrin
Rlac0637|CDS|CDS	4.8	1.5	14.4	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Fae08714|CDS|CDS	19.0	6.0	14.4	C	COG2025|COG2086	Electron transfer flavoprotein, alpha subunit|Electron transfer flavoprotein, beta subunit
TS29Rum20003|CDS|CDS	23.6	7.5	14.3	C	COG0822	NifU homolog involved in Fe-S cluster formation
TS28Eub0367|CDS|CDS	11.0	3.5	14.3	C	COG0554	Glycerol kinase
TS28Rum09777|CDS|CDS	38.3	12.3	14.1	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Fae01835|CDS|CDS	10.8	3.5	14.1	C	COG1882	Pyruvate-formate lyase
TS28Dor0740|CDS|CDS	8.7	2.8	13.9	C	COG1592	Rubrerythrin
TS29Clo0432|CDS|CDS	19.7	6.5	13.7	C	COG1882	Pyruvate-formate lyase
Bova3669|CDS|CDS	1.0	0.3	13.6	C	COG1007	NADH:ubiquinone oxidoreductase subunit 2 (chain N)
Bxyl1379|CDS|CDS	1.0	0.3	13.6	C	COG1014|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28Met1148|CDS|CDS	2.5	0.8	13.6	C	COG1145	Ferredoxin
TS29Clo0895|CDS|CDS	6.0	2.0	13.6	C	COG0280|COG0857	Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
TS28Rum03174|CDS|CDS	1.5	0.5	13.6	C	COG0356	F0F1-type ATP synthase, subunit a
Rumhyd2637|CDS|CDS	3.0	1.0	13.6	C	COG0281|COG0280|COG0857	Malic enzyme|Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
Robe3511|CDS|CDS	1.5	0.5	13.6	C	COG0356	F0F1-type ATP synthase, subunit a
Buni1806|CDS|CDS	3.0	1.0	13.6	C	COG4658|COG1805	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD|Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrB
TS28Dor2656|CDS|CDS	3.0	1.0	13.6	C	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I
TS28Met0556|CDS|CDS	3.0	1.0	13.6	C	COG1145	Ferredoxin
Rumhyd2688|CDS|CDS	3.0	1.0	13.6	C	COG1614	CO dehydrogenase/acetyl-CoA synthase beta subunit
Acac0251|CDS|CDS	3.0	1.0	13.6	C	COG2086	Electron transfer flavoprotein, beta subunit
Aput1545|CDS|CDS	3.0	1.0	13.6	C	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family
TS28Rum04771|CDS|CDS	1.5	0.5	13.6	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
Csym1329|CDS|CDS	3.0	1.0	13.6	C	COG2086	Electron transfer flavoprotein, beta subunit
TS29Bac02279|CDS|CDS	4.5	1.5	13.6	C	COG1592	Rubrerythrin
Dlon0162|CDS|CDS	4.5	1.5	13.6	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
TS28Met1190|CDS|CDS	4.8	1.6	13.5	C	COG1145	Ferredoxin
TS28Rum11190|CDS|CDS	16.3	5.5	13.4	C	COG0282	Acetate kinase
Msmi751009|CDS|CDS	2.9	1.0	13.2	C	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit
Bova3395|CDS|CDS	12.8	4.5	12.9	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS28Rum11776|CDS|CDS	8.5	3.0	12.9	C	COG0056	F0F1-type ATP synthase, alpha subunit
Buni2097|CDS|CDS	8.5	3.0	12.9	C	COG0224	F0F1-type ATP synthase, gamma subunit
Rumhyd1672|CDS|CDS	2.8	1.0	12.9	C	COG0055	F0F1-type ATP synthase, beta subunit
Bhan2076|CDS|CDS	2.8	1.0	12.9	C	COG1614	CO dehydrogenase/acetyl-CoA synthase beta subunit
TS29Met0823|CDS|CDS	31.1	11.0	12.8	C	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit
TS29Rum14199|CDS|CDS	39.5	14.0	12.8	C	COG1592	Rubrerythrin
TS29Rum11000|CDS|CDS	31.0	11.0	12.8	C	COG2025|COG2086	Electron transfer flavoprotein, alpha subunit|Electron transfer flavoprotein, beta subunit
TS29Rum13363|CDS|CDS	222.2	79.0	12.8	C	COG1456	CO dehydrogenase/acetyl-CoA synthase gamma subunit (corrinoid Fe-S protein)
BactD11824|CDS|CDS	8.4	3.0	12.7	C	COG0224	F0F1-type ATP synthase, gamma subunit
Msmi740375|CDS|CDS	1.4	0.5	12.7	C	COG2218	Formylmethanofuran dehydrogenase subunit C
Dlon2091|CDS|CDS	4.2	1.5	12.7	C	COG1592	Rubrerythrin
BactD12161|CDS|CDS	1.9	0.7	12.6	C	COG1979|COG1454	Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family|Alcohol dehydrogenase, class IV
Bxyl0241|CDS|CDS	12.4	4.5	12.6	C	COG0711	F0F1-type ATP synthase, subunit b
Cbol3054|CDS|CDS	11.0	4.0	12.5	C	COG1529|COG2080	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs|Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs
TS29Met0285|CDS|CDS	24.4	9.0	12.3	C	COG2048|COG0247|COG1150	Heterodisulfide reductase, subunit B|Fe-S oxidoreductase|Heterodisulfide reductase, subunit C
Bxyl0844|CDS|CDS	8.1	3.0	12.2	C	COG1145	Ferredoxin
TS28Met1301|CDS|CDS	7.0	2.6	12.2	C	COG2048|COG0479|COG0247|COG1139	Heterodisulfide reductase, subunit B|Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit|Fe-S oxidoreductase|Uncharacterized conserved protein containing a ferredoxin-like domain

BactD10967|CDS|CDS	4.3	1.6	12.2	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
TS29Rum13367|CDS|CDS	124.6	46.5	12.2	C	COG1151	6Fe-6S prismane cluster-containing protein
TS29Bac00274|CDS|CDS	25.3	9.5	12.1	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
TS28Fae10823|CDS|CDS	2.7	1.0	12.1	C	COG1454	Alcohol dehydrogenase, class IV
Buni0871|CDS|CDS	4.0	1.5	12.1	C	COG1145	Ferredoxin
TS28Rum16063|CDS|CDS	8.0	3.0	12.1	C	COG3383|COG0243	Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
TS29Clo4498|CDS|CDS	8.0	3.0	12.1	C	COG1620	L-lactate permease
TS29Met0924|CDS|CDS	21.2	8.0	12.0	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
TS29Bac10921|CDS|CDS	13.1	5.0	11.9	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS29Rum13368|CDS|CDS	69.6	26.5	11.9	C	COG1151	6Fe-6S prismane cluster-containing protein
Msmi740099|CDS|CDS	1.8	0.7	11.9	C	COG1436	Archaeal/vacuolar-type H+-ATPase subunit F
Msmi751596|CDS|CDS	1.8	0.7	11.9	C	COG1436	Archaeal/vacuolar-type H+-ATPase subunit F
BDI3032|CDS|rubrerythrin	9.0	3.5	11.7	C	COG1592	Rubrerythrin
TS28Rum15923|CDS|CDS	36.0	14.0	11.7	C	COG4624|COG1034|COG3383|COG0243	Iron only hydrogenase large subunit, C-terminal domain|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Uncharacterized anaerobic dehydrogenase|Anaerobic dehydrogenases, typically selenocysteine-containing
Bxyl1962|CDS|CDS	3.4	1.3	11.6	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Msm1348|CDS|rubrerythrin	2.6	1.0	11.6	C	COG1592	Rubrerythrin
TS28Met0463|CDS|CDS	2.6	1.0	11.6	C	COG1592	Rubrerythrin
TS29Clo0166|CDS|CDS	144.0	56.5	11.6	C	COG1882	Pyruvate-formate lyase
BactD13022|CDS|CDS	10.2	4.0	11.6	C	COG0822	NifU homolog involved in Fe-S cluster formation
Acac0053|CDS|CDS	5.0	2.0	11.3	C	COG3808	Inorganic pyrophosphatase
Rgna1692|CDS|CDS	10.0	4.0	11.3	C	COG0224	F0F1-type ATP synthase, gamma subunit
Rumhyd2795|CDS|CDS	5.0	2.0	11.3	C	COG0508|COG1071|COG0022	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes|Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit|Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit
TS28Fae09992|CDS|CDS	2.5	1.0	11.3	C	COG0280|COG0857	Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
TS28Rum01176|CDS|CDS	2.5	1.0	11.3	C	COG2878|COG1145	Predicted NADH:ubiquinone oxidoreductase, subunit RnfB|Ferredoxin
TS29Dor0452|CDS|CDS	5.0	2.0	11.3	C	COG1014|COG4231|COG1146	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits|Ferredoxin
TS28Rum15926|CDS|CDS	7.5	3.0	11.3	C	COG1905	NADH:ubiquinone oxidoreductase 24 kD subunit
Msmi740095|CDS|CDS	6.3	2.5	11.3	C	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I
TS29Par274|CDS|CDS	7.3	3.0	11.1	C	COG1592	Rubrerythrin
TS28Rum09669|CDS|CDS	74.1	30.5	11.0	C	COG0822	NifU homolog involved in Fe-S cluster formation
Msmi740379|CDS|CDS	0.6	0.3	10.9	C	COG1145	Ferredoxin
TS29Met0497|CDS|CDS	0.6	0.3	10.9	C	COG1145	Ferredoxin
Msmi751298|CDS|CDS	0.6	0.3	10.9	C	COG1145	Ferredoxin
TS28Met1191|CDS|CDS	0.6	0.3	10.9	C	COG1145	Ferredoxin
Msmi740384|CDS|CDS	6.7	2.8	10.8	C	COG1035|COG1145|COG1908	Coenzyme F420-reducing hydrogenase, beta subunit|Ferredoxin|Coenzyme F420-reducing hydrogenase, delta subunit
Bhan1765|CDS|CDS	7.2	3.0	10.8	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)
TS28Rum15656|CDS|CDS	10.8	4.5	10.8	C	COG2080|COG1529	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs
Robe2012|CDS|CDS	17.8	7.5	10.8	C	COG1151	6Fe-6S prismane cluster-containing protein
TS29Rum21138|CDS|CDS	99.2	42.0	10.7	C	COG1592	Rubrerythrin
TS29Met0431|CDS|CDS	11.8	5.0	10.7	C	COG3259	Coenzyme F420-reducing hydrogenase, alpha subunit
Msmi750888|CDS|CDS	2.8	1.2	10.7	C	COG1145	Ferredoxin
TS28Fae16104|CDS|CDS	8.6	3.7	10.6	C	COG4656	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC
Acac1342|CDS|CDS	2.3	1.0	10.6	C	COG0822	NifU homolog involved in Fe-S cluster formation
Bxyl1361|CDS|CDS	3.5	1.5	10.6	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS28Rum08609|CDS|CDS	3.5	1.5	10.6	C	COG5016|COG1038	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
Cbol4185|CDS|CDS	7.0	3.0	10.6	C	COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains
TS28Fae20696|CDS|CDS	2.3	1.0	10.6	C	COG0584|COG4781	Glycerophosphoryl diester phosphodiesterase|Membrane domain of membrane-anchored glycerophosphoryl diester phosphodiesterase
TS29Bac03237|CDS|CDS	11.5	5.0	10.4	C	COG1394	Archaeal/vacuolar-type H+-ATPase subunit D
TS28Met1779|CDS|CDS	3.1	1.4	10.4	C	COG1527|COG1436	Archaeal/vacuolar-type H+-ATPase subunit C|Archaeal/vacuolar-type H+-ATPase subunit F
Bfra31121738|CDS|CDS	2.3	1.0	10.2	C	COG2086	Electron transfer flavoprotein, beta subunit
Rumhyd1367|CDS|CDS	4.5	2.0	10.2	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
TS29Rum05362|CDS|CDS	4.5	2.0	10.2	C	COG1902	NADH:flavin oxidoreductases, Old Yellow Enzyme family
FpraM2120923|CDS|CDS	3.3	1.5	10.1	C	COG1454	Alcohol dehydrogenase, class IV
FpraM2121279|CDS|CDS	208.8	94.0	10.1	C	COG1014|COG1013|COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Msmi750891|CDS|CDS	4.4	2.0	10.0	C	COG1908|COG1941	Coenzyme F420-reducing hydrogenase, delta subunit|Coenzyme F420-reducing hydrogenase, gamma subunit
TS28Met0354|CDS|CDS	4.4	2.0	10.0	C	COG1908|COG1941	Coenzyme F420-reducing hydrogenase, delta subunit|Coenzyme F420-reducing hydrogenase, gamma subunit
TS28Bif4766|CDS|CDS	1.3	57.5	0.1	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS28Bif0847|CDS|CDS	2.8	130.5	0.1	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
TS29Bif3771|CDS|CDS	2.8	130.5	0.1	C	COG1454|COG1012	Alcohol dehydrogenase, class IV|NAD-dependent aldehyde dehydrogenases
TS29Col0474|CDS|CDS	1.0	48.0	0.1	C	COG0554	Glycerol kinase
TS29Bif2730|CDS|CDS	0.5	24.8	0.1	C	COG0039	Malate/lactate dehydrogenases
Bpse1451|CDS|CDS	0.3	16.8	0.1	C	COG1804	Predicted acyl-CoA transferases/carnitine dehydratase
TS29Bif1456|CDS|CDS	0.7	33.8	0.1	C	COG1454	Alcohol dehydrogenase, class IV
TS29Rum13605|CDS|CDS	1.0	51.0	0.1	C	COG1151	6Fe-6S prismane cluster-containing protein
TS29Bif2221|CDS|CDS	1.5	77.0	0.1	C	COG1048	Aconitase A
TS29Rum00849|CDS|CDS	1.0	55.0	0.1	C	COG1409|COG0584	Predicted phosphohydrolases|Glycerophosphoryl diester phosphodiesterase
TS28Fae12108|CDS|CDS	0.5	28.5	0.1	C	COG4658|COG1805	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD|Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrB

TS29Col0483|CDS|CDS	1.0	57.5	0.1	C	COG0055	F0F1-type ATP synthase, beta subunit
TS28Bif4574|CDS|CDS	0.5	29.8	0.1	C	COG0039	Malate/lactate dehydrogenases
TS29Bif0986|CDS|CDS	0.7	39.8	0.1	C	COG0039	Malate/lactate dehydrogenases
TS29Col0805|CDS|CDS	0.5	30.0	0.1	C	COG0656|COG0667|COG1453	Aldo/keto reductases, related to diketogulonate reductase|Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)|Predicted oxidoreductases of the aldo/keto reductase family
TS28Bif5371|CDS|CDS	0.5	27.3	0.1	C	COG0282	Acetate kinase
TS29RumUnc0107|CDS|CDS	1.0	64.0	0.1	C	COG0056	F0F1-type ATP synthase, alpha subunit
TS29Bif0211|CDS|CDS	0.3	21.3	0.1	C	COG1804	Predicted acyl-CoA transferases/carnitine dehydratase
TS29Rum13342|CDS|CDS	0.3	22.0	0.1	C	COG0716	Flavodoxins
TS28Fae17794|CDS|CDS	0.4	27.0	0.1	C	COG0056|COG4933	F0F1-type ATP synthase, alpha subunit|Uncharacterized conserved protein
TS29Bif0507|CDS|CDS	3.8	258.7	0.1	C	COG2352	Phosphoenolpyruvate carboxylase
Bpse1442|CDS|CDS	0.1	9.8	0.1	C	COG0055	F0F1-type ATP synthase, beta subunit
TS28Bif3354|CDS|CDS	0.5	35.3	0.1	C	COG1048	Aconitase A
TS29Rum00947|CDS|CDS	0.5	37.5	0.1	C	COG1882	Pyruvate-formate lyase
TS29Bif3900|CDS|CDS	1.5	113.2	0.1	C	COG1454|COG1979	Alcohol dehydrogenase, class IV|Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family
TS28Fae07401|CDS|CDS	0.5	38.5	0.1	C	COG0426|COG0446|COG1773|COG1853	Uncharacterized flavoproteins|Uncharacterized NAD(FAD)-dependent dehydrogenases|Rubredoxin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
TS29Rum20557|CDS|CDS	0.5	39.5	0.1	C	COG1454|COG1979	Alcohol dehydrogenase, class IV|Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family
TS28Bif0786|CDS|CDS	0.8	67.2	0.1	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS29Bif3820|CDS|CDS	0.8	67.2	0.1	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS29Bif1598|CDS|CDS	0.3	29.0	0.1	C	COG1454	Alcohol dehydrogenase, class IV
TS29Bif2955|CDS|CDS	0.3	21.8	0.1	C	COG0822	NifU homolog involved in Fe-S cluster formation
TS28Bif0237|CDS|CDS	0.3	21.8	0.1	C	COG0822	NifU homolog involved in Fe-S cluster formation
TS29Rum14576|CDS|CDS	0.5	44.0	0.1	C	COG1148|COG1908	Heterodisulfide reductase, subunit A and related polyferredoxins|Coenzyme F420-reducing hydrogenase, delta subunit
TS29Rum15722|CDS|CDS	0.5	44.5	0.1	C	COG1012	NAD-dependent aldehyde dehydrogenases
TS29Bif2805|CDS|CDS	0.3	29.7	0.1	C	COG0045	Succinyl-CoA synthetase, beta subunit
TS28Bif1906|CDS|CDS	0.3	29.7	0.1	C	COG0045	Succinyl-CoA synthetase, beta subunit
TS28Bif3811|CDS|CDS	0.2	17.8	0.1	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS28Fae14489|CDS|CDS	0.3	24.0	0.0	C	COG4658	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD
TS28Bif1622|CDS|CDS	0.1	14.3	0.0	C	COG0055	F0F1-type ATP synthase, beta subunit
TS29Clo3364|CDS|CDS	0.3	39.0	0.0	C	COG1894|COG1905	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|NADH:ubiquinone oxidoreductase 24 kD subunit
TS29Bif3391|CDS|CDS	0.8	99.1	0.0	C	COG1757	Na+/H+ antiporter
TS29Bif3354|CDS|CDS	0.3	34.5	0.0	C	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
TS29Bif1208|CDS|CDS	0.2	27.8	0.0	C	COG0240	Glycerol-3-phosphate dehydrogenase
TS29Bif0245|CDS|CDS	0.1	21.8	0.0	C	COG0055	F0F1-type ATP synthase, beta subunit
TS29Bif3083|CDS|CDS	0.5	69.0	0.0	C	COG0282	Acetate kinase
TS29Bif3039|CDS|CDS	0.5	79.8	0.0	C	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit
TS29Bif2942|CDS|CDS	0.3	43.3	0.0	C	COG1282	NAD/NADP transhydrogenase beta subunit
TS29Bif3407|CDS|CDS	0.7	117.5	0.0	C	COG1012	NAD-dependent aldehyde dehydrogenases
TS29Bif3301|CDS|CDS	0.3	55.8	0.0	C	COG0656|COG0667	Aldo/keto reductases, related to diketogulonate reductase|Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
TS29Bif3082|CDS|CDS	0.5	143.8	0.0	C	COG0280|COG0857	Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
TS28Bif4538|CDS|CDS	0.3	72.7	0.0	C	COG0778	Nitroreductase
TS29Bif3534|CDS|CDS	0.3	72.7	0.0	C	COG0778	Nitroreductase
TS28Fae16539|CDS|CDS	0.1	67.0	0.0	C	COG1882	Pyruvate-formate lyase
Robe0280|CDS|CDS	2.0	0.5	18.2	C|F	COG1319|COG4630	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs|Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A
Cbol3053|CDS|CDS	3.0	1.0	13.6	C|F	COG1319|COG2080|COG4630	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs|Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A
FpraM2121978|CDS|CDS	8.0	3.5	10.4	C|F	COG1529|COG2080|COG4631	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs|Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Xanthine dehydrogenase, molybdopterin-binding subunit B
BactD20750|CDS|CDS	1.2	0.5	10.9	C|G	COG1070|COG1069	Sugar (pentulose and hexulose) kinases|Ribulose kinase
Bova1898|CDS|CDS	1.2	0.5	10.9	C|G	COG1070|COG1069	Sugar (pentulose and hexulose) kinases|Ribulose kinase
TS28Rum11278|CDS|CDS	1.7	0.3	22.7	C|H	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
TS29Rum07782|CDS|CDS	1.7	0.3	22.7	C|H	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
TS28Rum04107|CDS|CDS	1.7	0.5	15.1	C|H	COG2243|COG2073|COG2241|COG2082|COG1010|COG1251|COG1492|COG2158	Precorrin-2 methylase|Cobalamin biosynthesis protein CbiG|Precorrin-6B methylase 1|Precorrin isomerase|Precorrin-3B methylase|NAD(P)H-nitrite reductase|Cobyric acid synthase|Uncharacterized protein containing a Zn-finger-like domain
TS29Rum13395|CDS|CDS	94.0	41.0	10.4	C|H	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
TS28Bac1795|CDS|CDS	4.3	0.7	29.5	C|I	COG2030|COG0280|COG0857	Acyl dehydratase|Phosphotransacetylase|BioD-like N-terminal domain of phosphotransacetylase
TS28Fae18582|CDS|CDS	13.0	2.0	29.5	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
TS29Rum10998|CDS|CDS	13.0	2.0	29.5	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
M23Apeg4243|CDS|Rubrerythrin	6.0	1.0	27.2	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Rumhyd1369|CDS|CDS	6.0	1.0	27.2	C|I	COG1038|COG0439|COG4770	Pyruvate carboxylase|Biotin carboxylase|Acetyl/propionyl-CoA carboxylase, alpha subunit
Bxyl2120|CDS|CDS	4.8	1.0	21.7	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
TS29Rum10997|CDS|CDS	19.5	5.0	17.7	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
TS28Col1695|CDS|CDS	15.5	4.0	17.6	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
TS28Fae08712|CDS|CDS	26.5	7.0	17.2	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
Acac2774|CDS|CDS	7.0	2.0	15.9	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
BactD22531|CDS|CDS	3.3	1.0	14.9	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
TS28Fae20638|CDS|CDS	41.5	13.0	14.5	C|I	COG1960|COG2025	Acyl-CoA dehydrogenases|Electron transfer flavoprotein, alpha subunit
Buni0918|CDS|CDS	12.0	4.5	12.1	C|I	COG5016|COG1038|COG0511	Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase|Biotin carboxyl carrier protein
Buni0879|CDS|CDS	5.2	2.0	11.7	C|I	COG2025|COG1960	Electron transfer flavoprotein, alpha subunit|Acyl-CoA dehydrogenases
CspL21839|CDS|CDS	3.2	1.3	10.9	C|I	COG1592|COG1853|COG1607	Rubrerythrin|Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family|Acyl-CoA hydrolase
BactD14019|CDS|CDS	5.2	2.3	10.1	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
Bova2162|CDS|CDS	5.2	2.3	10.1	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase
TS29Bac03567|CDS|CDS	5.2	2.3	10.1	C|I	COG1592|COG1607	Rubrerythrin|Acyl-CoA hydrolase

TS28Fae20631|CDS|CDS	4.5	1.0	20.4	C|K	COG0427|COG0454	Acetyl-CoA hydrolase|Histone acetyltransferase HPA2 and related acetyltransferases
TS28Bac0879|CDS|CDS	14.3	5.0	13.0	C|K	COG1595|COG5016|COG1038	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog|Pyruvate/oxaloacetate carboxyltransferase|Pyruvate carboxylase
TS28Bac6174|CDS|CDS	3.3	0.5	30.3	C|L	COG1372|COG1155	Intein/homing endonuclease|Archaeal/vacuolar-type H+-ATPase subunit A
TS29Met0241|CDS|CDS	2.2	0.9	11.1	C|L	COG1156|COG1372|COG1155	Archaeal/vacuolar-type H+-ATPase subunit B|Intein/homing endonuclease|Archaeal/vacuolar-type H+-ATPase subunit A
Bxyl1990|CDS|CDS	11.7	1.0	53.0	C|M|G	COG3507|COG3291|COG2273|COG5498|COG3488	Beta-xylosidase|FOG: PKD repeat|Beta-glucanase/Beta-glucan synthetase|Predicted glycosyl hydrolase|Predicted thiol oxidoreductase
Cbol1698|CDS|CDS	62.0	4.0	70.4	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
BDI1978|CDS|thioredoxin	19.0	2.0	43.1	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
Dfor0624|CDS|CDS	42.5	6.0	32.2	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Dfor0623|CDS|CDS	7.0	1.0	31.8	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
BDI1711|CDS|thioredoxin	16.0	3.0	24.2	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
Cbol1697|CDS|CDS	10.0	2.0	22.7	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Dfor2069|CDS|CDS	7.0	2.0	15.9	C|O	COG0526	Thiol-disulfide isomerase and thioredoxins
Buni1323|CDS|CDS	6.0	2.0	13.6	C|O	COG0526|COG0229|COG0225	Thiol-disulfide isomerase and thioredoxins|Conserved domain frequently associated with peptide methionine sulfoxide reductase|Peptide methionine sulfoxide reductase
Aput2323|CDS|CDS	6.0	2.0	13.6	C|O	COG0526|COG0785	Thiol-disulfide isomerase and thioredoxins|Cytochrome c biogenesis protein
Dlon0990|CDS|CDS	6.0	2.0	13.6	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Ccom1705|CDS|CDS	11.0	4.0	12.5	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Dfor2070|CDS|CDS	11.0	4.0	12.5	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Cbol5405|CDS|CDS	5.0	2.0	11.3	C|O	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
Bxyl4091|CDS|CDS	9.0	4.0	10.2	C|O	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
TS29Col1519|CDS|CDS	2.0	137.0	0.1	C|P	COG1009|COG2111|COG0650	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit|Multisubunit Na+/H+ antiporter, MnhB subunit|Formate hydrogenlyase subunit 4
TS28Dor3117|CDS|CDS	3.0	1.3	10.2	C|P|V	COG1131|COG4152|COG4555	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component|ABC-type Na+ transport system, ATPase component
TS29Bif3316|CDS|CDS	0.2	25.9	0.0	C|P|V	COG1131|COG4152|COG4586|COG4555	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component|ABC-type Na+ transport system, ATPase component
TS28Bif4720|CDS|CDS	0.2	25.9	0.0	C|P|V	COG1131|COG4152|COG4586|COG4555	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component|ABC-type Na+ transport system, ATPase component
TS28Rum15626|CDS|CDS	42.8	1.5	129.5	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
Robe3271|CDS|CDS	12.5	0.5	113.5	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
Ehal0413|CDS|CDS	6.0	0.5	54.5	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS28Eub0625|CDS|CDS	6.0	0.5	54.5	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS28Bac7267|CDS|CDS	6.0	0.7	40.9	C|Q	COG0282|COG4869	Acetate kinase|Propanediol utilization protein
Buni0164|CDS|CDS	6.0	0.7	40.9	C|Q	COG0282|COG4869	Acetate kinase|Propanediol utilization protein
Robe3277|CDS|CDS	2.7	0.5	24.5	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS28Rum15682|CDS|CDS	7.0	1.5	21.3	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS29Rum08440|CDS|CDS	16.0	4.0	18.2	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS29Rum00111|CDS|CDS	64.8	17.5	16.8	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS29Rum12353|CDS|CDS	26.3	8.0	14.9	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
Cbol6610|CDS|CDS	3.0	1.0	13.6	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
TS28Rum04248|CDS|CDS	3.0	1.0	13.6	C|Q	COG0282|COG4869	Acetate kinase|Propanediol utilization protein
Rumhyd2638|CDS|CDS	3.0	1.0	13.6	C|Q	COG0282|COG4869	Acetate kinase|Propanediol utilization protein
TS28Rum15627|CDS|CDS	8.8	3.5	11.3	C|Q	COG4577	Carbon dioxide concentrating mechanism/carboxysome shell protein
Bbre1583|CDS|CDS	3.3	0.3	44.3	C|V|O	COG2274|COG1132|COG4987|COG4988|COG5265	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
RintL11975|CDS|CDS	8.0	3.0	12.1	C|V|O	COG1132|COG4988|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS28Rum13672|CDS|CDS	20.5	1.0	93.1	D	COG3640	CO dehydrogenase maturation factor
TS29Fae09031|CDS|CDS	5.5	0.5	49.9	D	COG2184	Protein involved in cell division
TS28Col1205|CDS|CDS	10.0	1.0	45.4	D	COG0206	Cell division GTPase
Rumhyd2687|CDS|CDS	9.0	1.0	40.9	D	COG3640	CO dehydrogenase maturation factor
TS29Rum13366|CDS|CDS	206.5	28.5	32.9	D	COG3640	CO dehydrogenase maturation factor
TS28Fae02149|CDS|CDS	19.0	3.0	28.8	D	COG3599	Cell division initiation protein
Casp3452|CDS|CDS	12.3	2.0	27.8	D	COG0206	Cell division GTPase
Dlon1840|CDS|CDS	6.0	1.0	27.2	D	COG0772	Bacterial cell division membrane protein
TS29Rum17365|CDS|CDS	3.0	0.5	27.2	D	COG3640	CO dehydrogenase maturation factor
Buni3012|CDS|CDS	14.0	2.5	25.4	D	COG0206	Cell division GTPase
Bxyl2772|CDS|CDS	1.8	0.3	25.0	D	COG0489	ATPases involved in chromosome partitioning
BactD11569|CDS|CDS	1.8	0.3	25.0	D	COG0489	ATPases involved in chromosome partitioning
BactD12549|CDS|CDS	1.8	0.3	23.8	D	COG2385	Sporulation protein and related proteins
Buni2388|CDS|CDS	7.5	1.5	22.7	D	COG0489	ATPases involved in chromosome partitioning
Rumhyd0764|CDS|CDS	4.0	1.0	18.2	D	COG0206	Cell division GTPase
Bova2776|CDS|CDS	1.0	0.3	18.2	D	COG1077	Actin-like ATPase involved in cell morphogenesis
BactD21851|CDS|CDS	1.0	0.3	18.2	D	COG1077	Actin-like ATPase involved in cell morphogenesis
Robe2011|CDS|CDS	16.5	4.5	16.6	D	COG3640	CO dehydrogenase maturation factor
Bple3408|CDS|CDS	3.3	1.0	15.1	D	COG1192	ATPases involved in chromosome partitioning
Bcoproc1024|CDS|CDS	3.3	1.0	15.1	D	COG1192	ATPases involved in chromosome partitioning
Msmi751409|CDS|CDS	3.3	1.0	14.8	D	COG0206	Cell division GTPase
Msmi740271|CDS|CDS	3.3	1.0	14.8	D	COG0206	Cell division GTPase
TS28Rum10356|CDS|CDS	8.0	2.5	14.5	D	COG1196	Chromosome segregation ATPases
Clep0715|CDS|CDS	5.0	1.7	13.6	D	COG2894|COG0455	Septum formation inhibitor-activating ATPase|ATPases involved in chromosome partitioning

TS29Clo4347|CDS|CDS	5.0	1.7	13.6	D	COG2894|COG0455	Septum formation inhibitor-activating ATPase|ATPases involved in chromosome partitioning
Bthe3730956|CDS|CDS	1.0	0.3	13.6	D	COG1192	ATPases involved in chromosome partitioning
TS28Fae18349|CDS|CDS	1.5	0.5	13.6	D	COG0772	Bacterial cell division membrane protein
TS28Rum12409|CDS|CDS	1.5	0.5	13.6	D	COG1196	Chromosome segregation ATPases
Acol2658|CDS|CDS	3.0	1.0	13.6	D	COG1196	Chromosome segregation ATPases
TS28Rum00123|CDS|CDS	4.5	1.5	13.6	D	COG0489	ATPases involved in chromosome partitioning
ShigspD90371|CDS|CDS	2.8	1.0	12.9	D	COG3096	Uncharacterized protein involved in chromosome partitioning
Aput0467|CDS|CDS	33.5	12.0	12.7	D	COG0206	Cell division GTPase
TS28Clo10667|CDS|CDS	11.0	4.0	12.5	D	COG3599	Cell division initiation protein
Buni3010|CDS|CDS	16.2	6.0	12.2	D	COG0849	Actin-like ATPase involved in cell division
Rtor2137|CDS|CDS	1.3	0.5	12.1	D	COG0850	Septum formation inhibitor
TS29Rum19274|CDS|CDS	45.8	19.5	10.7	D	COG0206	Cell division GTPase
TS28Fae19350|CDS|CDS	7.0	3.0	10.6	D	COG3599	Cell division initiation protein
TS29Fae08499|CDS|CDS	1.0	49.0	0.1	D	COG1192	ATPases involved in chromosome partitioning
TS29Bif2523|CDS|CDS	2.0	105.0	0.1	D	COG1674	DNA segregation ATPase FtsK/SpoIIIE and related proteins
TS29Fae09303|CDS|CDS	1.5	79.0	0.1	D	COG1674	DNA segregation ATPase FtsK/SpoIIIE and related proteins
TS29Rum00036|CDS|CDS	0.5	28.0	0.1	D	COG0424	Nucleotide-binding protein implicated in inhibition of septum formation
TS28Fae18705|CDS|CDS	0.5	28.0	0.1	D	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control
Dfor3114|CDS|CDS	0.5	30.8	0.1	D	COG1192	ATPases involved in chromosome partitioning
TS29RumUnc1679|CDS|CDS	1.0	66.0	0.1	D	COG0772	Bacterial cell division membrane protein
CspM6211948|CDS|CDS	0.5	34.7	0.1	D	COG1192	ATPases involved in chromosome partitioning
TS29Rum19437|CDS|CDS	1.0	74.5	0.1	D	COG1674	DNA segregation ATPase FtsK/SpoIIIE and related proteins
TS28Fae18143|CDS|CDS	0.5	37.5	0.1	D	COG1192	ATPases involved in chromosome partitioning
TS29Fae00047|CDS|CDS	0.5	37.5	0.1	D	COG1192	ATPases involved in chromosome partitioning
TS29Fae00895|CDS|CDS	1.5	124.5	0.1	D	COG5279	Uncharacterized protein involved in cytokinesis, contains TGc (transglutaminase/protease-like) domain
TS29Rum12397|CDS|CDS	0.5	47.5	0.0	D	COG0445	NAD/FAD-utilizing enzyme apparently involved in cell division
TS29Fae08494|CDS|CDS	1.1	110.5	0.0	D	COG0445	NAD/FAD-utilizing enzyme apparently involved in cell division
TS29Rum16532|CDS|CDS	0.3	32.3	0.0	D	COG2184	Protein involved in cell division
TS29Rum11742|CDS|CDS	1.0	104.0	0.0	D	COG1192	ATPases involved in chromosome partitioning
TS29Bac07786|CDS|CDS	0.3	28.2	0.0	D	COG0772	Bacterial cell division membrane protein
TS29Bac09561|CDS|CDS	0.2	25.0	0.0	D	COG0445	NAD/FAD-utilizing enzyme apparently involved in cell division
TS29Bif0528|CDS|CDS	0.3	78.9	0.0	D	COG0772	Bacterial cell division membrane protein
TS28Bif4497|CDS|CDS	0.3	78.9	0.0	D	COG0772	Bacterial cell division membrane protein
TS29Bif2423|CDS|CDS	0.3	91.8	0.0	D	COG0772	Bacterial cell division membrane protein
TS29Bif2465|CDS|CDS	0.3	234.7	0.0	D	COG1196	Chromosome segregation ATPases
Rumhyd1512|CDS|CDS	0.2	28.0	0.0	D|V|Q	COG1136|COG4181|COG2884	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component|Predicted ATPase involved in cell division
TS28Dor0707|CDS|CDS	14.9	0.5	135.4	E	COG0686	Alanine dehydrogenase
Dlon0626|CDS|CDS	12.9	0.5	117.3	E	COG0686	Alanine dehydrogenase
BDI2672|CDS|arginase	20.0	1.0	90.8	E	COG1359|COG4992|COG1982|COG0010	Uncharacterized conserved protein|Ornithine/acetylornithine aminotransferase|Arginine/lysine/ornithine decarboxylases|Arginase/agmatinase/formimionoglutamate hydrolase, arginase family
Buni2819|CDS|CDS	14.0	1.0	63.6	E	COG2195	Di- and tripeptidases
Buni3421|CDS|CDS	6.5	0.5	59.0	E	COG0019|COG0527	Diaminopimelate decarboxylase|Aspartokinases
TS28Fae18414|CDS|CDS	6.5	0.5	59.0	E	COG0460	Homoserine dehydrogenase
TS28Rum13611|CDS|CDS	32.0	2.5	58.1	E	COG0014	Gamma-glutamyl phosphate reductase
Buni1224|CDS|CDS	43.9	4.0	49.8	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
CspM6212980|CDS|CDS	30.5	3.0	46.2	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
FpraM2120941|CDS|CDS	5.0	0.5	45.4	E	COG2502	Asparagine synthetase A
TS28Ali0217|CDS|CDS	10.0	1.0	45.4	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
TS28Dor0655|CDS|CDS	9.0	1.0	40.9	E	COG0531	Amino acid transporters
Caer1800|CDS|CDS	8.0	1.0	36.3	E	COG0722	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase
TS28Rum16250|CDS|CDS	4.0	0.5	36.3	E	COG4810	Ethanolamine utilization protein
Acac3379|CDS|CDS	8.0	1.0	36.3	E	COG0128|COG0287	5-enolpyruvylshikimate-3-phosphate synthase|Prephenate dehydrogenase
TS28RumUnc1995|CDS|CDS	8.0	1.0	36.3	E	COG1126|COG4598	ABC-type polar amino acid transport system, ATPase component|ABC-type histidine transport system, ATPase component
Aput1087|CDS|CDS	8.0	1.0	36.3	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Buni0628|CDS|CDS	7.7	1.0	34.8	E	COG0006	Xaa-Pro aminopeptidase
ShigspD92234|CDS|CDS	3.5	0.5	31.8	E	COG2981	Uncharacterized protein involved in cysteine biosynthesis
TS28Bac2692|CDS|CDS	4.3	0.7	29.5	E	COG2987	Urocanate hydratase
CspM6210827|CDS|CDS	6.5	1.0	29.5	E	COG1775	Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB
Dfor0629|CDS|CDS	19.0	3.0	28.8	E	COG1115	Na+/alanine symporter
ShigspD91594|CDS|CDS	6.3	1.0	28.8	E	COG0070	Glutamate synthase domain 3
Dfor1168|CDS|CDS	6.0	1.0	27.2	E	COG2008	Threonine aldolase
Rlac1849|CDS|CDS	6.0	1.0	27.2	E	COG0253	Diaminopimelate epimerase
Cbol5528|CDS|CDS	6.0	1.0	27.2	E	COG0078	Ornithine carbamoyltransferase
TS28Col1292|CDS|CDS	6.0	1.0	27.2	E	COG0548|COG1364	Acetylglutamate kinase|N-acetylglutamate synthase (N-acetylornithine aminotransferase)
TS28Fae19190|CDS|CDS	6.0	1.0	27.2	E	COG1123|COG4608	ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type oligopeptide transport system, ATPase component
Bxyl3854|CDS|CDS	4.0	0.7	27.2	E	COG0040	ATP phosphoribosyltransferase
BactD13049|CDS|CDS	4.0	0.7	27.2	E	COG0040	ATP phosphoribosyltransferase
TS28Rum01864|CDS|CDS	33.5	6.0	25.3	E	COG1171	Threonine dehydratase
TS28Rum01867|CDS|CDS	24.3	4.5	24.5	E	COG0078	Ornithine carbamoyltransferase
BactD20947|CDS|CDS	5.3	1.0	24.0	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Rum13305|CDS|CDS	26.0	5.0	23.6	E	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases
TS28Rum11259|CDS|CDS	5.0	1.0	22.7	E	COG1748	Saccharopine dehydrogenase and related proteins
Aput0292|CDS|CDS	5.0	1.0	22.7	E	COG0686	Alanine dehydrogenase
Cbol6056|CDS|CDS	5.0	1.0	22.7	E	COG0410|COG0411	ABC-type branched-chain amino acid transport systems, ATPase component|ABC-type branched-chain amino acid transport systems, ATPase component
TS28Col1313|CDS|CDS	15.0	3.0	22.7	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Csci2185|CDS|CDS	4.7	1.0	21.3	E	COG3938	Proline racemase
TS28Rum02864|CDS|CDS	7.0	1.5	21.2	E	COG0747	ABC-type dipeptide transport system, periplasmic component
Cbol1397|CDS|CDS	9.0	2.0	20.4	E	COG1003|COG0403	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain|Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain
TS28Rum13723|CDS|CDS	9.0	2.0	20.4	E	COG0436|COG1168	Aspartate/tyrosine/aromatic aminotransferase|Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities

BactD14479|CDS|CDS	4.3	1.0	19.7	E	COG2987	Urocanate hydratase
TS29Rum06400|CDS|CDS	42.0	10.0	19.1	E	COG0624|COG3195	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases|Uncharacterized protein conserved in bacteria
TS28Rum01868|CDS|CDS	8.0	2.0	18.2	E	COG0549	Carbamate kinase
Bova0736|CDS|CDS	4.0	1.0	18.2	E	COG2987	Urocanate hydratase
Aput0090|CDS|CDS	4.0	1.0	18.2	E	COG1045	Serine acetyltransferase
BactD11115|CDS|CDS	2.0	0.5	18.2	E	COG0509	Glycine cleavage system H protein (lipoate-binding)
TS29Rum11025|CDS|CDS	4.0	1.0	18.2	E	COG1003|COG0403	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain|Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain
Ehal1409|CDS|CDS	2.0	0.5	18.2	E	COG0665|COG0579	Glycine/D-amino acid oxidases (deaminating)|Predicted dehydrogenase
Acac2993|CDS|CDS	4.0	1.0	18.2	E	COG0703	Shikimate kinase
TS28Fae10841|CDS|CDS	4.0	1.0	18.2	E	COG1171	Threonine dehydratase
Buni3618|CDS|CDS	2.0	0.5	18.2	E	COG0110|COG1605	Acetyltransferase (isoleucine patch superfamily)|Chorismate mutase
BFnctc1597|CDS|histidinol-phosphatase	2.0	0.5	18.2	E	COG1387	Histidinol phosphatase and related hydrolases of the PHP family
TS28Dor1889|CDS|CDS	2.0	0.5	18.2	E	COG3104	Dipeptide/tripeptide permease
TS28Fae02113|CDS|CDS	8.0	2.0	18.2	E	COG1897	Homoserine trans-succinylase
TS28Rum11533|CDS|CDS	2.0	0.5	18.2	E	COG0141	Histidinol dehydrogenase
Dlon0125|CDS|CDS	2.0	0.5	18.2	E	COG3104	Dipeptide/tripeptide permease
Even0466|CDS|CDS	4.0	1.0	18.2	E	COG0460	Homoserine dehydrogenase
Rgna3372|CDS|CDS	4.0	1.0	18.2	E	COG0289	Dihydrodipicolinate reductase
BactD11193|CDS|CDS	1.3	0.3	18.2	E	COG2066	Glutaminase
TS28Bac5565|CDS|CDS	1.3	0.3	18.2	E	COG1305	Transglutaminase-like enzymes, putative cysteine proteases
TS28Clo09626|CDS|CDS	1.3	0.3	18.2	E	COG0263	Glutamate 5-kinase
Buni3364|CDS|CDS	1.3	0.3	18.2	E	COG1305	Transglutaminase-like enzymes, putative cysteine proteases
Bova1829|CDS|CDS	2.0	0.5	17.9	E	COG0112	Glycine/serine hydroxymethyltransferase
BactD20631|CDS|CDS	2.0	0.5	17.9	E	COG0112	Glycine/serine hydroxymethyltransferase
TS28Rum13609|CDS|CDS	3.8	1.0	17.4	E	COG0263	Glutamate 5-kinase
Bova2853|CDS|CDS	3.1	0.8	16.8	E	COG0070	Glutamate synthase domain 3
Bxyl1344|CDS|CDS	1.8	0.5	16.6	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
Robe2006|CDS|CDS	9.0	2.5	16.3	E	COG1410	Methionine synthase I, cobalamin-binding domain
Buni3493|CDS|CDS	7.7	2.2	16.1	E	COG0174	Glutamine synthetase
TS28Bac2259|CDS|CDS	7.7	2.2	16.1	E	COG0174	Glutamine synthetase
TS28Eub5273|CDS|CDS	1.2	0.3	15.9	E	COG3869	Arginine kinase
FpraM2121980|CDS|CDS	3.5	1.0	15.9	E	COG0709	Selenophosphate synthase
TS29Rum08488|CDS|CDS	7.0	2.0	15.9	E	COG0136	Aspartate-semialdehyde dehydrogenase
TS29Clo3826|CDS|CDS	14.0	4.0	15.9	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
TS28Col0144|CDS|CDS	7.0	2.0	15.9	E	COG2987	Urocanate hydratase
TS28Fae18755|CDS|CDS	3.5	1.0	15.9	E	COG1126	ABC-type polar amino acid transport system, ATPase component
TS28Rum14197|CDS|CDS	3.5	1.0	15.9	E	COG0410|COG0411	ABC-type branched-chain amino acid transport systems, ATPase component|ABC-type branched-chain amino acid transport systems, ATPase component
BactD11007|CDS|CDS	1.7	0.5	15.1	E	COG3579	Aminopeptidase C
TS28Rum13573|CDS|CDS	5.0	1.5	15.1	E	COG1362	Aspartyl aminopeptidase
Cbol2809|CDS|CDS	10.0	3.0	15.1	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases
TS29Bac07339|CDS|CDS	10.0	3.0	15.1	E	COG0140|COG0139	Phosphoribosyl-ATP pyrophosphohydrolase|Phosphoribosyl-AMP cyclohydrolase
Caer0388|CDS|CDS	69.3	21.0	15.0	E	COG2235	Arginine deiminase
Aput2087|CDS|CDS	23.0	7.0	14.9	E	COG1770|COG1505	Protease II|Serine proteases of the peptidase family S9A
Chyl3169|CDS|CDS	3.1	1.0	14.0	E	COG0686	Alanine dehydrogenase
BactD11839|CDS|CDS	3.1	1.0	13.9	E	COG0112	Glycine/serine hydroxymethyltransferase
ShigspD90033|CDS|CDS	1.0	0.3	13.6	E	COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases
Bpse0051|CDS|CDS	1.0	0.3	13.6	E	COG2873	O-acetylhomoserine sulfhydrylase
TS28Bac3870|CDS|CDS	1.0	0.3	13.6	E	COG1166	Arginine decarboxylase (spermidine biosynthesis)
Bxyl2491|CDS|CDS	1.0	0.3	13.6	E	COG0548	Acetylglutamate kinase
TS28Clo02956|CDS|CDS	6.0	2.0	13.6	E	COG0165|COG1246	Argininosuccinate lyase|N-acetylglutamate synthase and related acetyltransferases
Dfor1586|CDS|CDS	6.0	2.0	13.6	E	COG0136	Aspartate-semialdehyde dehydrogenase
Ccom1370|CDS|CDS	6.0	2.0	13.6	E	COG0289	Dihydrodipicolinate reductase
Cbol4326|CDS|CDS	3.0	1.0	13.6	E	COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog
Ccom1359|CDS|CDS	3.0	1.0	13.6	E	COG4608|COG1123	ABC-type oligopeptide transport system, ATPase component|ATPase components of various ABC-type transport systems, contain duplicated ATPase
Cbol2464|CDS|CDS	3.0	1.0	13.6	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS28Bac6124|CDS|CDS	3.0	1.0	13.6	E	COG1410|COG0646	Methionine synthase I, cobalamin-binding domain|Methionine synthase I (cobalamin-dependent), methyltransferase domain
TS28Fae19128|CDS|CDS	6.0	2.0	13.6	E	COG1177	ABC-type spermidine/putrescine transport system, permease component II
Bcap1238|CDS|CDS	6.0	2.0	13.6	E	COG4303	Ethanolamine ammonia-lyase, large subunit
Cnex2500|CDS|CDS	3.0	1.0	13.6	E	COG0136	Aspartate-semialdehyde dehydrogenase
Bcap3331|CDS|CDS	6.0	2.0	13.6	E	COG0006	Xaa-Pro aminopeptidase
TS28Rum15684|CDS|CDS	9.9	3.3	13.5	E	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases
TS29Bac03111|CDS|CDS	26.7	9.0	13.5	E	COG0031	Cysteine synthase
TS29Dor1624|CDS|CDS	17.8	6.0	13.4	E	COG0686	Alanine dehydrogenase
TS29Bac03244|CDS|CDS	11.5	4.0	13.1	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Bfin0217|CDS|CDS	1.4	0.5	12.9	E	COG2873	O-acetylhomoserine sulfhydrylase
Buni0596|CDS|CDS	4.7	1.7	12.7	E	COG3643	Glutamate formiminotransferase
TS28Bif2245|CDS|CDS	2.3	0.8	12.7	E	COG1760	L-serine deaminase
Bxyl2991|CDS|CDS	7.4	2.7	12.6	E	COG2755|COG3401	Lysophospholipase L1 and related esterases|Fibronectin type 3 domain-containing protein
Bova0053|CDS|CDS	2.7	1.0	12.4	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Dlon0161|CDS|CDS	5.5	2.0	12.4	E	COG3938	Proline racemase
TS28Fae03687|CDS|CDS	8.0	3.0	12.1	E	COG1760	L-serine deaminase
BactD11598|CDS|CDS	1.3	0.5	12.1	E	COG0287	Prephenate dehydrogenase
TS28Dor0367|CDS|CDS	8.0	3.0	12.0	E	COG3938	Proline racemase
TS28Rum01865|CDS|CDS	25.2	10.0	11.4	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases
Robe3472|CDS|CDS	0.8	0.3	11.3	E	COG0079	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase
TS29Bac04218|CDS|CDS	2.5	1.0	11.3	E	COG1760	L-serine deaminase
Buni2088|CDS|CDS	2.5	1.0	11.3	E	COG0112	Glycine/serine hydroxymethyltransferase
Acol3044|CDS|CDS	10.0	4.0	11.3	E	COG3033	Tryptophanase
TS28Rum09533|CDS|CDS	5.0	2.0	11.3	E	COG0440	Acetolactate synthase, small (regulatory) subunit
TS29Rum10908|CDS|CDS	5.0	2.0	11.3	E	COG1362	Aspartyl aminopeptidase
Bova4190|CDS|CDS	1.3	0.5	11.3	E	COG1760	L-serine deaminase

TS29Rum19010|CDS|CDS	27.0	11.0	11.1	E	COG1410	Methionine synthase I, cobalamin-binding domain
TS28Fae01474|CDS|CDS	3.7	1.5	11.1	E	COG0460	Homoserine dehydrogenase
TS29Bac11144|CDS|CDS	40.9	17.0	10.9	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Bthe7335567|CDS|CDS	6.0	2.5	10.9	E	COG0686	Alanine dehydrogenase
BactD20930|CDS|CDS	2.4	1.0	10.9	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Rum09539|CDS|CDS	9.3	4.0	10.6	E	COG0136	Aspartate-semialdehyde dehydrogenase
Clep0705|CDS|CDS	7.0	3.0	10.6	E	COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes
Dlon2773|CDS|CDS	2.3	1.0	10.6	E	COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog
TS28Bac5243|CDS|CDS	2.3	1.0	10.6	E	COG2008	Threonine aldolase
TS28Eub8503|CDS|CDS	8.0	3.5	10.4	E	COG0520	Selenocysteine lyase
BactD22465|CDS|CDS	0.8	0.3	10.2	E	COG1045|COG2151	Serine acetyltransferase|Predicted metal-sulfur cluster biosynthetic enzyme
TS28Rum11618|CDS|CDS	4.5	2.0	10.2	E	COG0174	Glutamine synthetase
TS28Bif2022|CDS|CDS	0.5	22.8	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS29Bif3311|CDS|CDS	1.0	45.5	0.1	E	COG0014	Gamma-glutamyl phosphate reductase
TS29Bif2878|CDS|CDS	0.5	22.8	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS28Bif3412|CDS|CDS	0.8	34.5	0.1	E	COG0006	Xaa-Pro aminopeptidase
TS29Rum11505|CDS|CDS	1.0	46.0	0.1	E	COG1123|COG4608	ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type oligopeptide transport system, ATPase component
TS29Col1172|CDS|CDS	1.0	47.0	0.1	E	COG0460	Homoserine dehydrogenase
TS29Bac08799|CDS|CDS	0.5	23.5	0.1	E	COG4690	Dipeptidase
TS29Bif3924|CDS|CDS	0.7	31.7	0.1	E	COG0110|COG1605	Acetyltransferase (isoleucine patch superfamily)|Chorismate mutase
TS29RumUnc0615|CDS|CDS	2.0	97.0	0.1	E	COG1305	Transglutaminase-like enzymes, putative cysteine proteases
TS29Bif3520|CDS|CDS	2.2	105.3	0.1	E	COG1505|COG1770	Serine proteases of the peptidase family S9A|Protease II
TS28Bif4961|CDS|CDS	2.2	105.3	0.1	E	COG1505|COG1770	Serine proteases of the peptidase family S9A|Protease II
TS29RumUnc0655|CDS|CDS	1.0	50.0	0.1	E	COG0367	Asparagine synthase (glutamine-hydrolyzing)
TS29Rum20044|CDS|CDS	1.0	50.0	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS28Fae16508|CDS|CDS	0.5	25.0	0.1	E	COG0031	Cysteine synthase
TS29Rum19983|CDS|CDS	1.0	51.0	0.1	E	COG2873	O-acetylhomoserine sulfhydrylase
TS29Bif3486|CDS|CDS	2.5	129.5	0.1	E	COG0308	Aminopeptidase N
TS29Bac03354|CDS|CDS	0.5	26.0	0.1	E	COG0006	Xaa-Pro aminopeptidase
Bxyl1347|CDS|CDS	0.1	6.5	0.1	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
TS28Fae18160|CDS|CDS	0.5	26.0	0.1	E	COG2008	Threonine aldolase
Buni2157|CDS|CDS	0.3	17.8	0.1	E	COG0591|COG4146	Na+/proline symporter|Predicted symporter
Robe0045|CDS|CDS	0.6	32.0	0.1	E	COG3340	Peptidase E
TS29RumUnc1228|CDS|CDS	1.0	54.0	0.1	E	COG0367	Asparagine synthase (glutamine-hydrolyzing)
TS28Fae21249|CDS|CDS	0.3	18.0	0.1	E	COG0137	Argininosuccinate synthase
Clep1279|CDS|CDS	0.1	7.0	0.1	E	COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog
TS28Fae10044|CDS|CDS	0.3	14.0	0.1	E	COG4992	Ornithine/acetylornithine aminotransferase
TS28Fae14980|CDS|CDS	0.5	28.0	0.1	E	COG4177	ABC-type branched-chain amino acid transport system, permease component
Rbro0079|CDS|CDS	0.5	28.3	0.1	E	COG0070	Glutamate synthase domain 3
TS29Fae08560|CDS|CDS	1.5	85.5	0.1	E	COG0367	Asparagine synthase (glutamine-hydrolyzing)
TS29RumUnc0021|CDS|CDS	1.0	58.0	0.1	E	COG1760	L-serine deaminase
TS28Rum13901|CDS|CDS	0.3	19.3	0.1	E	COG3968|COG0174	Uncharacterized protein related to glutamine synthetase|Glutamine synthetase
TS28Fae19462|CDS|CDS	1.0	58.5	0.1	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS29Fae09984|CDS|CDS	1.5	88.5	0.1	E	COG1982	Arginine/lysine/ornithine decarboxylases
TS28Fae01764|CDS|CDS	0.7	39.5	0.1	E	COG1982	Arginine/lysine/ornithine decarboxylases
TS28Fae12080|CDS|CDS	0.5	30.0	0.1	E	COG0263	Glutamate 5-kinase
TS29Rum17182|CDS|CDS	0.5	30.0	0.1	E	COG2755	Lysophospholipase L1 and related esterases
TS29Fae08006|CDS|CDS	0.5	30.5	0.1	E	COG0070	Glutamate synthase domain 3
TS29RumUnc0053|CDS|CDS	1.0	63.0	0.1	E	COG4992	Ornithine/acetylornithine aminotransferase
TS29Bif3640|CDS|CDS	0.8	49.5	0.1	E	COG0019	Diaminopimelate decarboxylase
TS28Bif0858|CDS|CDS	0.7	44.3	0.1	E	COG0346	Lactoylglutathione lyase and related lyases
TS28Bif3788|CDS|CDS	0.3	16.7	0.1	E	COG4690	Dipeptidase
TS29Bif3982|CDS|CDS	2.0	133.5	0.1	E	COG0436|COG1168	Aspartate/tyrosine/aromatic aminotransferase|Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities
TS29Bac05576|CDS|CDS	0.3	22.3	0.1	E	COG0591|COG4146	Na+/proline symporter|Predicted symporter
Rtor2036|CDS|CDS	0.6	40.5	0.1	E	COG3340	Peptidase E
TS29Fae00433|CDS|CDS	0.5	35.0	0.1	E	COG4177	ABC-type branched-chain amino acid transport system, permease component
TS28Bif3097|CDS|CDS	0.3	18.0	0.1	E	COG0006	Xaa-Pro aminopeptidase
TS29Bif2494|CDS|CDS	0.4	29.0	0.1	E	COG1605|COG0077	Chorismate mutase|Prephenate dehydratase
TS29Bif1333|CDS|CDS	0.7	49.0	0.1	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
TS29Bif1105|CDS|CDS	1.0	75.0	0.1	E	COG4690	Dipeptidase
TS28Bif0201|CDS|CDS	1.8	133.8	0.1	E	COG0070	Glutamate synthase domain 3
TS29Fae00851|CDS|CDS	1.0	77.5	0.1	E	COG0141	Histidinol dehydrogenase
Robe3181|CDS|CDS	0.2	15.5	0.1	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
Bpse0846|CDS|CDS	0.1	7.9	0.1	E	COG0174	Glutamine synthetase
TS29Bac07802|CDS|CDS	0.3	27.0	0.1	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
TS29Fae00077|CDS|CDS	0.5	41.0	0.1	E	COG2755	Lysophospholipase L1 and related esterases
TS28Bif2059|CDS|CDS	0.4	30.9	0.1	E	COG0460	Homoserine dehydrogenase
TS29Bac07219|CDS|CDS	0.3	27.8	0.1	E	COG0531	Amino acid transporters
TS29Fae03184|CDS|CDS	1.0	86.5	0.1	E	COG4690	Dipeptidase
TS29Fae00664|CDS|CDS	0.3	30.0	0.1	E	COG1115	Na+/alanine symporter
Bpse1086|CDS|CDS	0.3	22.7	0.1	E	COG4690	Dipeptidase
TS29Bif1190|CDS|CDS	0.3	22.7	0.1	E	COG4690	Dipeptidase
TS29Bac09129|CDS|CDS	0.2	18.3	0.0	E	COG1506	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
TS29Fae08425|CDS|CDS	0.2	18.5	0.0	E	COG0141	Histidinol dehydrogenase
TS29Rum15995|CDS|CDS	0.5	46.5	0.0	E	COG0687|COG1177	Spermidine/putrescine-binding periplasmic protein|ABC-type spermidine/putrescine transport system, permease component II
TS29Bif2257|CDS|CDS	0.3	23.5	0.0	E	COG0006	Xaa-Pro aminopeptidase
TS28Bif2887|CDS|CDS	0.1	9.4	0.0	E	COG0174	Glutamine synthetase
TS29Bac00843|CDS|CDS	0.3	31.5	0.0	E	COG0263	Glutamate 5-kinase
TS29Bif1146|CDS|CDS	0.3	31.5	0.0	E	COG0136	Aspartate-semialdehyde dehydrogenase
TS28Eub4474|CDS|CDS	0.3	32.5	0.0	E	COG3340	Peptidase E
TS29Bif2919|CDS|CDS	1.8	173.9	0.0	E	COG0070	Glutamate synthase domain 3
TS29Rum11664|CDS|CDS	1.0	100.0	0.0	E	COG0747	ABC-type dipeptide transport system, periplasmic component
Cnex0637|CDS|CDS	0.3	25.2	0.0	E	COG3340	Peptidase E
TS29Fae03211|CDS|CDS	0.7	69.5	0.0	E	COG1982	Arginine/lysine/ornithine decarboxylases
TS29Bif2734|CDS|CDS	1.0	106.5	0.0	E	COG1114	Branched-chain amino acid permeases
TS28Fae01739|CDS|CDS	0.5	55.0	0.0	E	COG0710	3-dehydroquinate dehydratase
TS28Bif0199|CDS|CDS	0.5	51.1	0.0	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
TS28Fae18412|CDS|CDS	0.5	58.0	0.0	E	COG0527	Aspartokinases
TS28Bif4745|CDS|CDS	0.3	29.0	0.0	E	COG0137	Argininosuccinate synthase
TS29Col0167|CDS|CDS	0.5	58.5	0.0	E	COG0498	Threonine synthase

TS29Bif2462|CDS|CDS	0.8	88.3	0.0	E	COG0006	Xaa-Pro aminopeptidase
TS29Bif3864|CDS|CDS	0.3	29.6	0.0	E	COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)
TS28Bif0738|CDS|CDS	0.3	29.6	0.0	E	COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)
TS29Fae01113|CDS|CDS	0.5	59.5	0.0	E	COG4166	ABC-type oligopeptide transport system, periplasmic component
TS29Bif2095|CDS|CDS	0.1	12.4	0.0	E	COG0174	Glutamine synthetase
TS29Fae08348|CDS|CDS	0.5	64.5	0.0	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
Dfor2604|CDS|CDS	0.1	18.5	0.0	E	COG2856	Predicted Zn peptidase
TS29Rum18693|CDS|CDS	0.1	18.5	0.0	E	COG2856	Predicted Zn peptidase
TS29Bac06512|CDS|CDS	0.1	16.3	0.0	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases
TS29Bif3356|CDS|CDS	0.8	101.3	0.0	E	COG0174	Glutamine synthetase
TS28Bif2005|CDS|CDS	0.3	37.2	0.0	E	COG0620	Methionine synthase II (cobalamin-independent)
TS28Fae18783|CDS|CDS	0.5	75.5	0.0	E	COG1775	Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB
TS28Fae21242|CDS|CDS	0.3	38.0	0.0	E	COG4992	Ornithine/acetylornithine aminotransferase
TS28Bif1004|CDS|CDS	0.3	42.6	0.0	E	COG0747|COG4166|COG4533	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component|ABC-type uncharacterized transport system, periplasmic component
TS28Bif4769|CDS|CDS	0.1	17.1	0.0	E	COG0174	Glutamine synthetase
TS29Bif0256|CDS|CDS	0.3	42.8	0.0	E	COG0019	Diaminopimelate decarboxylase
TS29Bif3641|CDS|CDS	0.4	68.4	0.0	E	COG0460	Homoserine dehydrogenase
TS29Rum20032|CDS|CDS	1.0	183.0	0.0	E	COG0070	Glutamate synthase domain 3
TS29Bif3343|CDS|CDS	0.3	49.5	0.0	E	COG1364	N-acetylglutamate synthase (N-acetylornithine aminotransferase)
TS29Bif3642|CDS|CDS	0.3	50.0	0.0	E	COG0083	Homoserine kinase
TS29Bif2917|CDS|CDS	0.5	92.0	0.0	E	COG0747|COG4166	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component
TS29Bif3338|CDS|CDS	0.3	53.5	0.0	E	COG0137	Argininosuccinate synthase
TS29Bif3655|CDS|CDS	0.3	60.2	0.0	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS29Bif3553|CDS|CDS	0.3	65.4	0.0	E	COG1113	Gamma-aminobutyrate permease and related permeases
TS29Bif3497|CDS|CDS	0.3	90.2	0.0	E	COG1305	Transglutaminase-like enzymes, putative cysteine proteases
TS28Bif4936|CDS|CDS	0.3	90.2	0.0	E	COG1305	Transglutaminase-like enzymes, putative cysteine proteases
TS29Bif2893|CDS|CDS	0.3	69.2	0.0	E	COG0620	Methionine synthase II (cobalamin-independent)
TS29Bif0481|CDS|CDS	0.3	69.3	0.0	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS29Bif0983|CDS|CDS	0.2	46.8	0.0	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS28Bif4432|CDS|CDS	0.3	70.3	0.0	E	COG0334	Glutamate dehydrogenase/leucine dehydrogenase
TS29Bif0708|CDS|CDS	0.3	75.6	0.0	E	COG0747|COG4166|COG4533	ABC-type dipeptide transport system, periplasmic component|ABC-type oligopeptide transport system, periplasmic component|ABC-type uncharacterized transport system, periplasmic component
TS29Bif3342|CDS|CDS	0.3	78.5	0.0	E	COG0548|COG1364	Acetylglutamate kinase|N-acetylglutamate synthase (N-acetylornithine aminotransferase)
TS28Bif2042|CDS|CDS	0.3	83.2	0.0	E	COG0436	Aspartate/tyrosine/aromatic aminotransferase
TS29Bif3033|CDS|CDS	0.3	112.0	0.0	E	COG2873	O-acetylhomoserine sulfhydrylase
TS28Bif2177|CDS|CDS	0.3	113.4	0.0	E	COG1113	Gamma-aminobutyrate permease and related permeases
Acac1337|CDS|CDS	19.0	1.0	86.3	E|C	COG1063|COG1064|COG1062	Threonine dehydrogenase and related Zn-dependent dehydrogenases|Zn-dependent alcohol dehydrogenases|Zn-dependent alcohol dehydrogenases, class III
CspM6210670|CDS|CDS	4.0	1.0	18.2	E|C	COG0473	Isocitrate/isopropylmalate dehydrogenase
TS28Fae20772|CDS|CDS	22.5	6.0	17.0	E|C	COG1252|COG0709	NADH dehydrogenase, FAD-containing subunit|Selenophosphate synthase
Dfor0576|CDS|CDS	3.0	1.0	13.6	E|C	COG0473	Isocitrate/isopropylmalate dehydrogenase
TS28Rum12958|CDS|CDS	3.0	1.0	13.6	E|C	COG1063|COG1062	Threonine dehydrogenase and related Zn-dependent dehydrogenases|Zn-dependent alcohol dehydrogenases, class III
Bfin3168|CDS|CDS	3.0	1.0	13.5	E|C	COG0473	Isocitrate/isopropylmalate dehydrogenase
TS28Eub6200|CDS|CDS	4.0	1.5	12.1	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS28Rum13906|CDS|CDS	13.3	5.5	10.9	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS28Fae20375|CDS|CDS	1.0	53.0	0.1	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS29Fae04274|CDS|CDS	1.0	59.0	0.1	E|C	COG0578|COG0579|COG0665	Glycerol-3-phosphate dehydrogenase|Predicted dehydrogenase|Glycine/D-amino acid oxidases (deaminating)
TS29Bif0808|CDS|CDS	0.6	59.6	0.0	E|C	COG1027|COG0114	Aspartate ammonia-lyase|Fumarase
TS29Col1392|CDS|CDS	0.5	60.0	0.0	E|C	COG0065|COG1048	3-isopropylmalate dehydratase large subunit|Aconitase A
TS28Bif0478|CDS|CDS	0.6	75.1	0.0	E|C	COG1027|COG0114	Aspartate ammonia-lyase|Fumarase
TS29Dor0636|CDS|CDS	74.0	8.0	42.0	E|C|H	COG1148|COG4624|COG0493|COG0543|COG1034|COG1142|COG1894|COG1144	Heterodisulfide reductase, subunit A and related polyferredoxins|Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
TS28Rum13304|CDS|CDS	33.0	7.5	20.0	E|C|H	COG1148|COG4624|COG0493|COG0543|COG1034|COG1894|COG1145|COG1143|COG1144|COG1319	Heterodisulfide reductase, subunit A and related polyferredoxins|Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin|Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit|Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs
TS29Bif0562|CDS|CDS	1.3	63.8	0.1	E|C|H	COG0493|COG0543|COG1034|COG1142|COG1894|COG1146	NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin
TS28Bif1219|CDS|CDS	1.3	63.8	0.1	E|C|H	COG0493|COG0543|COG1034|COG1142|COG1894|COG1146	NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Ferredoxin

TS29Fae09240|CDS|CDS	0.3	17.0	0.1	E|C|H	COG4624|COG0493|COG0543|COG1034|COG1142|COG1894	Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit
TS29Fae03160|CDS|CDS	1.0	87.5	0.1	E|C|H	COG4624|COG0493|COG0543|COG1034|COG1142|COG1894	Iron only hydrogenase large subunit, C-terminal domain|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Fe-S-cluster-containing hydrogenase components 2|NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit
TS29Clo2732|CDS|CDS	5.0	1.0	22.7	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
Bova0252|CDS|CDS	7.0	2.0	15.8	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
Dlon0288|CDS|CDS	1.5	0.5	13.6	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
TS29Rum06710|CDS|CDS	3.0	1.0	13.6	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
Buni2883|CDS|CDS	4.3	1.5	13.1	E|F	COG0283|COG0128|COG0287	Cytidylate kinase|5-enolpyruvylshikimate-3-phosphate synthase|Prephenate dehydrogenase
Bpse0389|CDS|CDS	0.3	19.0	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS28Fae18950|CDS|CDS	0.3	23.0	0.1	E|F	COG0505	Carbamoylphosphate synthase small subunit
TS29Bif4095|CDS|CDS	2.9	206.4	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS29Fae08614|CDS|CDS	1.0	82.5	0.1	E|F	COG0505	Carbamoylphosphate synthase small subunit
TS28Bif4271|CDS|CDS	0.3	29.5	0.1	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS29Bif0682|CDS|CDS	0.3	31.8	0.0	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
TS28Bif5326|CDS|CDS	0.3	43.3	0.0	E|F	COG0462	Phosphoribosylpyrophosphate synthetase
TS29Bif1622|CDS|CDS	0.3	58.5	0.0	E|F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)
TS28Bif1907|CDS|CDS	0.3	15.0	0.1	E|F|P	COG0601|COG0503	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components|Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins
TS29Bif2804|CDS|CDS	0.3	15.0	0.1	E|F|P	COG0601|COG0503	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components|Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins
TS29Fae09059|CDS|CDS	5.3	1.0	23.8	E|G	COG2190|COG2008	Phosphotransferase system IIA components|Threonine aldolase
TS28Clo06242|CDS|CDS	5.0	1.0	22.7	E|G	COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase
TS28Rum10836|CDS|CDS	2.7	0.8	14.5	E|G	COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase
Cbol2052|CDS|CDS	7.0	3.0	10.6	E|G	COG3842|COG3839	ABC-type spermidine/putrescine transport systems, ATPase components|ABC-type sugar transport systems, ATPase components
ShigspD90225|CDS|CDS	2.3	1.0	10.6	E|G	COG0129|COG0676	Dihydroxyacid dehydratase/phosphogluconate dehydratase|Uncharacterized enzymes related to aldose 1-epimerase
TS29Fae06074|CDS|CDS	3.0	142.0	0.1	E|G	COG0129|COG0676	Dihydroxyacid dehydratase/phosphogluconate dehydratase|Uncharacterized enzymes related to aldose 1-epimerase
TS29Bif3992|CDS|CDS	1.8	83.8	0.1	E|G	COG0129|COG0676	Dihydroxyacid dehydratase/phosphogluconate dehydratase|Uncharacterized enzymes related to aldose 1-epimerase
FpraM2120170|CDS|CDS	0.3	16.5	0.1	E|G	COG2610	H+/gluconate symporter and related permeases
TS28Bif3344|CDS|CDS	0.5	30.5	0.1	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
TS29Bif2518|CDS|CDS	0.5	75.0	0.0	E|G	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily
TS29Bac09681|CDS|CDS	0.3	23.7	0.1	E|G|K|T	COG0642|COG5002|COG2202|COG0834|COG0745|COG4753|COG2770|COG0784|COG2198|COG3322|COG3292|COG2972|COG5001|COG3706|COG4251|COG1879|COG2114|COG3447	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|FOG: HAMP domain|FOG: CheY-like receiver|FOG: HPt domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Predicted integral membrane sensor domain
TS29Bac12244|CDS|CDS	0.3	54.5	0.0	E|G|N|K|T	COG0642|COG5002|COG2202|COG0834|COG0745|COG4753|COG2207|COG2770|COG0784|COG5278|COG3322|COG3292|COG2972|COG5001|COG3706|COG4251|COG1879|COG2114|COG2201	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain
TS28Dor0653|CDS|CDS	6.0	1.0	27.2	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS28Rum12730|CDS|CDS	5.0	2.0	11.3	E|G|P	COG3842|COG3839|COG1118|COG4149|COG4148	ABC-type spermidine/putrescine transport systems, ATPase components|ABC-type sugar transport systems, ATPase components|ABC-type sulfate/molybdate transport systems, ATPase component|ABC-type molybdate transport system, permease component|ABC-type molybdate transport system, ATPase component
TS29Bac10282|CDS|CDS	3.3	1.5	10.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS29Bif1708|CDS|CDS	0.7	47.0	0.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS29Bac10582|CDS|CDS	0.3	24.0	0.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS29Bif3824|CDS|CDS	0.8	70.4	0.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS28Bif0781|CDS|CDS	0.8	70.4	0.1	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS28Bif5009|CDS|CDS	0.3	33.8	0.0	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS29Bif3012|CDS|CDS	0.7	156.0	0.0	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS29Bif3011|CDS|CDS	0.5	123.3	0.0	E|G|P	COG0477	Permeases of the major facilitator superfamily
TS29Bif4135|CDS|CDS	0.3	66.8	0.0	E|G|P	COG0477	Permeases of the major facilitator superfamily

Msmi741008|CDS|CDS	8.1	1.5	24.5	E|G|U	COG2730|COG3291|COG5563|COG3210|COG1305	Endoglucanase|FOG: PKD repeat|Predicted integral membrane proteins containing uncharacterized repeats|Large exoproteins involved in heme utilization or adhesion|Transglutaminase-like enzymes, putative cysteine proteases
TS28Met1041|CDS|CDS	12.8	4.8	12.1	E|G|U	COG3210|COG1305|COG2730|COG3291|COG5563	Large exoproteins involved in heme utilization or adhesion|Transglutaminase-like enzymes, putative cysteine proteases|Endoglucanase|FOG: PKD repeat|Predicted integral membrane proteins containing uncharacterized repeats
TS29Bac10848|CDS|CDS	0.5	27.0	0.1	E|G|V	COG2755|COG1680|COG1472	Lysophospholipase L1 and related esterases|Beta-lactamase class C and other penicillin binding proteins|Beta-glucosidase-related glycosidases
Aput0330|CDS|CDS	27.0	1.0	122.6	E|H	COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases
BactD13411|CDS|CDS	1.3	0.2	34.0	E|H	COG1932	Phosphoserine aminotransferase
Bxyl1468|CDS|CDS	2.7	0.5	24.2	E|H	COG0175	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes
TS28Rum03611|CDS|CDS	20.0	4.0	22.7	E|H	COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
TS28Col1472|CDS|CDS	5.0	1.0	22.7	E|H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
Bxyl2769|CDS|CDS	1.3	0.3	18.2	E|H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
Dlon2364|CDS|CDS	2.0	0.5	18.2	E|H	COG1932	Phosphoserine aminotransferase
TS28Col0576|CDS|CDS	4.0	1.0	18.2	E|H	COG1932	Phosphoserine aminotransferase
Aput1837|CDS|CDS	4.0	1.0	18.2	E|H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
Dlon1801|CDS|CDS	2.0	0.5	18.2	E|H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
TS28Bac6149|CDS|CDS	1.2	0.3	16.3	E|H	COG0059	Ketol-acid reductoisomerase
Buni1293|CDS|CDS	1.2	0.3	16.3	E|H	COG0059	Ketol-acid reductoisomerase
TS28Rum14812|CDS|CDS	5.0	1.5	15.1	E|H	COG0111|COG1760	Phosphoglycerate dehydrogenase and related dehydrogenases|L-serine deaminase
Acac1383|CDS|CDS	3.2	1.0	14.4	E|H	COG0059	Ketol-acid reductoisomerase
BactD11026|CDS|CDS	3.0	1.0	13.6	E|H	COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
TS28Fae16928|CDS|CDS	1.5	0.5	13.6	E|H	COG1932	Phosphoserine aminotransferase
ShigspD91018|CDS|CDS	1.5	0.5	13.6	E|H	COG0028|COG3960	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]|Glyoxylate carboligase
BactD23903|CDS|CDS	1.5	0.5	13.6	E|H	COG0028|COG1165	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]|2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
Ceut0171|CDS|CDS	1.5	0.5	13.6	E|H	COG0059	Ketol-acid reductoisomerase
TS28Clo08016|CDS|CDS	5.5	2.0	12.5	E|H	COG0059	Ketol-acid reductoisomerase
BactD11906|CDS|CDS	4.9	2.0	11.0	E|H	COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
Buni2385|CDS|CDS	5.7	2.5	10.3	E|H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
TS28Fae18673|CDS|CDS	0.5	29.5	0.1	E|H	COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
TS29RumUnc0266|CDS|CDS	1.0	64.0	0.1	E|H	COG0175	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes
TS28Fae20464|CDS|CDS	0.3	29.5	0.1	E|H	COG0059	Ketol-acid reductoisomerase
TS29Bif0489|CDS|CDS	1.3	120.5	0.1	E|H	COG0161|COG4992|COG0160	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase|Ornithine/acetylornithine aminotransferase|4-aminobutyrate aminotransferase and related aminotransferases
TS29Fae08210|CDS|CDS	0.5	84.0	0.0	E|H	COG1932	Phosphoserine aminotransferase
TS29Fae08234|CDS|CDS	0.5	94.5	0.0	E|H	COG0028	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
Cbol2801|CDS|CDS	12.0	4.0	13.6	E|H|C	COG1894|COG4624|COG1034|COG1145|COG0493|COG1142|COG0543|COG1148|COG1319|COG1144	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit|Iron only hydrogenase large subunit, C-terminal domain|NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)|Ferredoxin|NADPH-dependent glutamate synthase beta chain and related oxidoreductases|Fe-S-cluster-containing hydrogenase components 2|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Heterodisulfide reductase, subunit A and related polyferredoxins|Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs|Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
TS28Rum14306|CDS|CDS	5.0	1.0	22.7	E|K	COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
Bcap0277|CDS|CDS	5.0	1.0	22.7	E|K	COG1725|COG1167	Predicted transcriptional regulators|Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
TS29Fae06276|CDS|CDS	2.0	97.5	0.1	E|K	COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
TS28Bif4197|CDS|CDS	0.3	18.3	0.1	E|K	COG0517|COG0031|COG0626|COG3620	FOG: CBS domain|Cysteine synthase|Cystathionine beta-lyases/cystathionine gamma-synthases|Predicted transcriptional regulator with C-terminal CBS domains
TS29Fae09891|CDS|CDS	0.5	30.5	0.1	E|K	COG1725|COG1167	Predicted transcriptional regulators|Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
TS29Rum20126|CDS|CDS	1.0	70.0	0.1	E|K	COG1167	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
Bfra31124183|CDS|CDS	2.7	0.5	24.2	E|K|M|U|Q	COG0793|COG1506|COG4946|COG0823|COG1228|COG3710|COG2319	Periplasmic protease|Dipeptidyl aminopeptidases/acylaminoacyl-peptidases|Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system|Periplasmic component of the Tol biopolymer transport system|Imidazolonepropionase and related amidohydrolases|DNA-binding winged-HTH domains|FOG: WD40 repeat

TS29Rum16981|CDS|CDS	2.3	131.0	0.1	E|K|T	COG0642|COG0834|COG3452|COG2770|COG2198|COG2203|COG3300|COG3437	Signal transduction histidine kinase|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|FOG: HAMP domain|FOG: HPt domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and an HD-GYP domain
TS29Rum14501|CDS|CDS	0.3	85.0	0.0	E|K|T	COG0642|COG2202|COG0834|COG3452|COG0784|COG3614|COG2198|COG2203|COG3300|COG3437	Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|FOG: HPt domain|FOG: GAF domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and an HD-GYP domain
TS29Bif3488|CDS|CDS	0.5	82.7	0.0	E|M	COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase
TS28Fae16417|CDS|CDS	5.5	1.5	16.6	E|N|P|K|T	COG5001|COG3706|COG2199|COG0004|COG0840|COG2208|COG0347	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|FOG: GGDEF domain|Ammonia permease|Methyl-accepting chemotaxis protein|Serine phosphatase RsbU, regulator of sigma subunit|Nitrogen regulatory protein PII
TS29Clo3828|CDS|CDS	17.0	3.0	25.7	E|P	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
TS29Clo3829|CDS|CDS	14.0	5.0	12.7	E|P	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
TS29Bif3453|CDS|CDS	0.5	33.7	0.1	E|P	COG1173|COG0444|COG1123|COG4608|COG4172	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components|ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component|ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type oligopeptide transport system, ATPase component|ABC-type uncharacterized transport system, duplicated ATPase component
TS29Bif2499|CDS|CDS	0.3	76.0	0.0	E|P	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
TS28Bac5663|CDS|CDS	1.7	0.3	22.7	E|T	COG0642|COG2202|COG0834|COG3452|COG2770|COG2198|COG2203|COG5278	Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|FOG: HAMP domain|FOG: HPt domain|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain
TS28Fae16116|CDS|CDS	6.0	1.5	18.2	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS28Dor0126|CDS|CDS	1.5	0.5	13.6	E|T	COG0589|COG0531	Universal stress protein UspA and related nucleotide-binding proteins|Amino acid transporters
TS28Rum01026|CDS|CDS	8.5	3.0	12.9	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS29Bac00259|CDS|CDS	0.3	16.0	0.1	E|T	COG0642|COG5002|COG2202|COG0834|COG3452|COG2770|COG2198|COG3300|COG3322	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|FOG: HAMP domain|FOG: HPt domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain
TS29Col0809|CDS|CDS	0.5	32.0	0.1	E|T	COG0834|COG0765	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component
TS29Bac09401|CDS|CDS	0.3	24.8	0.1	E|T	COG0642|COG2202|COG0834|COG2770|COG0784|COG3614|COG2198|COG3300|COG3322	Signal transduction histidine kinase|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|FOG: HPt domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain
TS28Bif4907|CDS|CDS	0.3	31.3	0.0	E|T	COG0834|COG0765|COG4160	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component|ABC-type arginine/histidine transport system, permease component
TS29Bif3471|CDS|CDS	0.3	31.3	0.0	E|T	COG0834|COG0765|COG4160	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|ABC-type amino acid transport system, permease component|ABC-type arginine/histidine transport system, permease component
TS28Bif4821|CDS|CDS	0.3	26.8	0.0	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS29Bif3400|CDS|CDS	0.3	26.8	0.0	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS29Bif3473|CDS|CDS	0.3	28.2	0.0	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS28Bif4909|CDS|CDS	0.3	35.2	0.0	E|T	COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain
TS29Bif1558|CDS|CDS	0.3	16.0	0.1	E|V	COG1123|COG4608|COG4172|COG4167	ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type oligopeptide transport system, ATPase component|ABC-type uncharacterized transport system, duplicated ATPase component|ABC-type antimicrobial peptide transport system, ATPase component
TS28Rum01433|CDS|CDS	11.0	0.5	99.9	F	COG1781	Aspartate carbamoyltransferase, regulatory subunit
Caer0679|CDS|CDS	8.0	0.5	72.6	F	COG0540	Aspartate carbamoyltransferase, catalytic chain
TS28Col0100|CDS|CDS	10.0	1.0	45.4	F	COG2759	Formyltetrahydrofolate synthetase
Buni3233|CDS|CDS	5.0	0.5	45.4	F	COG0151	Phosphoribosylamine-glycine ligase
TS28Rum13596|CDS|CDS	4.8	0.5	43.9	F	COG0461	Orotate phosphoribosyltransferase
Caer0038|CDS|CDS	4.7	0.5	42.7	F	COG0628|COG0152|COG1828	Predicted permease|Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase|Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component
BactD12686|CDS|CDS	4.6	0.5	41.8	F	COG0461|COG0284	Orotate phosphoribosyltransferase|Orotidine-5'-phosphate decarboxylase
TS29Bac04006|CDS|CDS	8.0	1.0	36.3	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
CspM6212487|CDS|CDS	8.0	1.0	36.3	F	COG0104	Adenylosuccinate synthase
Dfor2397|CDS|CDS	7.0	1.0	31.8	F	COG0041|COG0151	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase|Phosphoribosylamine glycine ligase
Caer1152|CDS|CDS	3.5	0.5	31.8	F	COG0150	Phosphoribosylaminoimidazole (AIR) synthetase
TS28Rum01565|CDS|CDS	3.5	0.5	31.8	F	COG0194	Guanylate kinase

Buni2664|CDS|CDS	2.3	0.3	31.8	F	COG0628|COG0152|COG1828	Predicted permease|Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase|Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component
TS28Bac3721|CDS|CDS	2.3	0.3	31.8	F	COG0628|COG0152|COG1828	Predicted permease|Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase|Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component
Buni1076|CDS|CDS	3.4	0.5	31.0	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
Buni2114|CDS|CDS	6.2	1.0	28.0	F	COG0504	CTP synthase (UTP-ammonia lyase)
Bxyl0136|CDS|CDS	2.0	0.3	27.2	F	COG0504	CTP synthase (UTP-ammonia lyase)
Cbol2804|CDS|CDS	6.0	1.0	27.2	F	COG0402	Cytosine deaminase and related metal-dependent hydrolases
TS28Col1501|CDS|CDS	6.0	1.0	27.2	F	COG0104	Adenylosuccinate synthase
TS28Rum11469|CDS|CDS	6.0	1.0	27.2	F	COG0563	Adenylate kinase and related kinases
Bxyl2800|CDS|CDS	3.0	0.5	27.2	F	COG0105	Nucleoside diphosphate kinase
TS28Fae12461|CDS|CDS	3.0	0.5	27.2	F	COG0213	Thymidine phosphorylase
Aput1498|CDS|CDS	17.0	3.0	25.7	F	COG1864	DNA/RNA endonuclease G, NUC1
TS28Dor0623|CDS|CDS	2.7	0.5	24.2	F	COG0015	Adenylosuccinate lyase
TS28Rum11255|CDS|CDS	207.8	40.8	23.1	F	COG2759	Formyltetrahydrofolate synthetase
TS28Clo03814|CDS|CDS	2.5	0.5	22.7	F	COG0015	Adenylosuccinate lyase
Buni2085|CDS|CDS	7.5	1.5	22.7	F	COG0540	Aspartate carbamoyltransferase, catalytic chain
TS28Met0774|CDS|CDS	1.5	0.3	20.4	F	COG2019	Archaeal adenylate kinase
TS28Bac1849|CDS|CDS	4.2	1.0	18.9	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS29Bac02991|CDS|CDS	16.5	4.0	18.7	F	COG0005	Purine nucleoside phosphorylase
TS29Bac11630|CDS|CDS	1.0	0.3	18.2	F	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain
Casp0141|CDS|CDS	4.0	1.0	18.2	F	COG0209	Ribonucleotide reductase, alpha subunit
Cbol2796|CDS|CDS	8.0	2.0	18.2	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
Acod1471|CDS|CDS	4.0	1.0	18.2	F	COG0138	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)
TS28Fae08603|CDS|CDS	4.0	1.0	18.2	F	COG0528	Uridylate kinase
TS28Eub3124|CDS|CDS	11.0	3.0	16.6	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS29Rum00369|CDS|CDS	214.8	60.8	16.0	F	COG2759	Formyltetrahydrofolate synthetase
TS28Fae18538|CDS|CDS	3.5	1.0	15.9	F	COG0104	Adenylosuccinate synthase
BactD24022|CDS|CDS	2.8	0.8	15.4	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
TS28Rum11152|CDS|CDS	1.7	0.5	15.1	F	COG0737	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases
Robe3140|CDS|CDS	1.7	0.5	15.1	F	COG0737	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases
TS28Rum13591|CDS|CDS	15.0	4.5	15.1	F	COG0402	Cytosine deaminase and related metal-dependent hydrolases
Aput0452|CDS|CDS	13.0	4.0	14.8	F	COG1864	DNA/RNA endonuclease G, NUC1
Bsp1160292|CDS|CDS	3.3	1.0	14.8	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
BactD20170|CDS|CDS	3.2	1.0	14.4	F	COG0138|COG0299	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)|Folate-dependent phosphoribosylglycinamide formyltransferase PurN
TS28Fae00252|CDS|CDS	17.2	5.5	14.2	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS28Met0704|CDS|CDS	3.1	1.0	14.0	F	COG0104	Adenylosuccinate synthase
Msmi741106|CDS|CDS	3.1	1.0	14.0	F	COG0104	Adenylosuccinate synthase
TS28Fae12449|CDS|CDS	1.0	0.3	13.6	F	COG0634	Hypoxanthine-guanine phosphoribosyltransferase
Robe0274|CDS|CDS	3.0	1.0	13.6	F	COG0402	Cytosine deaminase and related metal-dependent hydrolases
BactD10713|CDS|CDS	3.0	1.0	13.6	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
Caer1176|CDS|CDS	1.5	0.5	13.6	F	COG0104	Adenylosuccinate synthase
TS28Met0716|CDS|CDS	0.8	0.3	13.6	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
RintL12790|CDS|CDS	3.0	1.0	13.6	F	COG0461	Orotate phosphoribosyltransferase
Dfor1645|CDS|CDS	3.0	1.0	13.6	F	COG0756	dUTPase
Dfor0658|CDS|CDS	3.0	1.0	13.6	F	COG0528	Uridylate kinase
TS28Rum07207|CDS|CDS	1.5	0.5	13.6	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS28Met0771|CDS|CDS	3.0	1.0	13.6	F	COG1102	Cytidylate kinase
TS28Bac0463|CDS|CDS	13.4	4.8	12.6	F	COG0519	GMP synthase, PP-ATPase domain/subunit
Bova0255|CDS|CDS	0.9	0.3	12.5	F	COG0015	Adenylosuccinate lyase
Bxyl3255|CDS|CDS	0.9	0.3	12.5	F	COG0563	Adenylate kinase and related kinases
FpraM2121674|CDS|CDS	1.3	0.5	12.1	F	COG0540	Aspartate carbamoyltransferase, catalytic chain
Bxyl0267|CDS|CDS	1.3	0.5	12.1	F	COG1781|COG0540	Aspartate carbamoyltransferase, regulatory subunit|Aspartate carbamoyltransferase, catalytic chain
TS28Bac2305|CDS|CDS	1.3	0.5	12.1	F	COG4085|COG0737	Predicted RNA-binding protein, contains TRAM domain|5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases
Buni0314|CDS|CDS	1.3	0.5	12.1	F	COG0737|COG4085	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases|Predicted RNA-binding protein, contains TRAM domain
Dfor2394|CDS|CDS	2.5	1.0	11.3	F	COG0151	Phosphoribosylamine-glycine ligase
Bcap0049|CDS|CDS	5.0	2.0	11.3	F	COG2820|COG0813	Uridine phosphorylase|Purine-nucleoside phosphorylase
BFnctc2965|CDS|dihydroorotase	2.5	1.0	11.3	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
ShigspD91910|CDS|CDS	2.5	1.0	11.3	F	COG0402	Cytosine deaminase and related metal-dependent hydrolases
TS28Rum01303|CDS|CDS	5.0	2.0	11.3	F	COG2759	Formyltetrahydrofolate synthetase
Rtor0303|CDS|CDS	5.0	2.0	11.3	F	COG2131	Deoxycytidylate deaminase
BFych463129|CDS|dihydroorotase	2.5	1.0	11.3	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
Bxyl3060|CDS|CDS	3.8	1.5	11.3	F	COG0461|COG0284	Orotate phosphoribosyltransferase|Orotidine-5'-phosphate decarboxylase
TS28Rum07577|CDS|CDS	7.0	3.0	10.6	F	COG2233	Xanthine/uracil permeases
Acac2193|CDS|CDS	7.0	3.0	10.6	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
TS28Rum10128|CDS|CDS	3.0	1.3	10.2	F	COG0563	Adenylate kinase and related kinases
TS29Rum01847|CDS|CDS	3.0	1.3	10.2	F	COG0563	Adenylate kinase and related kinases
TS29Bif3957|CDS|CDS	2.6	118.3	0.1	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS29Bif3435|CDS|CDS	1.5	68.7	0.1	F	COG0232	dGTP triphosphohydrolase
TS28Fae18590|CDS|CDS	1.0	46.0	0.1	F	COG2759	Formyltetrahydrofolate synthetase
FpraM2120495|CDS|CDS	0.3	15.5	0.1	F	COG0151	Phosphoribosylamine-glycine ligase
TS29Bif4130|CDS|CDS	1.8	82.5	0.1	F	COG1957	Inosine-uridine nucleoside N-ribohydrolase
TS28Bif3382|CDS|CDS	0.3	12.0	0.1	F	COG1051|COG4111	ADP-ribose pyrophosphatase|Uncharacterized conserved protein
TS28Rum01287|CDS|CDS	0.3	16.0	0.1	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS28Bif4955|CDS|CDS	0.8	41.3	0.1	F	COG0167	Dihydroorotate dehydrogenase
TS28Bif1061|CDS|CDS	1.0	49.8	0.1	F	COG1957	Inosine-uridine nucleoside N-ribohydrolase
TS29Bif3977|CDS|CDS	1.0	49.8	0.1	F	COG1957	Inosine-uridine nucleoside N-ribohydrolase
TS28Fae13852|CDS|CDS	0.3	17.5	0.1	F	COG0572	Uridine kinase
TS29Bif1808|CDS|CDS	0.5	26.5	0.1	F	COG2233	Xanthine/uracil permeases
BLD0532|CDS|Dihydroorotase	0.3	13.8	0.1	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS29Bif1915|CDS|CDS	0.3	14.2	0.1	F	COG0517|COG0516	FOG: CBS domain|IMP dehydrogenase/GMP reductase
Bpse0403|CDS|CDS	0.2	11.7	0.1	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS28Bif2011|CDS|CDS	0.3	15.0	0.1	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS28Fae20471|CDS|CDS	0.2	10.0	0.1	F	COG2131	Deoxycytidylate deaminase

TS28Bif0542|CDS|CDS	0.5	30.0	0.1	F	COG0209|COG1780	Ribonucleotide reductase, alpha subunit|Protein involved in ribonucleotide reduction
TS29Rum15735|CDS|CDS	1.0	65.0	0.1	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS28Fae18849|CDS|CDS	1.0	67.0	0.1	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS29Fae00514|CDS|CDS	0.5	34.5	0.1	F	COG0528	Uridylate kinase
TS29Fae00439|CDS|CDS	0.5	35.0	0.1	F	COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins
Bcat0239|CDS|CDS	0.2	12.0	0.1	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase
TS28Bif0289|CDS|CDS	0.4	30.1	0.1	F	COG2233	Xanthine/uracil permeases
TS28Bif1981|CDS|CDS	0.3	19.5	0.1	F	COG0517|COG0516	FOG: CBS domain|IMP dehydrogenase/GMP reductase
TS28Bif4257|CDS|CDS	0.2	16.7	0.1	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS29Fae04525|CDS|CDS	0.2	14.0	0.1	F	COG2131	Deoxycytidylate deaminase
TS29Bif2554|CDS|CDS	0.3	21.8	0.1	F	COG0756	dUTPase
TS29Col0937|CDS|CDS	0.5	47.0	0.0	F	COG0504	CTP synthase (UTP-ammonia lyase)
TS28Bif2012|CDS|CDS	0.3	24.4	0.0	F	COG0284|COG0461	Orotidine-5'-phosphate decarboxylase|Orotate phosphoribosyltransferase
TS29Bif2886|CDS|CDS	0.3	24.4	0.0	F	COG0284|COG0461	Orotidine-5'-phosphate decarboxylase|Orotate phosphoribosyltransferase
TS29Bif3404|CDS|CDS	0.5	50.8	0.0	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
TS29Bif3512|CDS|CDS	0.8	91.3	0.0	F	COG0167	Dihydroorotate dehydrogenase
TS29Bif3001|CDS|CDS	0.4	45.4	0.0	F	COG2233	Xanthine/uracil permeases
TS29Rum00528|CDS|CDS	0.5	58.5	0.0	F	COG1957	Inosine-uridine nucleoside N-ribohydrolase
TS28Bif5130|CDS|CDS	0.3	43.3	0.0	F	COG0015	Adenylosuccinate lyase
TS29Bif4005|CDS|CDS	0.3	43.3	0.0	F	COG0015	Adenylosuccinate lyase
TS29Bif1802|CDS|CDS	0.3	44.0	0.0	F	COG0519	GMP synthase, PP-ATPase domain/subunit
BL0792|CDS|dihydroorotase	0.3	37.6	0.0	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS29RumUnc1503|CDS|CDS	0.3	53.0	0.0	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
TS29Rum20027|CDS|CDS	0.5	85.0	0.0	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase
TS29Bif3398|CDS|CDS	0.3	44.2	0.0	F	COG0402	Cytosine deaminase and related metal-dependent hydrolases
TS29Bif2887|CDS|CDS	0.3	69.0	0.0	F	COG0044	Dihydroorotase and related cyclic amidohydrolases
TS29Bif1607|CDS|CDS	0.2	58.7	0.0	F	COG0047|COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain|Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain
TS29Fae05320|CDS|CDS	0.3	99.0	0.0	F	COG2233	Xanthine/uracil permeases
TS29Bif2486|CDS|CDS	0.3	76.0	0.0	F	COG1051|COG4111	ADP-ribose pyrophosphatase|Uncharacterized conserved protein
TS29Bif0445|CDS|CDS	0.5	203.3	0.0	F	COG0209|COG1780	Ribonucleotide reductase, alpha subunit|Protein involved in ribonucleotide reduction
TS28Rum13910|CDS|CDS	75.8	11.5	29.9	F|C	COG2080|COG1529|COG4631	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs|Xanthine dehydrogenase, molybdopterin-binding subunit B
TS28Rum01177|CDS|CDS	35.0	13.0	12.2	F|C	COG2080|COG1529|COG4631	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs|Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs|Xanthine dehydrogenase, molybdopterin-binding subunit B
TS28Rum13595|CDS|CDS	6.5	1.5	19.7	F|C|H	COG0167|COG0543|COG1146	Dihydroorotate dehydrogenase|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Ferredoxin
TS28Bac2680|CDS|CDS	4.7	0.3	63.6	F|H	COG0283|COG1160|COG0414	Cytidylate kinase|Predicted GTPases|Panthothenate synthetase
TS29Rum19901|CDS|CDS	1.0	64.0	0.1	F|J	COG0441|COG0572	Threonyl-tRNA synthetase|Uridine kinase
TS28Fae07806|CDS|CDS	2.0	0.5	18.2	F|J|D	COG0037|COG0634|COG0590	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control|Hypoxanthine-guanine phosphoribosyltransferase|Cytosine/adenosine deaminases
TS28Fae12448|CDS|CDS	3.0	1.0	13.6	F|J|D	COG0037|COG0634|COG0590	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control|Hypoxanthine-guanine phosphoribosyltransferase|Cytosine/adenosine deaminases
TS29Bif3875|CDS|CDS	2.0	133.0	0.1	F|J|D	COG0037|COG0634|COG0590	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control|Hypoxanthine-guanine phosphoribosyltransferase|Cytosine/adenosine deaminases
TS29Fae05449|CDS|CDS	0.3	78.8	0.0	F|K|L|T	COG4753|COG2207|COG2801|COG2169|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Transposase and inactivated derivatives|Adenosine deaminase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS28Bif2152|CDS|CDS	0.5	25.0	0.1	F|K|T	COG4753|COG2207|COG2169|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Adenosine deaminase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS29Bif3571|CDS|CDS	0.5	27.7	0.1	F|K|T	COG4753|COG2207|COG2169|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Adenosine deaminase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS29Rum20550|CDS|CDS	1.5	90.5	0.1	F|K|T	COG4753|COG2207|COG2204|COG4936|COG3706|COG2197|COG2169	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|Predicted sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Adenosine deaminase
TS29Fae07229|CDS|CDS	1.0	158.0	0.0	F|K|T	COG5002|COG0745|COG4753|COG2207|COG2204|COG4936|COG2169|COG4565	Signal transduction histidine kinase|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|Predicted sensor domain|Adenosine deaminase|Response regulator of citrate/malate metabolism
TS29Fae03757|CDS|CDS	0.3	54.0	0.0	F|K|T	COG4753|COG2207|COG2169|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Adenosine deaminase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
Chyl2219|CDS|CDS	299.6	1.0	1,360.1	G	COG1879	ABC-type sugar transport system, periplasmic component
TS28Rum14205|CDS|CDS	50.0	1.0	227.0	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
Bste1249|CDS|CDS	33.3	1.0	151.0	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes

Robe3405|CDS|CDS	27.5	1.0	124.8	G	COG1879|COG1129	ABC-type sugar transport system, periplasmic component|ABC-type sugar transport system, ATPase component
FpraM2122375|CDS|CDS	12.2	0.5	110.5	G	COG1129	ABC-type sugar transport system, ATPase component
Caer2199|CDS|CDS	11.0	0.5	99.9	G	COG1653	ABC-type sugar transport system, periplasmic component
BactD23013|CDS|CDS	5.2	0.3	93.8	G	COG0524	Sugar kinases, ribokinase family
TS28Eub0689|CDS|CDS	28.5	1.5	86.3	G	COG0296	1,4-alpha-glucan branching enzyme
Buni0654|CDS|CDS	35.3	2.0	80.0	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
TS29Rum18307|CDS|CDS	16.7	1.0	75.7	G	COG4214|COG1172	ABC-type xylose transport system, permease component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components
Cbol4780|CDS|CDS	16.0	1.0	72.6	G	COG0149	Triosephosphate isomerase
TS28Fae13066|CDS|CDS	15.7	1.0	71.3	G	COG2017	Galactose mutarotase and related enzymes
TS28Clo03232|CDS|CDS	15.2	1.0	69.0	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Even1737|CDS|CDS	4.9	0.3	66.1	G	COG2211	Na+/melibiose symporter and related transporters
TS28Fae19104|CDS|CDS	4.8	0.3	64.7	G	COG0448	ADP-glucose pyrophosphorylase
Bsp1164441|CDS|CDS	13.9	1.0	62.9	G	COG0021	Transketolase
Buni1344|CDS|CDS	11.3	0.8	61.7	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS28Bac6533|CDS|CDS	11.3	0.8	61.7	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
Dfor2810|CDS|CDS	26.0	2.0	59.0	G	COG1653	ABC-type sugar transport system, periplasmic component
Buni0506|CDS|CDS	13.0	1.0	59.0	G	COG1904	Glucuronate isomerase
TS28Rum14772|CDS|CDS	13.0	1.0	59.0	G	COG2407	L-fucose isomerase and related proteins
ShigspD91165|CDS|CDS	6.5	0.5	59.0	G	COG1653|COG2182	ABC-type sugar transport system, periplasmic component|Maltose-binding periplasmic proteins/domains
Buni0307|CDS|CDS	6.3	0.5	57.5	G	COG2730	Endoglucanase
Buni2718|CDS|CDS	10.2	0.8	55.4	G	COG1472	Beta-glucosidase-related glycosidases
Buni0942|CDS|CDS	23.5	2.0	53.3	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
BFych461653|CDS|galactokinase	11.5	1.0	52.2	G	COG0153	Galactokinase
Ehal0749|CDS|CDS	28.5	2.5	51.8	G	COG0296	1,4-alpha-glucan branching enzyme
Even1518|CDS|CDS	5.5	0.5	49.9	G	COG0574|COG1080|COG3412	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria
TS28Rum09615|CDS|CDS	5.5	0.5	49.9	G	COG1803	Methylglyoxal synthase
Bthe7331685|CDS|CDS	5.4	0.5	49.0	G	COG0205	6-phosphofructokinase
TS28Fae01867|CDS|CDS	10.7	1.0	48.6	G	COG0021|COG3959	Transketolase|Transketolase, N-terminal subunit
Clep0321|CDS|CDS	5.3	0.5	48.4	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bova3862|CDS|CDS	10.6	1.0	48.2	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29Rum05295|CDS|CDS	41.0	4.0	46.5	G	COG1523	Type II secretory pathway, pullulanase PulA and related glycosidases
Caer0050|CDS|CDS	5.0	0.5	45.4	G	COG0058	Glucan phosphorylase
TS29Rum12185|CDS|CDS	5.0	0.5	45.4	G	COG0366	Glycosidases
Bado1178|CDS|CDS	3.3	0.3	44.3	G	COG1653|COG2182	ABC-type sugar transport system, periplasmic component|Maltose-binding periplasmic proteins/domains
TS28Rum01018|CDS|CDS	14.5	1.5	43.9	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
Msmi751379|CDS|CDS	3.0	0.3	40.9	G	COG3635	Predicted phosphoglycerate mutase, AP superfamily
TS28Fae00371|CDS|CDS	179.8	20.5	39.8	G	COG0574|COG4668|COG1080|COG3412|COG2190	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components
TS28Clo08188|CDS|CDS	4.3	0.5	39.3	G	COG0574|COG4668|COG1080|COG3412|COG2190	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components
TS28Rum04748|CDS|CDS	12.8	1.5	38.8	G	COG1879	ABC-type sugar transport system, periplasmic component
TS28Fae08221|CDS|CDS	42.0	5.0	38.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum12400|CDS|CDS	158.0	19.0	37.8	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Bac0090|CDS|CDS	21.9	2.7	37.2	G	COG0366|COG1523|COG3281	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis
Buni1687|CDS|CDS	36.8	4.5	37.2	G	COG0364	Glucose-6-phosphate 1-dehydrogenase
BFych461191|CDS|alpha-glucosidase	4.0	0.5	36.3	G	COG2730	Endoglucanase
Bova2568|CDS|CDS	4.0	0.5	36.3	G	COG1472	Beta-glucosidase-related glycosidases
TS28Rum07352|CDS|CDS	8.0	1.0	36.3	G	COG3715	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIC
TS28RumUnc1416|CDS|CDS	8.0	1.0	36.3	G	COG1653	ABC-type sugar transport system, periplasmic component
Clep1247|CDS|CDS	39.5	5.0	35.9	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Clo10638|CDS|CDS	144.5	18.5	35.5	G	COG1082	Sugar phosphate isomerases/epimerases
TS29Clo0163|CDS|CDS	144.5	18.5	35.5	G	COG1082	Sugar phosphate isomerases/epimerases
TS28Rum12459|CDS|CDS	19.0	2.5	34.5	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
Robe3450|CDS|CDS	19.0	2.5	34.5	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
TS28Eub5920|CDS|CDS	7.5	1.0	34.0	G	COG1879|COG4214|COG1172|COG4211|COG4158	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, permease component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|ABC-type glucose/galactose transport system, permease component|Predicted ABC-type sugar transport system, permease component
TS29Fae06769|CDS|CDS	7.5	1.0	34.0	G	COG0176	Transaldolase
TS29Bac00193|CDS|CDS	10.3	1.4	33.4	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Ccom0204|CDS|CDS	11.0	1.5	33.3	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
BactD23607|CDS|CDS	2.4	0.3	32.7	G	COG0153	Galactokinase
Bova1248|CDS|CDS	2.4	0.3	32.7	G	COG0153	Galactokinase
Cbol0184|CDS|CDS	7.0	1.0	31.8	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
Ceut0367|CDS|CDS	7.0	1.0	31.8	G	COG3839	ABC-type sugar transport systems, ATPase components
Buni3294|CDS|CDS	3.5	0.5	31.8	G	COG2407	L-fucose isomerase and related proteins
TS29Rum14950|CDS|CDS	3.5	0.5	31.8	G	COG2182	Maltose-binding periplasmic proteins/domains
TS28Fae01993|CDS|CDS	35.0	5.0	31.8	G	COG1109	Phosphomannomutase
Buni0655|CDS|CDS	27.4	4.0	31.1	G	COG0588	Phosphoglycerate mutase 1
Cbol1349|CDS|CDS	33.0	5.0	30.0	G	COG3718	Uncharacterized enzyme involved in inositol metabolism
TS28Rum16267|CDS|CDS	6.6	1.0	29.9	G	COG1109	Phosphomannomutase
Buni1029|CDS|CDS	26.0	4.0	29.5	G	COG0153	Galactokinase
TS28Bif3421|CDS|CDS	4.3	0.7	29.5	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase

FpraM2122377|CDS|CDS	31.4	4.8	29.5	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
BactD12396|CDS|CDS	1.6	0.3	29.1	G	COG3537	Putative alpha-1,2-mannosidase
Bxyl4442|CDS|CDS	1.6	0.3	29.1	G	COG3537	Putative alpha-1,2-mannosidase
TS28Rum10083|CDS|CDS	6.3	1.0	28.8	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
BactD14124|CDS|CDS	2.1	0.3	28.4	G	COG1472	Beta-glucosidase-related glycosidases
TS28Fae16882|CDS|CDS	6.1	1.0	27.6	G	COG1879|COG1172|COG4211|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|ABC-type glucose/galactose transport system, permease component|Predicted ABC-type sugar transport system, permease component
Bthe7335520|CDS|CDS	6.1	1.0	27.6	G	COG0364	Glucose-6-phosphate 1-dehydrogenase
TS28Fae12407|CDS|CDS	9.1	1.5	27.5	G	COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component
TS28Rum15547|CDS|CDS	148.0	24.5	27.4	G	COG1129	ABC-type sugar transport system, ATPase component
TS28Bac4043|CDS|CDS	3.0	0.5	27.2	G	COG4124	Beta-mannanase
TS29Bac07452|CDS|CDS	8.0	1.3	27.2	G	COG0296	1,4-alpha-glucan branching enzyme
TS28Rum07429|CDS|CDS	6.0	1.0	27.2	G	COG0176	Transaldolase
BactD24560|CDS|CDS	3.0	0.5	27.2	G	COG4632	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase
TS28Rum07535|CDS|CDS	6.0	1.0	27.2	G	COG4468	Galactose-1-phosphate uridyltransferase
Bova1915|CDS|CDS	6.0	1.0	27.2	G	COG1904	Glucuronate isomerase
TS29Fae08908|CDS|CDS	3.0	0.5	27.2	G	COG1925	Phosphotransferase system, HPr-related proteins
BFnctc3537|CDS|6-phosphofructokinase	3.0	0.5	27.2	G	COG0205	6-phosphofructokinase
TS28Rum16436|CDS|CDS	3.0	0.5	27.2	G	COG0366	Glycosidases
BactD24420|CDS|CDS	3.0	0.5	27.2	G	COG3717	5-keto 4-deoxyuronate isomerase
TS28Dor1342|CDS|CDS	6.0	1.0	27.2	G	COG1653	ABC-type sugar transport system, periplasmic component
Svar1346|CDS|CDS	6.0	1.0	27.0	G	COG0574|COG1080|COG4668|COG3412|COG2190	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components
TS28Fae09505|CDS|CDS	14.8	2.5	26.8	G	COG3839	ABC-type sugar transport systems, ATPase components
Bfin0903|CDS|CDS	8.0	1.4	25.8	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Bthe3732371|CDS|CDS	8.0	1.4	25.8	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
BactD12630|CDS|CDS	8.0	1.4	25.8	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Bthe7331681|CDS|CDS	8.0	1.4	25.8	G	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
Robe1823|CDS|CDS	5.7	1.0	25.7	G	COG2017	Galactose mutarotase and related enzymes
Buni1688|CDS|CDS	8.5	1.5	25.7	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
TS28Fae21379|CDS|CDS	67.7	12.0	25.6	G	COG2182	Maltose-binding periplasmic proteins/domains
TS28Fae21323|CDS|CDS	134.8	24.0	25.5	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum18310|CDS|CDS	95.3	17.0	25.5	G	COG1879	ABC-type sugar transport system, periplasmic component
TS29Rum13498|CDS|CDS	98.0	17.5	25.4	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Rum01594|CDS|CDS	98.0	17.5	25.4	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Fae11115|CDS|CDS	3.7	0.7	25.0	G	COG1472	Beta-glucosidase-related glycosidases
TS28Eub4465|CDS|CDS	5.5	1.0	25.0	G	COG3839	ABC-type sugar transport systems, ATPase components
TS28Fae16913|CDS|CDS	16.4	3.0	24.8	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Fae12308|CDS|CDS	21.8	4.0	24.8	G	COG1653	ABC-type sugar transport system, periplasmic component
Bsp1162927|CDS|CDS	1.1	0.2	24.7	G	COG0205	6-phosphofructokinase
Bple2834|CDS|CDS	1.1	0.2	24.7	G	COG0205	6-phosphofructokinase
Bdor3667|CDS|CDS	1.1	0.2	24.7	G	COG0205	6-phosphofructokinase
BT1102|CDS|6-phosphofructokinase	1.1	0.2	24.7	G	COG0205	6-phosphofructokinase
Pmer3618|CDS|CDS	1.1	0.2	24.7	G	COG0205	6-phosphofructokinase
TS29Bac12223|CDS|CDS	5.4	1.0	24.4	G	COG3250	Beta-galactosidase/beta-glucuronidase
Robe3781|CDS|CDS	45.6	8.5	24.3	G	COG1653	ABC-type sugar transport system, periplasmic component
Robe3232|CDS|CDS	37.5	7.0	24.3	G	COG1879	ABC-type sugar transport system, periplasmic component
TS28Fae16880|CDS|CDS	41.6	7.8	24.1	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
TS28Rum02361|CDS|CDS	21.0	4.0	23.9	G	COG1129	ABC-type sugar transport system, ATPase component
Bthe3735712|CDS|CDS	1.8	0.3	23.8	G	COG1482	Phosphomannose isomerase
Bsp1164391|CDS|CDS	1.8	0.3	23.8	G	COG1482	Phosphomannose isomerase
Bthe7334894|CDS|CDS	1.8	0.3	23.8	G	COG1482	Phosphomannose isomerase
TS28Rum15519|CDS|CDS	20.8	4.0	23.6	G	COG1070|COG4806	Sugar (pentulose and hexulose) kinases|L-rhamnose isomerase
TS29Fae06979|CDS|CDS	2.6	0.5	23.6	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
Bfra31122209|CDS|CDS	4.3	0.8	23.6	G	COG2407	L-fucose isomerase and related proteins
TS28Fae12935|CDS|CDS	10.3	2.0	23.5	G	COG0366|COG3281|COG1640	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis|4-alpha-glucanotransferase
ShigspD90137|CDS|CDS	1.7	0.3	22.7	G	COG4806	L-rhamnose isomerase
TS28Bac5535|CDS|CDS	1.7	0.3	22.7	G	COG0297	Glycogen synthase
RintL10186|CDS|CDS	5.0	1.0	22.7	G	COG1175	ABC-type sugar transport systems, permease components
TS28RumUnc1503|CDS|CDS	5.0	1.0	22.7	G	COG2211	Na+/melibiose symporter and related transporters
Rtor1790|CDS|CDS	5.0	1.0	22.7	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
TS28Rum02515|CDS|CDS	2.5	0.5	22.7	G	COG0366	Glycosidases
Csci1385|CDS|CDS	5.0	1.0	22.7	G	COG1820	N-acetylglucosamine-6-phosphate deacetylase
TS28Eub0190|CDS|CDS	2.5	0.5	22.7	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum16245|CDS|CDS	5.0	1.0	22.7	G	COG1482	Phosphomannose isomerase
Cbol4823|CDS|CDS	5.0	1.0	22.7	G	COG2376	Dihydroxyacetone kinase
RintL13599|CDS|CDS	5.0	1.0	22.7	G	COG2182	Maltose-binding periplasmic proteins/domains
Rtor1784|CDS|CDS	12.5	2.5	22.7	G	COG1129	ABC-type sugar transport system, ATPase component
TS28Rum06501|CDS|CDS	12.5	2.5	22.7	G	COG1129	ABC-type sugar transport system, ATPase component
Rbro0248|CDS|CDS	7.5	1.5	22.7	G	COG3839	ABC-type sugar transport systems, ATPase components
BactD12575|CDS|CDS	6.7	1.3	22.7	G	COG1472	Beta-glucosidase-related glycosidases
BactD11766|CDS|CDS	5.0	1.0	22.6	G	COG0574|COG1080|COG4668	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain
BactD21441|CDS|CDS	4.0	0.8	22.0	G	COG0191	Fructose/tagatose bisphosphate aldolase
FpraM2122449|CDS|CDS	2.4	0.5	21.9	G	COG0296	1,4-alpha-glucan branching enzyme
Caer2021|CDS|CDS	33.8	7.0	21.9	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Fae16502|CDS|CDS	14.3	3.0	21.6	G	COG1925	Phosphotransferase system, HPr-related proteins
TS29Fae06725|CDS|CDS	216.2	46.0	21.3	G	COG2182	Maltose-binding periplasmic proteins/domains
BLD0895|CDS|Alpha-L-arabinofuranosidase	2.3	0.5	21.2	G	COG3534	Alpha-L-arabinofuranosidase

BactD11982|CDS|CDS	7.0	1.5	21.2	G	COG0176|COG0166	Transaldolase|Glucose-6-phosphate isomerase
TS28Bac1052|CDS|CDS	2.3	0.5	21.2	G	COG1109	Phosphomannomutase
Robe2835|CDS|CDS	20.5	4.5	20.7	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bfin1256|CDS|CDS	13.6	3.0	20.6	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Rum15751|CDS|CDS	25.0	5.5	20.6	G	COG1653	ABC-type sugar transport system, periplasmic component
BactD23946|CDS|CDS	13.6	3.0	20.6	G	COG3250	Beta-galactosidase/beta-glucuronidase
Buni2565|CDS|CDS	1.5	0.3	20.4	G	COG3250	Beta-galactosidase/beta-glucuronidase
CspM6211453|CDS|CDS	9.0	2.0	20.4	G	COG0448	ADP-glucose pyrophosphorylase
TS28Fae22183|CDS|CDS	4.5	1.0	20.4	G	COG1904	Glucuronate isomerase
TS28Rum15546|CDS|CDS	71.8	16.0	20.4	G	COG1879|COG1172|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component
TS29Rum19417|CDS|CDS	246.0	55.0	20.3	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum03672|CDS|CDS	38.0	8.5	20.3	G	COG3250|COG3525	Beta-galactosidase/beta-glucuronidase|N-acetyl-beta-hexosaminidase
TS29Rum03526|CDS|CDS	4.3	1.0	19.7	G	COG1653	ABC-type sugar transport system, periplasmic component
Clep1248|CDS|CDS	4.3	1.0	19.7	G	COG1175	ABC-type sugar transport systems, permease components
TS28Fae01078|CDS|CDS	13.0	3.0	19.7	G	COG1472	Beta-glucosidase-related glycosidases
BactD13714|CDS|CDS	6.5	1.5	19.7	G	COG1472	Beta-glucosidase-related glycosidases
TS28Eub5098|CDS|CDS	4.3	1.0	19.7	G	COG2182	Maltose-binding periplasmic proteins/domains
TS29Bac07451|CDS|CDS	2.2	0.5	19.7	G	COG0296	1,4-alpha-glucan branching enzyme
BDI0208|CDS|4-alpha-glucanotransferase	43.0	10.0	19.5	G	COG3408	Glycogen debranching enzyme
Buni1126|CDS|CDS	24.4	5.7	19.5	G	COG0366|COG1523|COG3281	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis
TS28Rum15491|CDS|CDS	8.5	2.0	19.4	G	COG3839	ABC-type sugar transport systems, ATPase components
TS29Fae07101|CDS|CDS	4.3	1.0	19.3	G	COG0149	Triosephosphate isomerase
Buni3019|CDS|CDS	8.5	2.0	19.3	G	COG0696	Phosphoglyceromutase
Rgna1670|CDS|CDS	10.5	2.5	19.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Bac2896|CDS|CDS	7.7	1.8	19.0	G	COG1472	Beta-glucosidase-related glycosidases
TS28Rum11756|CDS|CDS	14.5	3.5	18.8	G	COG1653	ABC-type sugar transport system, periplasmic component
Bxyl0043|CDS|CDS	6.2	1.5	18.7	G	COG0800	2-keto-3-deoxy-6-phosphogluconate aldolase
Bxyl0802|CDS|CDS	6.2	1.5	18.7	G	COG3525	N-acetyl-beta-hexosaminidase
TS29Rum20911|CDS|CDS	68.0	17.0	18.2	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Bcat0994|CDS|CDS	1.0	0.3	18.2	G	COG3839	ABC-type sugar transport systems, ATPase components
TS28Fae16440|CDS|CDS	4.0	1.0	18.2	G	COG0395	ABC-type sugar transport system, permease component
TS28Rum05122|CDS|CDS	4.0	1.0	18.2	G	COG1879	ABC-type sugar transport system, periplasmic component
TS28Rum00303|CDS|CDS	4.0	1.0	18.2	G	COG1129	ABC-type sugar transport system, ATPase component
Caer2202|CDS|CDS	2.0	0.5	18.2	G	COG0395|COG3833	ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component
TS28Fae21898|CDS|CDS	4.0	1.0	18.2	G	COG0176	Transaldolase
BFych463828|CDS|4-alpha-glucanotransferase	10.0	2.5	18.2	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
Casp4832|CDS|CDS	4.0	1.0	18.2	G	COG1129	ABC-type sugar transport system, ATPase component
BactD11061|CDS|CDS	2.0	0.5	18.2	G	COG2730	Endoglucanase
TS28Fae18738|CDS|CDS	4.0	1.0	18.2	G	COG3412|COG1925	Uncharacterized protein conserved in bacteria|Phosphotransferase system, HPr-related proteins
TS28Dor0052|CDS|CDS	4.0	1.0	18.2	G	COG3010	Putative N-acetylmannosamine-6-phosphate epimerase
TS28Rum11685|CDS|CDS	4.0	1.0	18.2	G	COG1653	ABC-type sugar transport system, periplasmic component
RintL12354|CDS|CDS	4.0	1.0	18.2	G	COG1554|COG1877	Trehalose and maltose hydrolases (possible phosphorylases)|Trehalose-6-phosphatase
Hfil0135|CDS|CDS	4.0	1.0	18.2	G	COG3010	Putative N-acetylmannosamine-6-phosphate epimerase
Bryfor3079|CDS|CDS	4.0	1.0	18.2	G	COG1472	Beta-glucosidase-related glycosidases
Dlon1532|CDS|CDS	2.0	0.5	18.2	G	COG4468	Galactose-1-phosphate uridyltransferase
Buni0258|CDS|CDS	4.0	1.0	18.2	G	COG3250	Beta-galactosidase/beta-glucuronidase
Buni2250|CDS|CDS	3.3	0.8	18.2	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Bac6120|CDS|CDS	1.3	0.3	18.2	G	COG3250	Beta-galactosidase/beta-glucuronidase
BactD21456|CDS|CDS	4.0	1.0	18.1	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
Buni1068|CDS|CDS	25.5	6.5	17.8	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
TS28Bac1544|CDS|CDS	15.0	3.8	17.8	G	COG3934	Endo-beta-mannanase
Buni0300|CDS|CDS	15.0	3.8	17.8	G	COG3934	Endo-beta-mannanase
TS29Fae06921|CDS|CDS	3.9	1.0	17.7	G	COG1109	Phosphomannomutase
TS29Rum10632|CDS|CDS	19.5	5.0	17.7	G	COG1879	ABC-type sugar transport system, periplasmic component
TS29Clo4778|CDS|CDS	35.0	9.0	17.7	G	COG1879	ABC-type sugar transport system, periplasmic component
Buni3322|CDS|CDS	5.8	1.5	17.7	G	COG1109	Phosphomannomutase
TS28Bif4566|CDS|CDS	13.4	3.5	17.4	G	COG0021	Transketolase
Buni0791|CDS|CDS	3.8	1.0	17.4	G	COG1472	Beta-glucosidase-related glycosidases
FpraM2122373|CDS|CDS	5.8	1.5	17.4	G	COG1879|COG1172|COG4158|COG4211	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component|ABC-type glucose/galactose transport system, permease component
Buni0659|CDS|CDS	3.8	1.0	17.3	G	COG0205	6-phosphofructokinase
TS28Fae01830|CDS|CDS	370.0	97.0	17.3	G	COG1653	ABC-type sugar transport system, periplasmic component
Robe3281|CDS|CDS	19.0	5.0	17.3	G	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases
TS28Rum01682|CDS|CDS	16.9	4.5	17.0	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Dfor1934|CDS|CDS	33.7	9.0	17.0	G	COG1879	ABC-type sugar transport system, periplasmic component
Bxyl3893|CDS|CDS	3.1	0.8	17.0	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
TS28Rum02685|CDS|CDS	43.0	11.5	17.0	G	COG1653	ABC-type sugar transport system, periplasmic component
Robe3782|CDS|CDS	7.4	2.0	16.9	G	COG1175	ABC-type sugar transport systems, permease components
FpraM2121175|CDS|CDS	88.8	24.0	16.8	G	COG1653	ABC-type sugar transport system, periplasmic component
BFych463252|CDS|phosphoglyceromutase	1.8	0.5	16.6	G	COG0588	Phosphoglycerate mutase 1
TS28RumUnc1985|CDS|CDS	11.0	3.0	16.6	G	COG3957	Phosphoketolase
BFnctc3091|CDS|phosphoglyceromutase	1.8	0.5	16.6	G	COG0588	Phosphoglycerate mutase 1
Aput0302|CDS|CDS	22.0	6.0	16.6	G	COG1109	Phosphomannomutase
TS28Rum12148|CDS|CDS	3.7	1.0	16.6	G	COG2160	L-arabinose isomerase
TS28Eub0950|CDS|CDS	1.8	0.5	16.6	G	COG0149	Triosephosphate isomerase

TS28Clo02971|CDS|CDS	14.5	4.0	16.5	G	COG0574|COG4668|COG1080|COG3412|COG2190	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components
Bxyl2948|CDS|CDS	4.7	1.3	15.9	G	COG3775	Phosphotransferase system, galactitol-specific IIC component
Cbol4937|CDS|CDS	7.0	2.0	15.9	G	COG1129	ABC-type sugar transport system, ATPase component
TS28Dor0107|CDS|CDS	14.0	4.0	15.9	G	COG1653	ABC-type sugar transport system, periplasmic component
Cbol0799|CDS|CDS	7.0	2.0	15.9	G	COG1129	ABC-type sugar transport system, ATPase component
Bova0285|CDS|CDS	3.5	1.0	15.7	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
FpraM2121630|CDS|CDS	8.6	2.5	15.6	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Fae13618|CDS|CDS	6.8	2.0	15.5	G	COG1904	Glucuronate isomerase
FpraM2122294|CDS|CDS	23.8	7.0	15.5	G	COG1653	ABC-type sugar transport system, periplasmic component
Dfor2293|CDS|CDS	17.0	5.0	15.4	G	COG0574|COG1080|COG4668|COG3412	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria
BactD12393|CDS|CDS	1.7	0.5	15.3	G	COG4833	Predicted glycosyl hydrolase
TS28Fae14035|CDS|CDS	15.1	4.5	15.3	G	COG0166|COG0176	Glucose-6-phosphate isomerase|Transaldolase
Bxyl0801|CDS|CDS	1.7	0.5	15.1	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Clo06640|CDS|CDS	3.3	1.0	15.1	G	COG1175	ABC-type sugar transport systems, permease components
TS28Bac1652|CDS|CDS	3.3	1.0	15.1	G	COG1472	Beta-glucosidase-related glycosidases
Cste1898|CDS|CDS	3.3	1.0	15.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Fae21445|CDS|CDS	5.0	1.5	15.1	G	COG1109	Phosphomannomutase
TS29Rum00102|CDS|CDS	320.6	98.0	14.9	G	COG2407	L-fucose isomerase and related proteins
Bxyl4452|CDS|CDS	5.5	1.7	14.8	G	COG4833	Predicted glycosyl hydrolase
TS29Rum00093|CDS|CDS	156.9	48.0	14.8	G	COG1879|COG4214|COG1172|COG4211|COG4158	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, permease component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|ABC-type glucose/galactose transport system, permease component|Predicted ABC-type sugar transport system, permease component
BactD12573|CDS|CDS	3.3	1.0	14.8	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
Clep1252|CDS|CDS	6.5	2.0	14.8	G	COG1082	Sugar phosphate isomerases/epimerases
Rtor0675|CDS|CDS	6.5	2.0	14.8	G	COG0366|COG1640|COG3281	Glycosidases|4-alpha-glucanotransferase|Uncharacterized protein, probably involved in trehalose biosynthesis
Buni1028|CDS|CDS	4.8	1.5	14.6	G	COG0738	Fucose permease
TS29Bac00498|CDS|CDS	27.3	8.5	14.6	G	COG0148	Enolase
TS28Fae19105|CDS|CDS	6.4	2.0	14.6	G	COG0297	Glycogen synthase
TS28Fae19101|CDS|CDS	6.3	2.0	14.3	G	COG0296	1,4-alpha-glucan branching enzyme
Rbro0630|CDS|CDS	7.8	2.5	14.2	G	COG2182	Maltose-binding periplasmic proteins/domains
TS29Rum17970|CDS|CDS	50.0	16.0	14.2	G	COG1653	ABC-type sugar transport system, periplasmic component
Buni1140|CDS|CDS	35.8	11.5	14.1	G	COG0148	Enolase
Bxyl3092|CDS|CDS	13.9	4.5	14.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
BactD12720|CDS|CDS	13.9	4.5	14.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Csci1941|CDS|CDS	1.0	0.3	13.6	G	COG1109	Phosphomannomutase
Bova0190|CDS|CDS	1.0	0.3	13.6	G	COG2942	N-acyl-D-glucosamine 2-epimerase
Bfra31121655|CDS|CDS	1.0	0.3	13.6	G	COG0191	Fructose/tagatose bisphosphate aldolase
BactD23173|CDS|CDS	1.0	0.3	13.6	G	COG3250	Beta-galactosidase/beta-glucuronidase
Ccom0503|CDS|CDS	21.0	7.0	13.6	G	COG3250	Beta-galactosidase/beta-glucuronidase
BactD21080|CDS|CDS	1.5	0.5	13.6	G	COG0176|COG0166	Transaldolase|Glucose-6-phosphate isomerase
TS28Dor0455|CDS|CDS	3.0	1.0	13.6	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Fae16439|CDS|CDS	3.0	1.0	13.6	G	COG1653	ABC-type sugar transport system, periplasmic component
Hfil2990|CDS|CDS	3.0	1.0	13.6	G	COG0153	Galactokinase
TS28Rum02438|CDS|CDS	1.5	0.5	13.6	G	COG1129	ABC-type sugar transport system, ATPase component
TS28Met1583|CDS|CDS	3.0	1.0	13.6	G	COG3635	Predicted phosphoglycerate mutase, AP superfamily
Bxyl4248|CDS|CDS	3.0	1.0	13.6	G	COG3669	Alpha-L-fucosidase
Rumhyd1082|CDS|CDS	3.0	1.0	13.6	G	COG1175|COG2182	ABC-type sugar transport systems, permease components|Maltose-binding periplasmic proteins/domains
BactD22086|CDS|CDS	0.6	0.2	13.6	G	COG4124	Beta-mannanase
BFnctc1811|CDS|beta-N-acetylhexosaminidase	3.0	1.0	13.6	G	COG3525	N-acetyl-beta-hexosaminidase
TS28Fae16441|CDS|CDS	3.0	1.0	13.6	G	COG1175|COG4209	ABC-type sugar transport systems, permease components|ABC-type polysaccharide transport system, permease component
Dlon1193|CDS|CDS	3.0	1.0	13.6	G	COG3534	Alpha-L-arabinofuranosidase
TS28Fae08223|CDS|CDS	3.0	1.0	13.6	G	COG1175|COG4209	ABC-type sugar transport systems, permease components|ABC-type polysaccharide transport system, permease component
Rumhyd2933|CDS|CDS	3.0	1.0	13.6	G	COG0296	1,4-alpha-glucan branching enzyme
CspM6212778|CDS|CDS	3.0	1.0	13.6	G	COG0296	1,4-alpha-glucan branching enzyme
TS28Rum10081|CDS|CDS	3.0	1.0	13.6	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
TS28Ali2049|CDS|CDS	3.0	1.0	13.6	G	COG0191	Fructose/tagatose bisphosphate aldolase
Rumhyd1270|CDS|CDS	6.0	2.0	13.6	G	COG0524|COG0800|COG3892|COG3718	Sugar kinases, ribokinase family|2-keto-3-deoxy-6-phosphogluconate aldolase|Uncharacterized protein conserved in bacteria|Uncharacterized enzyme involved in inositol metabolism
Bova1242|CDS|CDS	1.5	0.5	13.6	G	COG2160	L-arabinose isomerase
Acac2071|CDS|CDS	3.0	1.0	13.6	G	COG1082	Sugar phosphate isomerases/epimerases
Ccom0201|CDS|CDS	3.0	1.0	13.6	G	COG0149	Triosephosphate isomerase
Ccom0399|CDS|CDS	15.0	5.0	13.6	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum12988|CDS|CDS	3.0	1.0	13.6	G	COG3525	N-acetyl-beta-hexosaminidase
Cbol4296|CDS|CDS	3.0	1.0	13.6	G	COG0036	Pentose-5-phosphate-3-epimerase
Hfil2940|CDS|CDS	3.0	1.0	13.6	G	COG1904	Glucuronate isomerase
TS29Rum08265|CDS|CDS	3.0	1.0	13.6	G	COG0448	ADP-glucose pyrophosphorylase
TS29Rum07113|CDS|CDS	9.0	3.0	13.6	G	COG3250	Beta-galactosidase/beta-glucuronidase
Cbol1155|CDS|CDS	9.0	3.0	13.6	G	COG1879|COG1172|COG4158|COG4211	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component|ABC-type glucose/galactose transport system, permease component
TS28Rum10535|CDS|CDS	19.5	6.5	13.6	G	COG1879	ABC-type sugar transport system, periplasmic component
TS28Fae02318|CDS|CDS	9.0	3.0	13.6	G	COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component
BactD11785|CDS|CDS	2.0	0.7	13.6	G	COG1820	N-acetylglucosamine-6-phosphate deacetylase
FpraM2121455|CDS|CDS	9.8	3.3	13.4	G	COG0205	6-phosphofructokinase

Rtor1417|CDS|CDS	38.3	13.0	13.4	G	COG0574|COG1080|COG4668|COG3412	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria
Bfin0907|CDS|CDS	5.4	1.8	13.4	G	COG0205	6-phosphofructokinase
Bthe3732367|CDS|CDS	5.4	1.8	13.4	G	COG0205	6-phosphofructokinase
BactD12634|CDS|CDS	5.4	1.8	13.4	G	COG0205	6-phosphofructokinase
Buni0934|CDS|CDS	22.0	7.5	13.3	G	COG0366|COG3281|COG3408	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis|Glycogen debranching enzyme
FpraM2121173|CDS|CDS	7.3	2.5	13.3	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS28Fae10265|CDS|CDS	7.3	2.5	13.3	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
BLD0441|CDS|Transaldolase	1.5	0.5	13.2	G	COG0176	Transaldolase
TS29Rum16940|CDS|CDS	81.0	28.0	13.1	G	COG1082	Sugar phosphate isomerases/epimerases
TS28Rum00062|CDS|CDS	26.0	9.0	13.1	G	COG2017	Galactose mutarotase and related enzymes
BactD10542|CDS|CDS	4.3	1.5	13.1	G	COG1904	Glucuronate isomerase
BactD11454|CDS|CDS	4.3	1.5	13.1	G	COG3717	5-keto 4-deoxyuronate isomerase
Bxyl4446|CDS|CDS	4.3	1.5	13.0	G	COG4833	Predicted glycosyl hydrolase
TS29Bac06978|CDS|CDS	10.4	3.7	12.9	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Fae21419|CDS|CDS	35.6	12.5	12.9	G	COG3839	ABC-type sugar transport systems, ATPase components
TS29Rum05967|CDS|CDS	2.8	1.0	12.9	G	COG0448	ADP-glucose pyrophosphorylase
FpraM2121364|CDS|CDS	2.8	1.0	12.9	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Bac1222|CDS|CDS	5.7	2.0	12.9	G	COG2942	N-acyl-D-glucosamine 2-epimerase
TS28Bac1549|CDS|CDS	2.8	1.0	12.9	G	COG3459	Cellobiose phosphorylase
TS29Rum11085|CDS|CDS	14.0	5.0	12.7	G	COG3345	Alpha-galactosidase
TS29Bac08446|CDS|CDS	43.3	15.5	12.7	G	COG0364	Glucose-6-phosphate 1-dehydrogenase
TS29Rum03144|CDS|CDS	75.4	27.0	12.7	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Bac4132|CDS|CDS	2.8	1.0	12.7	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Bif2313|CDS|CDS	8.4	3.0	12.7	G	COG3957	Phosphoketolase
TS29RumUnc0176|CDS|CDS	139.0	50.0	12.6	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum00091|CDS|CDS	180.8	66.0	12.4	G	COG1879	ABC-type sugar transport system, periplasmic component
TS29Fae06789|CDS|CDS	151.3	56.0	12.3	G	COG1653	ABC-type sugar transport system, periplasmic component
Caer1707|CDS|CDS	13.5	5.0	12.3	G	COG3716	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IID
Rtor1782|CDS|CDS	14.8	5.5	12.2	G	COG1879	ABC-type sugar transport system, periplasmic component
Begg1320|CDS|CDS	2.7	1.0	12.1	G	COG2730	Endoglucanase
TS28Fae16912|CDS|CDS	2.7	1.0	12.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bac10809|CDS|CDS	5.3	2.0	12.1	G	COG2942	N-acyl-D-glucosamine 2-epimerase
Bxyl2836|CDS|CDS	2.7	1.0	12.1	G	COG3537	Putative alpha-1,2-mannosidase
Csci2634|CDS|CDS	2.7	1.0	12.1	G	COG3839	ABC-type sugar transport systems, ATPase components
TS28Rum15723|CDS|CDS	4.0	1.5	12.1	G	COG1472	Beta-glucosidase-related glycosidases
Cbol5496|CDS|CDS	8.0	3.0	12.1	G	COG0153	Galactokinase
Bxyl0308|CDS|CDS	1.3	0.5	12.1	G	COG2731	Beta-galactosidase, beta subunit
TS29Bac07455|CDS|CDS	1.3	0.5	12.1	G	COG2731	Beta-galactosidase, beta subunit
Bova2264|CDS|CDS	1.3	0.5	12.1	G	COG3635	Predicted phosphoglycerate mutase, AP superfamily
TS28Fae10269|CDS|CDS	34.5	13.0	12.0	G	COG1653	ABC-type sugar transport system, periplasmic component
Bova2416|CDS|CDS	10.5	4.0	11.9	G	COG0176|COG0166	Transaldolase|Glucose-6-phosphate isomerase
Cbol1156|CDS|CDS	13.0	5.0	11.8	G	COG1129	ABC-type sugar transport system, ATPase component
FpraM2120142|CDS|CDS	4.8	1.8	11.8	G	COG0448	ADP-glucose pyrophosphorylase
TS28Fae00616|CDS|CDS	20.7	8.0	11.7	G	COG1879	ABC-type sugar transport system, periplasmic component
TS28Fae13793|CDS|CDS	20.5	8.0	11.6	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum14900|CDS|CDS	10.2	4.0	11.5	G	COG1879|COG1172|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component
TS29Bac00648|CDS|CDS	73.7	29.3	11.4	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
Bxyl3805|CDS|CDS	0.8	0.3	11.3	G	COG3507	Beta-xylosidase
TS28Rum08450|CDS|CDS	2.5	1.0	11.3	G	COG0366	Glycosidases
Dfor0827|CDS|CDS	5.0	2.0	11.3	G	COG0448	ADP-glucose pyrophosphorylase
RintL13215|CDS|CDS	5.0	2.0	11.3	G	COG3250	Beta-galactosidase/beta-glucuronidase
Caer2203|CDS|CDS	2.5	1.0	11.3	G	COG3839	ABC-type sugar transport systems, ATPase components
Robe3411|CDS|CDS	2.5	1.0	11.3	G	COG2017	Galactose mutarotase and related enzymes
Dfor2481|CDS|CDS	12.5	5.0	11.3	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Rum11755|CDS|CDS	7.4	3.0	11.2	G	COG1175	ABC-type sugar transport systems, permease components
Rtor0337|CDS|CDS	12.3	5.0	11.2	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Fae00016|CDS|CDS	43.0	17.5	11.2	G	COG0448	ADP-glucose pyrophosphorylase
Bthe3732370|CDS|CDS	2.3	0.9	11.1	G	COG0588	Phosphoglycerate mutase 1
CspM6211083|CDS|CDS	2.5	1.0	11.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29RumUnc0460|CDS|CDS	7.3	3.0	11.1	G	COG1175	ABC-type sugar transport systems, permease components
TS28Rum02551|CDS|CDS	11.0	4.5	11.1	G	COG2706	3-carboxymuconate cyclase
Robe3235|CDS|CDS	12.2	5.0	11.0	G	COG1879|COG1172|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component
BactD10892|CDS|CDS	6.1	2.5	11.0	G	COG2721	Altronate dehydratase
TS29Rum19002|CDS|CDS	29.0	12.0	11.0	G	COG1879	ABC-type sugar transport system, periplasmic component
Rgna1505|CDS|CDS	4.8	2.0	11.0	G	COG0448	ADP-glucose pyrophosphorylase
TS28Bac3908|CDS|CDS	26.5	11.0	10.9	G	COG2730	Endoglucanase
Buni1138|CDS|CDS	26.5	11.0	10.9	G	COG2730	Endoglucanase
TS28Fae00017|CDS|CDS	39.5	16.5	10.9	G	COG0448	ADP-glucose pyrophosphorylase
TS28Eub7787|CDS|CDS	3.6	1.5	10.8	G	COG1653	ABC-type sugar transport system, periplasmic component
Robe3234|CDS|CDS	25.0	10.5	10.8	G	COG1129	ABC-type sugar transport system, ATPase component
TS28Fae01251|CDS|CDS	14.3	6.0	10.8	G	COG2190	Phosphotransferase system IIA components
Bfin0060|CDS|CDS	2.4	1.0	10.7	G	COG1472	Beta-glucosidase-related glycosidases
TS29RumUnc1456|CDS|CDS	33.0	14.0	10.7	G	COG3839	ABC-type sugar transport systems, ATPase components
Buni2622|CDS|CDS	17.6	7.5	10.6	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29Rum00094|CDS|CDS	148.7	63.5	10.6	G	COG1129	ABC-type sugar transport system, ATPase component
Svar1329|CDS|CDS	4.7	2.0	10.6	G	COG3507	Beta-xylosidase
BFych460380|CDS|beta-galactosidase	3.5	1.5	10.6	G	COG3250	Beta-galactosidase/beta-glucuronidase
Cbol4933|CDS|CDS	7.0	3.0	10.6	G	COG1129	ABC-type sugar transport system, ATPase component
TS29Fae04105|CDS|CDS	3.5	1.5	10.6	G	COG1904	Glucuronate isomerase
TS28Fae16796|CDS|CDS	7.0	3.0	10.6	G	COG0191	Fructose/tagatose bisphosphate aldolase
Msmi750774|CDS|CDS	0.6	0.3	10.6	G	COG0483|COG0061	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family|Predicted sugar kinase

BactD10197|CDS|CDS	2.3	1.0	10.6	G	COG2211	Na+/melibiose symporter and related transporters
TS28Fae10964|CDS|CDS	2.3	1.0	10.6	G	COG1653	ABC-type sugar transport system, periplasmic component
BactD12498|CDS|CDS	14.3	6.2	10.6	G	COG0296|COG0366|COG1523	1,4-alpha-glucan branching enzyme|Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases
Buni1039|CDS|CDS	15.0	6.5	10.5	G	COG0021	Transketolase
Cbol1789|CDS|CDS	11.5	5.0	10.4	G	COG0800	2-keto-3-deoxy-6-phosphogluconate aldolase
Bxyl1419|CDS|CDS	5.8	2.5	10.4	G	COG1482	Phosphomannose isomerase
TS28Fae18004|CDS|CDS	19.5	8.5	10.4	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
Bxyl0496|CDS|CDS	8.0	3.5	10.4	G	COG1904	Glucuronate isomerase
TS28Rum08404|CDS|CDS	3.0	1.3	10.2	G	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases
Clep0154|CDS|CDS	3.0	1.3	10.2	G	COG1070	Sugar (pentulose and hexulose) kinases
BactD13546|CDS|CDS	3.0	1.3	10.2	G	COG3250	Beta-galactosidase/beta-glucuronidase
Casp2879|CDS|CDS	4.5	2.0	10.2	G	COG1879|COG4213	ABC-type sugar transport system, periplasmic component|ABC-type xylose transport system, periplasmic component
Caer0051|CDS|CDS	4.5	2.0	10.2	G	COG0448	ADP-glucose pyrophosphorylase
Dfor1753|CDS|CDS	4.5	2.0	10.2	G	COG0205	6-phosphofructokinase
Bryfor3651|CDS|CDS	4.5	2.0	10.2	G	COG0149	Triosephosphate isomerase
Bpse1623|CDS|CDS	2.3	1.0	10.2	G	COG0191	Fructose/tagatose bisphosphate aldolase
TS29Rum09402|CDS|CDS	4.5	2.0	10.2	G	COG0366|COG3281|COG1640	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis|4-alpha-glucanotransferase
TS28Bac7178|CDS|CDS	1.1	0.5	10.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS28Fae21432|CDS|CDS	58.9	26.5	10.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
TS29Fae10163|CDS|CDS	58.9	26.5	10.1	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
Buni0566|CDS|CDS	20.0	9.0	10.1	G	COG0296	1,4-alpha-glucan branching enzyme
BFnctc0241|CDS|phosphoglyceromutase	3.3	1.5	10.1	G	COG0696	Phosphoglyceromutase
BFych460292|CDS|phosphoglyceromutase	3.3	1.5	10.1	G	COG0696	Phosphoglyceromutase
TS29Rum17063|CDS|CDS	132.0	59.5	10.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum19947|CDS|CDS	1.5	68.5	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Bac06649|CDS|CDS	0.3	15.5	0.1	G	COG3534	Alpha-L-arabinofuranosidase
TS29Bif3460|CDS|CDS	2.5	116.5	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29RumUnc1625|CDS|CDS	1.0	47.0	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum20774|CDS|CDS	3.0	141.5	0.1	G	COG0058	Glucan phosphorylase
TS29Fae10067|CDS|CDS	3.8	183.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Rum19427|CDS|CDS	1.0	48.0	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Rum00317|CDS|CDS	1.0	48.0	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bif2442|CDS|CDS	4.5	216.5	0.1	G	COG1472	Beta-glucosidase-related glycosidases
TS29Rum03154|CDS|CDS	1.0	49.0	0.1	G	COG0383	Alpha-mannosidase
TS29Rum16581|CDS|CDS	2.0	99.0	0.1	G	COG2190|COG1264	Phosphotransferase system IIA components|Phosphotransferase system IIB components
TS28Fae22252|CDS|CDS	0.5	25.0	0.1	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
TS28Fae18201|CDS|CDS	1.0	50.5	0.1	G	COG1109	Phosphomannomutase
TS28Bif1656|CDS|CDS	0.4	17.8	0.1	G	COG1874	Beta-galactosidase
FpraM2120602|CDS|CDS	1.0	51.0	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS28Fae16621|CDS|CDS	1.0	52.0	0.1	G	COG3459	Cellobiose phosphorylase
TS28Fae21374|CDS|CDS	0.5	26.0	0.1	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
TS29Rum16550|CDS|CDS	2.0	107.0	0.1	G	COG3345	Alpha-galactosidase
TS28Bif4951|CDS|CDS	0.3	13.5	0.1	G	COG0153	Galactokinase
TS28Fae20836|CDS|CDS	0.5	27.0	0.1	G	COG0153	Galactokinase
TS28Fae15027|CDS|CDS	0.5	27.0	0.1	G	COG0406	Fructose-2,6-bisphosphatase
TS29Fae07234|CDS|CDS	3.0	162.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Fae07251|CDS|CDS	1.0	54.0	0.1	G	COG1482	Phosphomannose isomerase
TS29Bif1408|CDS|CDS	0.7	36.0	0.1	G	COG2190|COG1264	Phosphotransferase system IIA components|Phosphotransferase system IIB components
TS29Fae01011|CDS|CDS	0.3	18.0	0.1	G	COG2942	N-acyl-D-glucosamine 2-epimerase
TS28Bif5093|CDS|CDS	1.0	55.0	0.1	G	COG1879|COG1172|COG4211|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|ABC-type glucose/galactose transport system, permease component|Predicted ABC-type sugar transport system, permease component
TS29Fae03198|CDS|CDS	1.0	55.5	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bac05994|CDS|CDS	0.2	11.2	0.1	G	COG1929	Glycerate kinase
TS29Bif0069|CDS|CDS	0.5	28.0	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum16743|CDS|CDS	1.0	57.5	0.1	G	COG3414|COG3037	Phosphotransferase system, galactitol-specific IIB component|Uncharacterized protein conserved in bacteria
TS28Bif5094|CDS|CDS	0.8	43.2	0.1	G	COG1879|COG1172|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component
TS29Bif4061|CDS|CDS	0.8	43.2	0.1	G	COG1879|COG1172|COG4158	ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component
Bpse0138|CDS|CDS	0.7	38.5	0.1	G	COG2190|COG1264	Phosphotransferase system IIA components|Phosphotransferase system IIB components
TS29Bif0349|CDS|CDS	0.7	38.7	0.1	G	COG0366	Glycosidases
TS29Bif1969|CDS|CDS	0.3	19.7	0.1	G	COG0126|COG0149	3-phosphoglycerate kinase|Triosephosphate isomerase
TS28Bif1192|CDS|CDS	0.8	44.3	0.1	G	COG0366	Glycosidases
TS28Bif0398|CDS|CDS	1.5	89.5	0.1	G	COG1070	Sugar (pentulose and hexulose) kinases
TS29Fae07226|CDS|CDS	2.0	120.0	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Col1892|CDS|CDS	0.5	30.0	0.1	G	COG3444|COG2893	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB|Phosphotransferase system, mannose/fructose-specific component IIA
Bcat1020|CDS|CDS	0.5	30.5	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bac03401|CDS|CDS	0.3	20.5	0.1	G	COG4806	L-rhamnose isomerase
TS29Fae09099|CDS|CDS	0.5	31.0	0.1	G	COG1482	Phosphomannose isomerase
TS29Bif0176|CDS|CDS	0.3	20.8	0.1	G	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)
TS29Fae05959|CDS|CDS	1.0	63.0	0.1	G	COG1175|COG4209	ABC-type sugar transport systems, permease components|ABC-type polysaccharide transport system, permease component
TS28Bif0871|CDS|CDS	0.3	21.0	0.1	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
TS29Bif0407|CDS|CDS	1.3	84.2	0.1	G	COG3345	Alpha-galactosidase
Bpse1406|CDS|CDS	0.7	42.2	0.1	G	COG0366	Glycosidases

TS29Fae01185|CDS|CDS	2.5	159.5	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS28Fae13802|CDS|CDS	0.5	32.0	0.1	G	COG1482	Phosphomannose isomerase
TS29RumUnc0132|CDS|CDS	1.0	64.0	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
Bbre0172|CDS|CDS	0.5	32.5	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS28Bif1183|CDS|CDS	1.5	97.7	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS29Fae05536|CDS|CDS	3.0	196.0	0.1	G	COG1501	Alpha-glucosidases, family 31 of glycosyl hydrolases
TS29Fae04921|CDS|CDS	0.7	44.0	0.1	G	COG0235|COG1720	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases|Uncharacterized conserved protein
Bbre0174|CDS|CDS	0.3	22.0	0.1	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
TS29Fae05958|CDS|CDS	1.0	67.0	0.1	G	COG0395|COG3833	ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component
TS29Rum00343|CDS|CDS	1.0	67.0	0.1	G	COG0406|COG2068	Fructose-2,6-bisphosphatase|Uncharacterized MobA-related protein
TS28Bif1921|CDS|CDS	0.3	16.8	0.1	G	COG3001	Fructosamine-3-kinase
TS29Bif3509|CDS|CDS	1.3	84.5	0.1	G	COG0153	Galactokinase
TS29Bac08433|CDS|CDS	0.3	22.7	0.1	G	COG3855	Uncharacterized protein conserved in bacteria
TS29Bif3459|CDS|CDS	1.3	85.2	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Bif0414|CDS|CDS	1.7	114.5	0.1	G	COG0366	Glycosidases
TS29RumUnc1629|CDS|CDS	1.0	69.0	0.1	G	COG1621	Beta-fructosidases (levanase/invertase)
TS29Bif3817|CDS|CDS	0.3	23.4	0.1	G	COG0120	Ribose 5-phosphate isomerase
TS28Bif0790|CDS|CDS	0.3	23.4	0.1	G	COG0120	Ribose 5-phosphate isomerase
TS29Fae01170|CDS|CDS	1.0	71.0	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29RumUnc0058|CDS|CDS	1.0	71.0	0.1	G	COG1109	Phosphomannomutase
TS29RumUnc0780|CDS|CDS	1.0	72.0	0.1	G	COG1472	Beta-glucosidase-related glycosidases
TS29Bif3887|CDS|CDS	0.8	54.4	0.1	G	COG4213	ABC-type xylose transport system, periplasmic component
TS28Bif0707|CDS|CDS	0.8	54.4	0.1	G	COG4213	ABC-type xylose transport system, periplasmic component
TS29Col0673|CDS|CDS	1.0	73.5	0.1	G	COG2190|COG1264|COG1263	Phosphotransferase system IIA components|Phosphotransferase system IIB components|Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific
TS29Fae07218|CDS|CDS	2.0	148.0	0.1	G	COG0366	Glycosidases
TS29Rum16785|CDS|CDS	0.5	37.5	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Fae22256|CDS|CDS	0.5	38.5	0.1	G	COG3090|COG1593	TRAP-type C4-dicarboxylate transport system, small permease component|TRAP-type C4-dicarboxylate transport system, large permease component
TS29Bac09566|CDS|CDS	0.3	26.5	0.1	G	COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase
TS28Bif1651|CDS|CDS	0.3	19.9	0.1	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Rum20799|CDS|CDS	0.5	40.0	0.1	G	COG0395|COG3833	ABC-type sugar transport system, permease component|ABC-type maltose transport systems, permease component
TS28Bif0682|CDS|CDS	1.0	80.0	0.1	G	COG3534	Alpha-L-arabinofuranosidase
TS29Bif3908|CDS|CDS	1.0	80.0	0.1	G	COG3534	Alpha-L-arabinofuranosidase
TS28Fae00257|CDS|CDS	0.5	41.0	0.1	G	COG1621	Beta-fructosidases (levanase/invertase)
TS28Bif4546|CDS|CDS	0.3	20.8	0.1	G	COG1175	ABC-type sugar transport systems, permease components
TS29Fae05440|CDS|CDS	2.0	167.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Bif3423|CDS|CDS	2.0	167.2	0.1	G	COG3534	Alpha-L-arabinofuranosidase
TS29Bif3905|CDS|CDS	1.0	84.0	0.1	G	COG3507	Beta-xylosidase
TS29Bac11072|CDS|CDS	0.3	28.0	0.1	G	COG1874	Beta-galactosidase
TS29Fae05964|CDS|CDS	1.0	85.0	0.1	G	COG2706	3-carboxymuconate cyclase
TS29RumUnc0074|CDS|CDS	1.0	85.0	0.1	G	COG0366|COG1523|COG3281|COG1640	Glycosidases|Type II secretory pathway, pullulanase PulA and related glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis|4-alpha-glucanotransferase
TS29Bif0429|CDS|CDS	3.0	257.3	0.1	G	COG3345	Alpha-galactosidase
TS29Col1463|CDS|CDS	0.5	43.0	0.1	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
TS29Bif0577|CDS|CDS	1.0	86.2	0.1	G	COG0366	Glycosidases
TS29Col1465|CDS|CDS	0.5	43.5	0.1	G	COG1455	Phosphotransferase system cellobiose-specific component IIC
TS29Fae07195|CDS|CDS	1.0	88.0	0.1	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Rum11959|CDS|CDS	0.5	45.0	0.1	G	COG0366|COG3281	Glycosidases|Uncharacterized protein, probably involved in trehalose biosynthesis
TS29Rum15476|CDS|CDS	1.0	90.5	0.1	G	COG2190|COG1264|COG1263	Phosphotransferase system IIA components|Phosphotransferase system IIB components|Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific
TS29Rum13471|CDS|CDS	1.0	91.0	0.0	G	COG3459	Cellobiose phosphorylase
TS29Bif0584|CDS|CDS	0.8	68.3	0.0	G	COG0366	Glycosidases
TS29Col0291|CDS|CDS	0.5	46.0	0.0	G	COG1109	Phosphomannomutase
TS29Bif0395|CDS|CDS	0.3	31.3	0.0	G	COG1109	Phosphomannomutase
Bcat1029|CDS|CDS	0.5	47.0	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
Bcat1016|CDS|CDS	0.5	47.0	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Bif0567|CDS|CDS	0.8	72.2	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Bac01349|CDS|CDS	0.3	32.7	0.0	G	COG1874	Beta-galactosidase
TS29Col0681|CDS|CDS	0.5	49.0	0.0	G	COG1640	4-alpha-glucanotransferase
TS29Rum13468|CDS|CDS	0.5	49.5	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Fae12536|CDS|CDS	0.3	33.0	0.0	G	COG0297	Glycogen synthase
TS29Bif0123|CDS|CDS	0.7	67.7	0.0	G	COG3345	Alpha-galactosidase
TS29Rum13422|CDS|CDS	0.5	52.0	0.0	G	COG2211	Na+/melibiose symporter and related transporters
TS29Rum20798|CDS|CDS	1.0	105.0	0.0	G	COG3534	Alpha-L-arabinofuranosidase
BLD0735|CDS|Pullulanase	0.7	70.2	0.0	G	COG1523	Type II secretory pathway, pullulanase PulA and related glycosidases
TS29Bif0660|CDS|CDS	0.8	79.2	0.0	G	COG0364	Glucose-6-phosphate 1-dehydrogenase
TS29Bif0269|CDS|CDS	0.3	26.4	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Bif0426|CDS|CDS	0.8	79.8	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Fae00657|CDS|CDS	0.5	53.5	0.0	G	COG0058	Glucan phosphorylase
TS29Bif3752|CDS|CDS	0.5	54.5	0.0	G	COG1175	ABC-type sugar transport systems, permease components
TS28Fae18040|CDS|CDS	0.3	37.0	0.0	G	COG1109	Phosphomannomutase
TS29Bif3094|CDS|CDS	0.7	74.7	0.0	G	COG1523	Type II secretory pathway, pullulanase PulA and related glycosidases
TS29Bac08162|CDS|CDS	0.3	28.5	0.0	G	COG1877|COG0561|COG0380	Trehalose-6-phosphatase|Predicted hydrolases of the HAD superfamily|Trehalose-6-phosphate synthase
TS29Fae09101|CDS|CDS	1.0	119.5	0.0	G	COG1109	Phosphomannomutase
TS29Bif2794|CDS|CDS	0.3	30.1	0.0	G	COG3001	Fructosamine-3-kinase
TS28Bif0577|CDS|CDS	0.3	41.0	0.0	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bif0418|CDS|CDS	0.3	41.0	0.0	G	COG1175	ABC-type sugar transport systems, permease components
TS29Bif0057|CDS|CDS	0.5	62.0	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS29Fae09121|CDS|CDS	1.0	124.0	0.0	G	COG0383	Alpha-mannosidase
TS28Fae18785|CDS|CDS	0.5	63.0	0.0	G	COG0205	6-phosphofructokinase
TS29Bac01484|CDS|CDS	0.3	42.0	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS28Bif0573|CDS|CDS	0.5	64.2	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS29Bif0421|CDS|CDS	0.5	64.2	0.0	G	COG1653	ABC-type sugar transport system, periplasmic component
TS28Bif3485|CDS|CDS	0.3	32.3	0.0	G	COG1070	Sugar (pentulose and hexulose) kinases
TS29Bif3539|CDS|CDS	0.3	32.8	0.0	G	COG1175	ABC-type sugar transport systems, permease components
TS28Fae17618|CDS|CDS	0.2	23.0	0.0	G	COG0058	Glucan phosphorylase

TS28Bif4918|CDS|CDS	0.3	35.0	0.0	G	COG1109	Phosphomannomutase
TS28Bif1655|CDS|CDS	0.5	71.5	0.0	G	COG0395	ABC-type sugar transport system, permease component
TS29Fae00319|CDS|CDS	0.5	73.0	0.0	G	COG1070|COG4806	Sugar (pentulose and hexulose) kinases|L-rhamnose isomerase
TS29Fae09165|CDS|CDS	2.0	292.0	0.0	G	COG4724	Endo-beta-N-acetylglucosaminidase D
TS28Fae19417|CDS|CDS	0.2	30.0	0.0	G	COG2017	Galactose mutarotase and related enzymes
TS28Bif0684|CDS|CDS	0.3	50.7	0.0	G	COG3507	Beta-xylosidase
TS28Fae17779|CDS|CDS	0.3	38.0	0.0	G	COG0296	1,4-alpha-glucan branching enzyme
Bbre0337|CDS|CDS	0.3	38.6	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS29Bif0093|CDS|CDS	0.7	103.2	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Fae08648|CDS|CDS	0.5	82.0	0.0	G	COG0205	6-phosphofructokinase
TS29Bif1341|CDS|CDS	0.1	25.5	0.0	G	COG3405	Endoglucanase Y
TS29Bif0041|CDS|CDS	0.7	122.3	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Rum20811|CDS|CDS	0.5	92.5	0.0	G	COG3534	Alpha-L-arabinofuranosidase
TS29Fae06380|CDS|CDS	0.5	98.5	0.0	G	COG1109	Phosphomannomutase
TS29Bif2392|CDS|CDS	0.3	49.8	0.0	G	COG1070	Sugar (pentulose and hexulose) kinases
TS29Rum17068|CDS|CDS	1.0	201.0	0.0	G	COG3090|COG1593|COG1638	TRAP-type C4-dicarboxylate transport system, small permease component|TRAP-type C4-dicarboxylate transport system, large permease component|TRAP-type C4-dicarboxylate transport system, periplasmic component
BL0527|CDS|4-alpha-glucanotransferase	0.3	54.9	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS29Fae05512|CDS|CDS	0.5	110.5	0.0	G	COG2211	Na+/melibiose symporter and related transporters
BLD1321|CDS|4-alpha-glucanotransferase	0.3	55.3	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS28Bif5365|CDS|CDS	0.3	55.4	0.0	G	COG2211	Na+/melibiose symporter and related transporters
TS29Bif0013|CDS|CDS	0.5	113.3	0.0	G	COG3250	Beta-galactosidase/beta-glucuronidase
TS29Bif3754|CDS|CDS	0.3	78.0	0.0	G	COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase
BLD1661|CDS|endo-1,4-beta-xylanase/Beta-xylosidase	0.3	68.2	0.0	G	COG3507	Beta-xylosidase
TS29Bif2547|CDS|CDS	0.3	73.0	0.0	G	COG0524	Sugar kinases, ribokinase family
TS29Fae08929|CDS|CDS	0.5	150.5	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS29Bif3698|CDS|CDS	0.3	76.0	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS29Bif3723|CDS|CDS	0.3	77.0	0.0	G	COG3507	Beta-xylosidase
TS29Bif2448|CDS|CDS	0.3	108.5	0.0	G	COG2942	N-acyl-D-glucosamine 2-epimerase
TS28Bif1189|CDS|CDS	0.3	89.9	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS29Bif0586|CDS|CDS	0.3	89.9	0.0	G	COG1640|COG3280	4-alpha-glucanotransferase|Maltooligosyl trehalose synthase
TS29Bif0273|CDS|CDS	0.1	37.8	0.0	G	COG1874	Beta-galactosidase
TS29Bif2809|CDS|CDS	0.2	76.3	0.0	G	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)
TS28Bif0908|CDS|CDS	0.3	95.7	0.0	G	COG3507	Beta-xylosidase
TS29Bif3087|CDS|CDS	0.3	97.4	0.0	G	COG2211	Na+/melibiose symporter and related transporters
TS29Bif3906|CDS|CDS	0.3	133.7	0.0	G	COG3507	Beta-xylosidase
TS29Bif3483|CDS|CDS	0.3	100.8	0.0	G	COG1109	Phosphomannomutase
TS29Fae07187|CDS|CDS	0.5	202.0	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS29Bif3962|CDS|CDS	0.3	105.6	0.0	G	COG1472	Beta-glucosidase-related glycosidases
TS28Clo06065|CDS|CDS	1.7	0.3	22.7	G|C	COG1070|COG0554	Sugar (pentulose and hexulose) kinases|Glycerol kinase
TS29Bif1503|CDS|CDS	0.3	39.8	0.0	G|C	COG1070|COG1069	Sugar (pentulose and hexulose) kinases|Ribulose kinase
TS29Bif2950|CDS|CDS	0.3	13.0	0.1	G|F	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases
TS28Bif0232|CDS|CDS	0.3	13.0	0.1	G|F	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases
TS29Bif2798|CDS|CDS	0.3	16.0	0.1	G|F	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases
TS28Bif1914|CDS|CDS	0.3	16.0	0.1	G|F	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases
TS29Bif3326|CDS|CDS	1.0	93.8	0.0	G|F	COG1051|COG0647	ADP-ribose pyrophosphatase|Predicted sugar phosphatases of the HAD superfamily
TS29Fae00655|CDS|CDS	1.0	49.5	0.1	G|F|K|L|T	COG4753|COG2207|COG4936|COG3706|COG2169|COG3449|COG3664	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Predicted sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Adenosine deaminase|DNA gyrase inhibitor|Beta-xylosidase
TS29Fae05476|CDS|CDS	1.0	79.0	0.1	G|F|K|T	COG4753|COG2207|COG2169|COG3664|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Adenosine deaminase|Beta-xylosidase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS29Rum04198|CDS|CDS	7.7	2.0	17.4	G|H	COG0698|COG2227	Ribose 5-phosphate isomerase RpiB|2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase
TS29Fae06767|CDS|CDS	0.5	54.5	0.0	G|I|H	COG0021|COG1154|COG3958	Transketolase|Deoxyxylulose-5-phosphate synthase|Transketolase, C-terminal subunit
BactD10540|CDS|CDS	2.8	0.5	25.0	G|I|Q	COG1028|COG1070|COG0246	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)|Sugar (pentulose and hexulose) kinases|Mannitol-1-phosphate/altronate dehydrogenases
TS28Bac6130|CDS|CDS	9.7	1.0	44.2	G|K	COG1940	Transcriptional regulator/sugar kinase
TS28Rum15621|CDS|CDS	4.5	0.5	40.9	G|K	COG1349	Transcriptional regulators of sugar metabolism
TS28Eub0585|CDS|CDS	3.5	0.5	31.8	G|K	COG2390|COG2376	Transcriptional regulator, contains sigma factor-related N-terminal domain|Dihydroxyacetone kinase
TS28Rum09030|CDS|CDS	8.0	3.0	12.1	G|K	COG1940	Transcriptional regulator/sugar kinase
TS28Rum14218|CDS|CDS	0.5	25.5	0.1	G|K	COG2390|COG2376	Transcriptional regulator, contains sigma factor-related N-terminal domain|Dihydroxyacetone kinase
TS29Rum21143|CDS|CDS	0.5	25.5	0.1	G|K	COG2390|COG2376	Transcriptional regulator, contains sigma factor-related N-terminal domain|Dihydroxyacetone kinase
TS29Col1119|CDS|CDS	0.5	31.0	0.1	G|K	COG1879|COG1609	ABC-type sugar transport system, periplasmic component|Transcriptional regulators
TS29Fae09117|CDS|CDS	0.5	37.0	0.1	G|K	COG1940	Transcriptional regulator/sugar kinase
TS29Bif3886|CDS|CDS	0.5	43.9	0.1	G|K	COG1940	Transcriptional regulator/sugar kinase
TS28Bif0708|CDS|CDS	0.5	43.9	0.1	G|K	COG1940	Transcriptional regulator/sugar kinase
TS29Bif2452|CDS|CDS	0.8	77.5	0.0	G|K	COG1940	Transcriptional regulator/sugar kinase
TS29Rum16852|CDS|CDS	0.5	67.0	0.0	G|K	COG1940	Transcriptional regulator/sugar kinase
TS29Col0739|CDS|CDS	0.3	45.0	0.0	G|K	COG1940	Transcriptional regulator/sugar kinase
TS29Rum16071|CDS|CDS	0.3	17.0	0.1	G|K|L|T	COG4753|COG2207|COG4936|COG3708|COG3449|COG3664	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Predicted sensor domain|Uncharacterized protein conserved in bacteria|DNA gyrase inhibitor|Beta-xylosidase

TS28Rum11663|CDS|CDS	3.0	1.0	13.6	G|K|T	COG4753|COG2207|COG3664	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Beta-xylosidase
TS29Bac08672|CDS|CDS	0.3	30.5	0.0	G|K|T	COG0642|COG5002|COG2202|COG0745|COG4753|COG2770|COG0784|COG2198|COG5278|COG3292|COG2972|COG5001|COG3706|COG4251|COG1879|COG2114	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|FOG: HAMP domain|FOG: CheY-like receiver|FOG: HPt domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)
TS29Fae05516|CDS|CDS	1.0	139.5	0.0	G|K|T	COG4753|COG2207|COG3437|COG4936|COG3664|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted sensor domain|Beta-xylosidase|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS28Met1503|CDS|CDS	0.8	0.3	13.6	G|L	COG0574|COG1372	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Intein/homing endonuclease
TS28Bac4814|CDS|CDS	4.0	0.3	54.5	G|M	COG0451	Nucleoside-diphosphate-sugar epimerases
TS28Fae10696|CDS|CDS	7.5	2.0	17.0	G|M	COG3507|COG2273|COG2730|COG5520	Beta-xylosidase|Beta-glucanase/Beta-glucan synthetase|Endoglucanase|O-Glycosyl hydrolase
TS28Par2344|CDS|CDS	4.6	1.3	15.6	G|M	COG0438|COG0058	Glycosyltransferase|Glucan phosphorylase
TS28Bac4238|CDS|CDS	2.0	0.7	13.6	G|M	COG1086	Predicted nucleoside-diphosphate sugar epimerases
TS28Ali2026|CDS|CDS	3.0	1.0	13.6	G|M	COG0451	Nucleoside-diphosphate-sugar epimerases
TS28Fae14958|CDS|CDS	2.5	1.0	11.3	G|M	COG0451|COG1087	Nucleoside-diphosphate-sugar epimerases|UDP-glucose 4-epimerase
TS29Bac01994|CDS|CDS	28.0	12.0	10.6	G|M	COG3594|COG0463|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS28Met1820|CDS|CDS	0.8	0.3	10.2	G|M	COG1086	Predicted nucleoside-diphosphate sugar epimerases
TS29Col0825|CDS|CDS	1.5	71.0	0.1	G|M	COG0463|COG0726|COG1216|COG1887|COG3754	Glycosyltransferases involved in cell wall biogenesis|Predicted xylanase/chitin deacetylase|Predicted glycosyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis protein
TS29Bac05078|CDS|CDS	0.5	28.5	0.1	G|M	COG3594|COG0463|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS29Fae01252|CDS|CDS	1.0	70.0	0.1	G|M	COG3594|COG0463|COG1215|COG1887|COG1442	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Glycosyltransferases, probably involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases
TS29Bac10867|CDS|CDS	0.3	18.0	0.1	G|M	COG0451	Nucleoside-diphosphate-sugar epimerases
TS29Fae10492|CDS|CDS	1.0	74.0	0.1	G|M	COG5632|COG4193	N-acetylmuramoyl-L-alanine amidase|Beta- N-acetylglucosaminidase
TS29Bif3604|CDS|CDS	1.0	99.3	0.0	G|M	COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component
TS29Bif3722|CDS|CDS	0.5	87.3	0.0	G|M	COG3507|COG5498	Beta-xylosidase|Predicted glycosyl hydrolase
TS28Bif1093|CDS|CDS	0.3	48.0	0.0	G|M	COG3594|COG0463|COG1215|COG1887	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Glycosyltransferases, probably involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC
TS29Bif0662|CDS|CDS	0.3	48.0	0.0	G|M	COG3594|COG0463|COG1215|COG1887	Fucose 4-O-acetylase and related acetyltransferases|Glycosyltransferases involved in cell wall biogenesis|Glycosyltransferases, probably involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC
TS28Bif0909|CDS|CDS	0.5	108.3	0.0	G|M	COG3507|COG5498	Beta-xylosidase|Predicted glycosyl hydrolase
TS29Rum20836|CDS|CDS	0.5	118.0	0.0	G|M	COG0451	Nucleoside-diphosphate-sugar epimerases
TS28Fae18814|CDS|CDS	13.5	1.5	40.9	G|M|T	COG3103|COG5632|COG4193	SH3 domain protein|N-acetylmuramoyl-L-alanine amidase|Beta- N-acetylglucosaminidase
TS28Rum01341|CDS|CDS	4.0	1.5	12.1	G|N	COG5492|COG1501	Bacterial surface proteins containing Ig-like domains|Alpha-glucosidases, family 31 of glycosyl hydrolases
TS28Rum01339|CDS|CDS	22.2	8.5	11.8	G|N	COG5492|COG1501	Bacterial surface proteins containing Ig-like domains|Alpha-glucosidases, family 31 of glycosyl hydrolases
TS29Bif3543|CDS|CDS	7.5	406.0	0.1	G|N	COG5492|COG3507	Bacterial surface proteins containing Ig-like domains|Beta-xylosidase
TS29Bif3542|CDS|CDS	3.3	203.4	0.1	G|N	COG5492|COG3507	Bacterial surface proteins containing Ig-like domains|Beta-xylosidase
TS29Bif3547|CDS|CDS	4.5	647.0	0.0	G|N|M	COG5492|COG3507|COG5498|COG3940|COG3533	Bacterial surface proteins containing Ig-like domains|Beta-xylosidase|Predicted glycosyl hydrolase|Predicted beta-xylosidase|Uncharacterized protein conserved in bacteria
TS28Rum13581|CDS|CDS	7.0	2.0	15.9	G|O	COG0637|COG1214|COG1554	Predicted phosphatase/phosphohexomutase|Inactive homolog of metal-dependent proteases, putative molecular chaperone|Trehalose and maltose hydrolases (possible phosphorylases)
TS28Rum01185|CDS|CDS	13.5	1.0	61.3	G|T	COG5002|COG1879	Signal transduction histidine kinase|ABC-type sugar transport system, periplasmic component
TS29Rum16901|CDS|CDS	501.3	59.0	38.6	G|T	COG5002|COG1879|COG1129	Signal transduction histidine kinase|ABC-type sugar transport system, periplasmic component|ABC-type sugar transport system, ATPase component
TS28Rum15515|CDS|CDS	7.0	2.0	15.9	G|T	COG0469|COG3848	Pyruvate kinase|Phosphohistidine swiveling domain
TS28Rum10868|CDS|CDS	2.3	0.7	15.9	G|T	COG4668|COG1080|COG3412|COG1762|COG3605|COG1925	Mannitol/fructose-specific phosphotransferase system, IIA domain|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Uncharacterized protein conserved in bacteria|Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)|Signal transduction protein containing GAF and PtsI domains|Phosphotransferase system, HPr-related proteins
TS28Bac0234|CDS|CDS	2.3	1.0	10.6	G|T	COG5002|COG1879	Signal transduction histidine kinase|ABC-type sugar transport system, periplasmic component

TS29Bac04953|CDS|CDS	0.5	42.0	0.1	G|T	COG0642|COG5002|COG2202|COG4753|COG2770|COG0784|COG3292|COG5001|COG3706|COG4251|COG1879|COG2114	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)
TS29Bif1788|CDS|CDS	0.3	44.0	0.0	G|T	COG0469|COG3848	Pyruvate kinase|Phosphohistidine swiveling domain
Rtor0098|CDS|CDS	44.0	13.5	14.8	G|U	COG3291|COG2273|COG3250|COG1472|COG3525|COG0823	FOG: PKD repeat|Beta-glucanase/Beta-glucan synthetase|Beta-galactosidase/beta-glucuronidase|Beta-glucosidase-related glycosidases|N-acetyl-beta-hexosaminidase|Periplasmic component of the Tol biopolymer transport system
Bxyl0042|CDS|CDS	4.4	0.7	29.7	G|V	COG1132|COG0524|COG0800	ABC-type multidrug transport system, ATPase and permease components|Sugar kinases, ribokinase family|2-keto-3-deoxy-6-phosphogluconate aldolase
TS29Fae05459|CDS|CDS	1.0	138.0	0.0	G|V	COG1680|COG1472	Beta-lactamase class C and other penicillin binding proteins|Beta-glucosidase-related glycosidases
TS28Rum10322|CDS|CDS	72.0	1.0	326.9	H	COG0181	Porphobilinogen deaminase
Msmi740778|CDS|CDS	19.3	0.5	175.5	H	COG4058	Methyl coenzyme M reductase, alpha subunit
Msmi750908|CDS|CDS	8.3	0.3	149.8	H	COG4055	Methyl coenzyme M reductase, subunit D
TS28Met0368|CDS|CDS	23.0	1.0	104.4	H	COG4058	Methyl coenzyme M reductase, alpha subunit
Msmi740775|CDS|CDS	5.3	0.3	95.3	H	COG4055	Methyl coenzyme M reductase, subunit D
Buni3420|CDS|CDS	30.0	1.5	90.8	H	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes
Msmi750905|CDS|CDS	22.6	1.5	68.3	H	COG4058	Methyl coenzyme M reductase, alpha subunit
TS28Met0372|CDS|CDS	20.3	1.4	64.9	H	COG4054	Methyl coenzyme M reductase, beta subunit
TS28Rum00060|CDS|CDS	36.0	3.0	54.5	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
Bfin0663|CDS|CDS	2.7	0.3	49.3	H	COG0379	Quinolinate synthase
Msmi750909|CDS|CDS	19.6	1.9	46.4	H	COG4054	Methyl coenzyme M reductase, beta subunit
Bxyl3983|CDS|CDS	3.3	0.3	45.2	H	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes
Buni1250|CDS|CDS	3.0	0.3	40.9	H	COG1575	1,4-dihydroxy-2-naphthoate octaprenyltransferase
BactD14059|CDS|CDS	2.0	0.3	36.8	H	COG0379	Quinolinate synthase
ShigspD90954|CDS|CDS	4.0	0.5	36.3	H	COG1985	Pyrimidine reductase, riboflavin biosynthesis
Aput1191|CDS|CDS	8.0	1.0	36.3	H	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases
TS29Met0756|CDS|CDS	13.0	1.7	35.4	H	COG1429	Cobalamin biosynthesis protein CobN and related Mg-chelatases
TS29Rum12347|CDS|CDS	4.7	0.7	31.8	H	COG0414	Panthothenate synthetase
Buni3404|CDS|CDS	3.3	0.5	30.3	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
TS28Bac2715|CDS|CDS	3.3	0.5	30.3	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
TS28Met0371|CDS|CDS	8.3	1.3	30.0	H	COG4055	Methyl coenzyme M reductase, subunit D
TS28Met0369|CDS|CDS	14.8	2.3	28.9	H	COG4057	Methyl coenzyme M reductase, gamma subunit
Msmi750906|CDS|CDS	14.8	2.3	28.9	H	COG4057	Methyl coenzyme M reductase, gamma subunit
TS28Rum15411|CDS|CDS	3.0	0.5	27.2	H	COG2875|COG2073|COG2241	Precorrin-4 methylase|Cobalamin biosynthesis protein CbiG|Precorrin-6B methylase 1
TS28Fae15359|CDS|CDS	3.0	0.5	27.2	H	COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase
TS29Clo3121|CDS|CDS	6.0	1.0	27.2	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
TS28Fae11385|CDS|CDS	6.0	1.0	27.2	H	COG0854|COG0319	Pyridoxal phosphate biosynthesis protein|Predicted metal-dependent hydrolase
Msmi750907|CDS|CDS	20.5	3.5	26.6	H	COG4056	Methyl coenzyme M reductase, subunit C
TS29Bac02278|CDS|CDS	5.5	1.0	25.0	H	COG0029	Aspartate oxidase
TS28Fae18410|CDS|CDS	8.0	1.5	24.2	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
Bxyl1095|CDS|CDS	2.7	0.5	24.2	H	COG0142	Geranylgeranyl pyrophosphate synthase
Msmi740774|CDS|CDS	20.6	3.9	23.9	H	COG4054	Methyl coenzyme M reductase, beta subunit
TS29Clo3112|CDS|CDS	10.0	2.0	22.7	H	COG0181	Porphobilinogen deaminase
Aput2034|CDS|CDS	9.5	2.0	21.6	H	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes
Aput1842|CDS|CDS	14.0	3.0	21.2	H	COG0320	Lipoate synthase
Begg0851|CDS|CDS	5.1	1.1	20.9	H	COG4206	Outer membrane cobalamin receptor protein
Dfor2466|CDS|CDS	4.3	1.0	19.7	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
Bcoproc1931|CDS|CDS	5.1	1.2	19.6	H	COG4206	Outer membrane cobalamin receptor protein
TS29Bac10512|CDS|CDS	98.3	23.0	19.4	H	COG0262	Dihydrofolate reductase
TS28Rum09613|CDS|CDS	8.5	2.0	19.3	H	COG0669	Phosphopantetheine adenylyltransferase
Bcap0729|CDS|CDS	4.0	1.0	18.2	H	COG0499	S-adenosylhomocysteine hydrolase
ShigspD90201|CDS|CDS	4.0	1.0	18.2	H	COG0181	Porphobilinogen deaminase
TS28Dor2344|CDS|CDS	2.0	0.5	18.2	H	COG0294	Dihydropteroate synthase and related enzymes
Dfor2233|CDS|CDS	8.0	2.0	18.2	H	COG5012|COG0407	Predicted cobalamin binding protein|Uroporphyrinogen-III decarboxylase
TS28Rum01588|CDS|CDS	4.0	1.0	18.2	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
TS28Fae02054|CDS|CDS	2.0	0.5	18.2	H	COG0854|COG0319	Pyridoxal phosphate biosynthesis protein|Predicted metal-dependent hydrolase
Bthe7332109|CDS|CDS	1.3	0.3	18.2	H	COG0212	5-formyltetrahydrofolate cyclo-ligase
BactD11322|CDS|CDS	5.1	1.3	18.0	H	COG4206	Outer membrane cobalamin receptor protein
ShigspD90103|CDS|CDS	3.8	1.0	17.4	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
BactD12122|CDS|CDS	3.7	1.0	16.9	H	COG0157	Nicotinate-nucleotide pyrophosphorylase
Bxyl1217|CDS|CDS	5.1	1.4	16.6	H	COG4206	Outer membrane cobalamin receptor protein
TS29Rum18053|CDS|CDS	18.0	5.0	16.3	H	COG2109	ATP:corrinoid adenosyltransferase
Cbol4859|CDS|CDS	7.0	2.0	15.9	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
TS28Rum13468|CDS|CDS	3.5	1.0	15.9	H	COG1060|COG0502	Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes|Biotin synthase and related enzymes
Robe2887|CDS|CDS	21.3	6.3	15.5	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
Msmi740777|CDS|CDS	13.5	4.0	15.3	H	COG4057	Methyl coenzyme M reductase, gamma subunit
TS29Clo3115|CDS|CDS	13.0	4.0	14.8	H	COG2038|COG2087	NaMN:DMB phosphoribosyltransferase|Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase
TS29Met0802|CDS|CDS	6.0	2.0	13.6	H	COG4063	Tetrahydromethanopterin S-methyltransferase, subunit A
Bcap0900|CDS|CDS	3.0	1.0	13.6	H	COG1270	Cobalamin biosynthesis protein CobD/CbiB
Msmi740484|CDS|CDS	3.0	1.0	13.6	H	COG0054	Riboflavin synthase beta-chain
Even1320|CDS|CDS	3.0	1.0	13.6	H	COG0192	S-adenosylmethionine synthetase
Buni0546|CDS|CDS	3.0	1.0	13.6	H	COG2022|COG2104	Uncharacterized enzyme of thiazole biosynthesis|Sulfur transfer protein involved in thiamine biosynthesis
Bthe7335450|CDS|CDS	1.5	0.5	13.6	H	COG0302	GTP cyclohydrolase I
TS28Rum04856|CDS|CDS	3.0	1.0	13.6	H	COG0196	FAD synthase
Bfin1127|CDS|CDS	5.1	1.8	13.1	H	COG4206	Outer membrane cobalamin receptor protein
TS28Rum02364|CDS|CDS	43.7	15.3	13.0	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
Aput0878|CDS|CDS	11.0	4.0	12.5	H	COG0190	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase
TS29Bac07332|CDS|CDS	31.0	11.5	12.2	H	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes
Buni3284|CDS|CDS	4.0	1.5	12.1	H	COG0502|COG0161	Biotin synthase and related enzymes|Adenosylmethionine-8-amino-7-oxononanoate aminotransferase

Clep0851|CDS|CDS	4.0	1.5	12.1	H	COG0192	S-adenosylmethionine synthetase
FpraM2121012|CDS|CDS	1.3	0.5	12.1	H	COG0388|COG0171	Predicted amidohydrolase|NAD synthase
Bsp1162030|CDS|CDS	5.1	2.0	11.7	H	COG4206	Outer membrane cobalamin receptor protein
Bste0639|CDS|CDS	5.1	2.0	11.7	H	COG4206	Outer membrane cobalamin receptor protein
Aput0643|CDS|CDS	5.1	2.0	11.7	H	COG4206	Outer membrane cobalamin receptor protein
TS28Par0017|CDS|CDS	5.1	2.0	11.7	H	COG4206	Outer membrane cobalamin receptor protein
Bthe3733898|CDS|CDS	4.6	1.8	11.7	H	COG4206	Outer membrane cobalamin receptor protein
Bthe7332527|CDS|CDS	4.6	1.8	11.7	H	COG4206	Outer membrane cobalamin receptor protein
Bova0454|CDS|CDS	5.0	2.0	11.3	H	COG0142	Geranylgeranyl pyrophosphate synthase
ShigspD90522|CDS|CDS	2.5	1.0	11.3	H	COG0156	7-keto-8-aminopelargonate synthetase and related enzymes
TS29Met0811|CDS|CDS	17.0	7.0	11.0	H	COG4058	Methyl coenzyme M reductase, alpha subunit
Msmi740673|CDS|CDS	62.0	26.0	10.8	H	COG1572|COG1429	Uncharacterized conserved protein|Cobalamin biosynthesis protein CobN and related Mg-chelatases
TS29Met0804|CDS|CDS	7.0	3.0	10.6	H	COG4062	Tetrahydromethanopterin S-methyltransferase, subunit B
TS28Rum02930|CDS|CDS	3.5	1.5	10.6	H	COG2091	Phosphopantetheinyl transferase
BactD11772|CDS|CDS	2.3	1.0	10.6	H	COG0422	Thiamine biosynthesis protein ThiC
Buni2607|CDS|CDS	1.1	0.5	10.4	H	COG0414	Panthothenate synthetase
TS29Rum18453|CDS|CDS	50.7	22.3	10.3	H	COG4822	Cobalamin biosynthesis protein CbiK, Co2+ chelatase
TS29Bac11507|CDS|CDS	3.0	1.3	10.2	H	COG1575	1,4-dihydroxy-2-naphthoate octaprenyltransferase
TS28Rum13361|CDS|CDS	9.0	4.0	10.2	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
TS29Clo3033|CDS|CDS	3.3	1.5	10.1	H	COG0192	S-adenosylmethionine synthetase
TS29Bif3990|CDS|CDS	1.1	48.3	0.1	H	COG0192	S-adenosylmethionine synthetase
TS28Bif2030|CDS|CDS	1.1	48.3	0.1	H	COG0192	S-adenosylmethionine synthetase
TS29Rum19401|CDS|CDS	1.0	48.0	0.1	H	COG2145	Hydroxyethylthiazole kinase, sugar kinase family
TS29Rum14558|CDS|CDS	0.3	12.3	0.1	H	COG0307	Riboflavin synthase alpha chain
TS29Rum00452|CDS|CDS	1.0	54.0	0.1	H	COG0157	Nicotinate-nucleotide pyrophosphorylase
TS29Fae10496|CDS|CDS	1.0	54.0	0.1	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
TS29Bac05452|CDS|CDS	0.3	18.0	0.1	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
TS29Rum00464|CDS|CDS	1.0	55.5	0.1	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
TS29Rum20157|CDS|CDS	1.0	59.0	0.1	H	COG0007|COG1648|COG1587	Uroporphyrinogen-III methylase|Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)|Uroporphyrinogen-III synthase
TS29Rum13454|CDS|CDS	0.5	29.5	0.1	H	COG0807	GTP cyclohydrolase II
TS29Fae10007|CDS|CDS	0.5	29.5	0.1	H	COG1713	Predicted HD superfamily hydrolase involved in NAD metabolism
TS29Bif3308|CDS|CDS	0.3	14.8	0.1	H	COG1057|COG1713	Nicotinic acid mononucleotide adenylyltransferase|Predicted HD superfamily hydrolase involved in NAD metabolism
TS29Fae00313|CDS|CDS	1.0	60.0	0.1	H	COG0192	S-adenosylmethionine synthetase
TS29Rum18775|CDS|CDS	0.3	20.0	0.1	H	COG0001	Glutamate-1-semialdehyde aminotransferase
TS29Rum00353|CDS|CDS	0.5	31.0	0.1	H	COG0535|COG2226	Predicted Fe-S oxidoreductases|Methylase involved in ubiquinone/menaquinone biosynthesis
TS28Bif0717|CDS|CDS	0.3	16.2	0.1	H	COG0302	GTP cyclohydrolase I
TS29Fae08158|CDS|CDS	1.0	66.0	0.1	H	COG0635	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases
TS29Bif0702|CDS|CDS	1.5	104.0	0.1	H	COG1232	Protoporphyrinogen oxidase
TS29Bif3878|CDS|CDS	0.8	52.2	0.1	H	COG0302	GTP cyclohydrolase I
TS28Bif0419|CDS|CDS	0.3	18.5	0.1	H	COG0669	Phosphopantetheine adenylyltransferase
TS29Rum00451|CDS|CDS	1.0	82.0	0.1	H	COG0029|COG0157	Aspartate oxidase|Nicotinate-nucleotide pyrophosphorylase
TS29Bif4142|CDS|CDS	0.2	20.1	0.0	H	COG0351|COG0352|COG1992	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase|Thiamine monophosphate synthase|Uncharacterized conserved protein
TS29Fae01154|CDS|CDS	0.5	54.5	0.0	H	COG2241|COG2242	Precorrin-6B methylase 1|Precorrin-6B methylase 2
TS29Bif2464|CDS|CDS	1.2	142.0	0.0	H	COG0285|COG0294	Folylpolyglutamate synthase|Dihydropteroate synthase and related enzymes
TS29Bif3430|CDS|CDS	0.5	66.0	0.0	H	COG0311	Predicted glutamine amidotransferase involved in pyridoxine biosynthesis
TS28Bif4959|CDS|CDS	0.5	72.2	0.0	H	COG0095	Lipoate-protein ligase A
TS28Bif0595|CDS|CDS	0.3	37.8	0.0	H	COG0388|COG0171	Predicted amidohydrolase|NAD synthase
TS28Bif5000|CDS|CDS	0.2	33.1	0.0	H	COG0351|COG0352|COG1992	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase|Thiamine monophosphate synthase|Uncharacterized conserved protein
TS29Bif4144|CDS|CDS	0.6	163.3	0.0	H	COG0422	Thiamine biosynthesis protein ThiC
TS29Bif3055|CDS|CDS	0.3	83.8	0.0	H	COG0388|COG0171	Predicted amidohydrolase|NAD synthase
Dlon2243|CDS|CDS	3.0	1.0	13.6	H|C	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
RintL12759|CDS|CDS	5.0	2.0	11.3	H|C	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
Rgna0524|CDS|CDS	4.5	2.0	10.2	H|C	COG0543	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
CspSS20024|CDS|CDS	5.0	1.0	22.7	H|C|F	COG1146|COG0543|COG0167	Ferredoxin|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Dihydroorotate dehydrogenase
Cbol3220|CDS|CDS	8.0	3.0	12.1	H|C|F	COG1146|COG0543|COG0167	Ferredoxin|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Dihydroorotate dehydrogenase
Robe1910|CDS|CDS	2.5	1.0	11.3	H|C|F	COG1146|COG0543|COG0167	Ferredoxin|2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Dihydroorotate dehydrogenase
Buni1281|CDS|CDS	4.7	1.3	15.9	H|F	COG1160|COG0283|COG0414	Predicted GTPases|Cytidylate kinase|Panthothenate synthetase
Cmet2013|CDS|CDS	3.0	1.0	13.6	H|I	COG1154	Deoxyxylulose-5-phosphate synthase
Buni2793|CDS|CDS	2.3	1.0	10.6	H|I	COG1154	Deoxyxylulose-5-phosphate synthase
Buni1583|CDS|CDS	1.5	0.5	13.6	H|Q	COG3321|COG0156	Polyketide synthase modules and related proteins|7-keto-8-aminopelargonate synthetase and related enzymes
TS29Rum10996|CDS|CDS	22.0	1.0	99.9	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
BactD10948|CDS|CDS	4.8	0.3	86.3	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Bxyl4296|CDS|CDS	4.8	0.3	86.3	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Buni1120|CDS|CDS	28.4	1.5	86.0	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Bxyl4163|CDS|CDS	8.1	0.5	73.5	I	COG1260	Myo-inositol-1-phosphate synthase
TS28Clo03439|CDS|CDS	12.0	1.0	54.5	I	COG0183	Acetyl-CoA acetyltransferase
Ceut0481|CDS|CDS	4.2	0.4	43.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
Buni1308|CDS|CDS	13.5	1.5	40.9	I	COG2185|COG1884	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)|Methylmalonyl-CoA mutase, N-terminal domain/subunit
TS29Par544|CDS|CDS	8.0	1.0	36.3	I	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
RintL12222|CDS|CDS	15.3	2.0	34.6	I	COG0183	Acetyl-CoA acetyltransferase
Acac0254|CDS|CDS	7.0	1.0	31.8	I	COG1024|COG1250	Enoyl-CoA hydratase/carnithine racemase|3-hydroxyacyl-CoA dehydrogenase
Rtor1700|CDS|CDS	3.5	0.5	31.8	I	COG0657	Esterase/lipase
Rumhyd2644|CDS|CDS	7.0	1.0	31.8	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
Buni1109|CDS|CDS	17.0	2.5	30.9	I	COG1260	Myo-inositol-1-phosphate synthase
TS28Bac5633|CDS|CDS	8.7	1.3	29.5	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
CspM6212613|CDS|CDS	25.0	4.0	28.4	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
Ccom1707|CDS|CDS	34.0	5.5	28.1	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
Casp1260|CDS|CDS	6.0	1.0	27.2	I	COG0657	Esterase/lipase
Csym2028|CDS|CDS	18.0	3.0	27.2	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)

CspL21154|CDS|CDS	5.9	1.0	25.7	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS28Fae18586|CDS|CDS	24.0	4.5	24.2	I	COG0183	Acetyl-CoA acetyltransferase
TS28Fae18583|CDS|CDS	31.8	6.0	24.1	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
Chyl0440|CDS|CDS	2.5	0.5	22.7	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
Clep1437|CDS|CDS	2.5	0.5	22.7	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
TS28Clo09644|CDS|CDS	2.5	0.5	22.7	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
TS29Bac08436|CDS|CDS	1.3	0.3	22.7	I	COG1022	Long-chain acyl-CoA synthetases (AMP-forming)
Bova3226|CDS|CDS	4.9	1.0	22.2	I	COG1260	Myo-inositol-1-phosphate synthase
BactD10050|CDS|CDS	3.1	0.7	21.3	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
TS28Fae20273|CDS|CDS	15.3	3.5	19.9	I	COG0183	Acetyl-CoA acetyltransferase
Robe0362|CDS|CDS	4.0	1.0	18.2	I	COG0020	Undecaprenyl pyrophosphate synthase
BDI0368|CDS|xylanase	4.0	1.0	18.2	I	COG0657	Esterase/lipase
TS28Eub0146|CDS|CDS	8.0	2.0	18.2	I	COG1024|COG1250	Enoyl-CoA hydratase/carnithine racemase|3-hydroxyacyl-CoA dehydrogenase
TS29Bac07191|CDS|CDS	4.0	1.0	18.2	I	COG0688	Phosphatidylserine decarboxylase
Bova3359|CDS|CDS	4.8	1.3	17.3	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Buni0342|CDS|CDS	7.6	2.0	17.2	I	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
Cbol1693|CDS|CDS	14.8	4.0	16.8	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
TS28Fae20637|CDS|CDS	51.8	14.5	16.2	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
TS28Clo04161|CDS|CDS	10.0	3.0	15.1	I	COG1250	3-hydroxyacyl-CoA dehydrogenase
TS28Fae20636|CDS|CDS	26.2	8.5	14.0	I	COG1024|COG1250	Enoyl-CoA hydratase/carnithine racemase|3-hydroxyacyl-CoA dehydrogenase
TS28Rum15679|CDS|CDS	1.5	0.5	13.6	I	COG0671	Membrane-associated phospholipid phosphatase
TS28Rum12255|CDS|CDS	6.0	2.0	13.6	I	COG2272	Carboxylesterase type B
ShigspD92111|CDS|CDS	1.5	0.5	13.6	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS28Dor0781|CDS|CDS	3.0	1.0	13.6	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
TS28Col0176|CDS|CDS	9.0	3.0	13.6	I	COG0183	Acetyl-CoA acetyltransferase
TS28Fae00074|CDS|CDS	10.0	3.5	13.0	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
TS28Fae20697|CDS|CDS	2.7	1.0	12.1	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
Aput1196|CDS|CDS	10.5	4.0	11.9	I	COG2185|COG1884	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)|Methylmalonyl-CoA mutase, N-terminal domain/subunit
Bova3818|CDS|CDS	1.3	0.5	11.8	I	COG0623	Enoyl-[acyl-carrier-protein] reductase (NADH)
Bxyl3046|CDS|CDS	1.3	0.5	11.8	I	COG0623	Enoyl-[acyl-carrier-protein] reductase (NADH)
Buni2290|CDS|CDS	8.7	3.3	11.8	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
Dfor0619|CDS|CDS	25.3	10.0	11.5	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme
TS28Clo06731|CDS|CDS	5.0	2.0	11.3	I	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
Aput1966|CDS|CDS	15.0	6.0	11.3	I	COG0821	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis
TS29Bac09616|CDS|CDS	5.7	2.3	11.0	I	COG2185|COG1884	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)|Methylmalonyl-CoA mutase, N-terminal domain/subunit
Buni0348|CDS|CDS	3.5	1.5	10.6	I	COG0020	Undecaprenyl pyrophosphate synthase
Aput1559|CDS|CDS	14.0	6.0	10.6	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
TS29Bif1296|CDS|CDS	0.3	15.5	0.1	I	COG4221|COG1211	Short-chain alcohol dehydrogenase of unknown specificity|4-diphosphocytidyl-2-methyl-D-erithritol synthase
CspM6210568|CDS|CDS	2.9	142.0	0.1	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS29Col1489|CDS|CDS	1.0	50.0	0.1	I	COG2084	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases
TS29Bac01857|CDS|CDS	0.5	25.0	0.1	I	COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III
TS29Bif2696|CDS|CDS	1.5	76.1	0.1	I	COG1022	Long-chain acyl-CoA synthetases (AMP-forming)
TS29Bif4129|CDS|CDS	1.5	77.0	0.1	I	COG0020	Undecaprenyl pyrophosphate synthase
TS29Rum01464|CDS|CDS	0.5	26.0	0.1	I	COG0439	Biotin carboxylase
TS28Bif0631|CDS|CDS	1.0	56.7	0.1	I	COG1022	Long-chain acyl-CoA synthetases (AMP-forming)
TS28Bif0934|CDS|CDS	0.8	43.1	0.1	I	COG4982|COG4981	3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
TS29Col0912|CDS|CDS	0.5	29.0	0.1	I	COG1597	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase
TS29Fae00646|CDS|CDS	0.5	32.5	0.1	I	COG2267	Lysophospholipase
TS28Bif0551|CDS|CDS	0.5	35.9	0.1	I	COG0657	Esterase/lipase
TS29Bif0438|CDS|CDS	0.5	35.9	0.1	I	COG0657	Esterase/lipase
TS28Bif4503|CDS|CDS	0.5	36.3	0.1	I	COG2267	Lysophospholipase
TS28Bif3336|CDS|CDS	0.3	20.3	0.1	I	COG0558	Phosphatidylglycerophosphate synthase
TS29Rum11767|CDS|CDS	0.5	42.5	0.1	I	COG3884	Acyl-ACP thioesterase
TS29Bif3960|CDS|CDS	4.3	368.7	0.1	I	COG3581|COG3580| COG1924	Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria|Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)
TS29Bac05147|CDS|CDS	0.3	22.0	0.1	I	COG0657	Esterase/lipase
TS29Bif2345|CDS|CDS	0.3	29.7	0.1	I	COG0821	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis
TS29Bif0533|CDS|CDS	0.5	52.3	0.0	I	COG2267	Lysophospholipase
TS29Bif3953|CDS|CDS	1.0	112.2	0.0	I	COG1022	Long-chain acyl-CoA synthetases (AMP-forming)
TS29Col1437|CDS|CDS	0.5	56.5	0.0	I	COG1835	Predicted acyltransferases
TS29Col0136|CDS|CDS	1.0	120.0	0.0	I	COG3581|COG3580| COG1924	Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria|Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)
TS28Bif5375|CDS|CDS	0.5	62.1	0.0	I	COG1835	Predicted acyltransferases
FpraM2120014|CDS|CDS	0.2	40.4	0.0	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS29Bif2374|CDS|CDS	0.5	108.3	0.0	I	COG4799	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)
TS29Bif3077|CDS|CDS	0.5	111.6	0.0	I	COG1835	Predicted acyltransferases
TS29Fae06010|CDS|CDS	0.1	25.4	0.0	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes
TS28Bif4811|CDS|CDS	0.3	73.5	0.0	I	COG0657	Esterase/lipase
TS29Col0144|CDS|CDS	1.0	60.0	0.1	I|H	COG1154	Deoxyxylulose-5-phosphate synthase
TS28Rum14309|CDS|CDS	2.0	0.5	18.2	I|J	COG1211|COG0336| COG0245	4-diphosphocytidyl-2-methyl-D-erithritol synthase|tRNA-(guanine-N1)-methyltransferase|2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
Bthe7333249|CDS|CDS	16.0	0.7	109.0	I|Q	COG0236	Acyl carrier protein
Cbol4432|CDS|CDS	45.0	2.0	102.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Ccom2044|CDS|CDS	30.0	2.0	68.1	I|Q	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase
TS29Dor0403|CDS|CDS	9.0	1.0	40.9	I|Q	COG1028|COG4221	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)|Short-chain alcohol dehydrogenase of unknown specificity
Bxyl2435|CDS|CDS	9.8	1.3	33.5	I|Q	COG0236	Acyl carrier protein
BactD13824|CDS|CDS	9.8	1.3	33.5	I|Q	COG0236	Acyl carrier protein

BactD13279|CDS|CDS	3.4	0.5	30.9	I|Q	COG0318|COG1022	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II|Long-chain acyl-CoA synthetases (AMP-forming)
TS28Rum13339|CDS|CDS	4.5	1.0	20.4	I|Q	COG0236	Acyl carrier protein
TS28Rum13342|CDS|CDS	2.0	0.5	18.2	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS28Bac2683|CDS|CDS	1.0	0.3	13.6	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Msmi741306|CDS|CDS	1.0	0.3	13.6	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Buni1284|CDS|CDS	1.0	0.3	13.6	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Msmi750377|CDS|CDS	1.0	0.3	13.6	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Csci2462|CDS|CDS	3.0	1.0	13.6	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS29Clo3876|CDS|CDS	6.0	2.0	13.6	I|Q	COG0236	Acyl carrier protein
TS28Bac3746|CDS|CDS	4.0	1.3	13.6	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS28Fae11131|CDS|CDS	22.6	8.5	12.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Dfor3139|CDS|CDS	5.0	2.0	11.3	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
Buni1916|CDS|CDS	5.7	2.3	11.0	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS29Bif0600|CDS|CDS	0.4	21.3	0.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS28Bif1169|CDS|CDS	0.4	21.3	0.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS28Fae18321|CDS|CDS	0.2	12.0	0.1	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
BL1537|CDS|Fas	1.0	120.1	0.0	I|Q	COG0331|COG3321|COG0304|COG4982|COG4981	(acyl-carrier-protein) S-malonyltransferase|Polyketide synthase modules and related proteins|3-oxoacyl-(acyl-carrier-protein) synthase|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
Robe0065|CDS|CDS	0.3	55.6	0.0	I|Q	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
TS28Bif0933|CDS|CDS	0.3	78.9	0.0	I|Q	COG0304|COG0331|COG3321|COG4982|COG4981	3-oxoacyl-(acyl-carrier-protein) synthase|(acyl-carrier-protein) S-malonyltransferase|Polyketide synthase modules and related proteins|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
TS29Bif2375|CDS|CDS	1.0	545.0	0.0	I|Q	COG0304|COG0331|COG3321|COG4982|COG4981	3-oxoacyl-(acyl-carrier-protein) synthase|(acyl-carrier-protein) S-malonyltransferase|Polyketide synthase modules and related proteins|3-oxoacyl-[acyl-carrier protein] reductase|Enoyl reductase domain of yeast-type FAS1
Bthe7330382|CDS|CDS	41.6	0.5	377.9	J	COG0097	Ribosomal protein L6P/L9E
Bthe7330390|CDS|CDS	8.5	0.2	231.5	J	COG0099	Ribosomal protein S13
Bthe3731272|CDS|CDS	8.5	0.2	231.5	J	COG0099	Ribosomal protein S13
Bfin3125|CDS|CDS	8.5	0.2	192.9	J	COG0480	Translation elongation factors (GTPases)
Buni0625|CDS|CDS	56.9	1.5	172.1	J	COG0050	GTPases - translation elongation factors
TS29Fae00136|CDS|CDS	17.3	0.5	157.4	J	COG1544	Ribosome-associated protein Y (PSrp-1)
CspSS21228|CDS|CDS	16.5	0.5	149.8	J	COG0050	GTPases - translation elongation factors
Begg2622|CDS|CDS	16.0	0.5	145.3	J	COG0186	Ribosomal protein S17
TS28Met1810|CDS|CDS	5.9	0.2	133.9	J	COG0081	Ribosomal protein L1
Buni3377|CDS|CDS	9.7	0.3	131.7	J	COG0008|COG0064	Glutamyl- and glutaminyl-tRNA synthetases|Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
Buni1600|CDS|CDS	14.4	0.5	130.5	J	COG0441	Threonyl-tRNA synthetase
Msmi751413|CDS|CDS	5.4	0.2	122.6	J	COG0081	Ribosomal protein L1
Bhan0175|CDS|CDS	26.6	1.0	120.9	J	COG0050	GTPases - translation elongation factors
Bthe7330386|CDS|CDS	25.7	1.0	116.8	J	COG0200	Ribosomal protein L15
TS28Rum08442|CDS|CDS	12.8	0.5	116.5	J	COG2868	Predicted ribosomal protein
TS28Fae20651|CDS|CDS	12.8	0.5	115.8	J	COG0049	Ribosomal protein S7
BactD20045|CDS|CDS	12.5	0.6	94.5	J	COG0092	Ribosomal protein S3
TS28Fae15009|CDS|CDS	9.5	0.5	86.3	J	COG0335	Ribosomal protein L19
TS29Bac10597|CDS|CDS	9.3	0.5	84.1	J	COG0230	Ribosomal protein L34
TS28Rum11480|CDS|CDS	27.0	1.5	81.8	J	COG0096	Ribosomal protein S8
Dlon0694|CDS|CDS	17.0	1.0	77.2	J	COG0291	Ribosomal protein L35
Robe1738|CDS|CDS	16.5	1.0	74.9	J	COG0186	Ribosomal protein S17
BactD12743|CDS|CDS	5.4	0.3	73.1	J	COG0172	Seryl-tRNA synthetase
Bthe7330383|CDS|CDS	23.8	1.5	72.1	J	COG0256	Ribosomal protein L18
TS29Bac09455|CDS|CDS	15.7	1.0	71.1	J	COG0091	Ribosomal protein L22
TS28Dor0304|CDS|CDS	61.5	4.0	69.8	J	COG0180	Tryptophanyl-tRNA synthetase
Buni2672|CDS|CDS	12.7	0.8	69.0	J	COG0216	Protein chain release factor A
Buni0620|CDS|CDS	45.2	3.0	68.3	J	COG0480	Translation elongation factors (GTPases)
TS28Fae01959|CDS|CDS	51.7	3.5	67.1	J	COG0050	GTPases - translation elongation factors
Bxyl1669|CDS|CDS	14.8	1.0	67.0	J	COG0256	Ribosomal protein L18
BactD14464|CDS|CDS	14.8	1.0	67.0	J	COG0256	Ribosomal protein L18
Bxyl1670|CDS|CDS	14.1	1.0	63.9	J	COG0097	Ribosomal protein L6P/L9E
Bcap2256|CDS|CDS	14.0	1.0	63.6	J	COG0089	Ribosomal protein L23
Bxyl1668|CDS|CDS	6.7	0.5	60.8	J	COG0098	Ribosomal protein S5
TS28Eub0672|CDS|CDS	6.5	0.5	59.0	J	COG0102	Ribosomal protein L13
Ehal0507|CDS|CDS	6.5	0.5	59.0	J	COG0102	Ribosomal protein L13
TS28Rum15873|CDS|CDS	12.8	1.0	58.3	J	COG0089	Ribosomal protein L23
TS28Rum00047|CDS|CDS	44.2	3.5	57.3	J	COG1544	Ribosome-associated protein Y (PSrp-1)
BactD14438|CDS|CDS	33.5	2.7	56.9	J	COG0050	GTPases - translation elongation factors
TS28Fae11958|CDS|CDS	6.3	0.5	56.7	J	COG0091	Ribosomal protein L22
Robe2987|CDS|CDS	6.3	0.5	56.7	J	COG0360	Ribosomal protein S6
Dlon0184|CDS|CDS	12.2	1.0	55.2	J	COG0093	Ribosomal protein L14
TS28Bac1326|CDS|CDS	20.1	1.7	54.7	J	COG0173	Aspartyl-tRNA synthetase
Buni2310|CDS|CDS	4.0	0.3	54.5	J	COG0180	Tryptophanyl-tRNA synthetase
TS28Fae22829|CDS|CDS	11.5	1.0	52.2	J	COG0097	Ribosomal protein L6P/L9E
BWH20064|CDS|CDS	3.8	0.3	52.0	J	COG0094	Ribosomal protein L5
BactD20035|CDS|CDS	22.4	2.0	50.9	J	COG0050	GTPases - translation elongation factors
TS29Rum11355|CDS|CDS	11.2	1.0	50.7	J	COG0089	Ribosomal protein L23
TS28CloUnc059|CDS|CDS	16.6	1.5	50.4	J	COG0050	GTPases - translation elongation factors
Buni2320|CDS|CDS	11.0	1.0	49.9	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
TS28Met1811|CDS|CDS	2.2	0.2	49.9	J	COG0080	Ribosomal protein L11
Msmi751412|CDS|CDS	2.2	0.2	49.9	J	COG0080	Ribosomal protein L11

Caer1178|CDS|CDS	5.5	0.5	49.9	J	COG0359	Ribosomal protein L9
Msmi740268|CDS|CDS	2.2	0.2	49.9	J	COG0080	Ribosomal protein L11
Cbol5431|CDS|CDS	11.0	1.0	49.9	J	COG0256	Ribosomal protein L18
TS28Clo04653|CDS|CDS	3.5	0.3	47.7	J	COG1236|COG1782	Predicted exonuclease of the beta-lactamase fold involved in RNA processing|Predicted metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain
TS28Rum01328|CDS|CDS	20.9	2.0	47.5	J	COG0050	GTPases - translation elongation factors
TS28Rum11479|CDS|CDS	56.7	5.5	46.8	J	COG0097	Ribosomal protein L6P/L9E
TS29Rum16476|CDS|CDS	20.5	2.0	46.5	J	COG0261	Ribosomal protein L21
Bova0745|CDS|CDS	11.2	1.1	46.4	J	COG0092	Ribosomal protein S3
Aput1412|CDS|CDS	10.0	1.0	45.4	J	COG0012	Predicted GTPase, probable translation factor
Aput0550|CDS|CDS	10.0	1.0	45.4	J	COG0024	Methionine aminopeptidase
TS29Bac09449|CDS|CDS	15.9	1.7	43.3	J	COG0198	Ribosomal protein L24
BactD14460|CDS|CDS	15.9	1.7	43.3	J	COG0198	Ribosomal protein L24
Bxyl1674|CDS|CDS	15.9	1.7	43.3	J	COG0198	Ribosomal protein L24
TS29Rum19788|CDS|CDS	9.5	1.0	43.1	J	COG0099	Ribosomal protein S13
Ceut0026|CDS|CDS	9.5	1.0	43.1	J	COG0050	GTPases - translation elongation factors
TS28Rum01329|CDS|CDS	9.2	1.0	41.9	J	COG0480	Translation elongation factors (GTPases)
Dlon0186|CDS|CDS	13.8	1.5	41.6	J	COG0094	Ribosomal protein L5
Buni0751|CDS|CDS	4.5	0.5	40.9	J	COG0215	Cysteinyl-tRNA synthetase
TS28Fae18265|CDS|CDS	22.5	2.5	40.9	J	COG0361	Translation initiation factor 1 (IF-1)
Rtor0509|CDS|CDS	4.5	0.5	40.9	J	COG0098	Ribosomal protein S5
Bcac2073|CDS|CDS	9.0	1.0	40.7	J	COG0256	Ribosomal protein L18
TS28Rum08441|CDS|CDS	17.3	2.0	39.2	J	COG0211	Ribosomal protein L27
Bthe7330426|CDS|CDS	12.6	1.5	38.0	J	COG0333	Ribosomal protein L32
Rumhyd0596|CDS|CDS	8.3	1.0	37.5	J	COG0087	Ribosomal protein L3
BactD14459|CDS|CDS	4.1	0.5	36.8	J	COG0186	Ribosomal protein S17
Bfin3716|CDS|CDS	8.1	1.0	36.7	J	COG0097	Ribosomal protein L6P/L9E
Casp2730|CDS|CDS	4.0	0.5	36.3	J	COG0335	Ribosomal protein L19
TS28Fae22841|CDS|CDS	4.0	0.5	36.3	J	COG0185	Ribosomal protein S19
Bcap2269|CDS|CDS	12.0	1.5	36.3	J	COG0097	Ribosomal protein L6P/L9E
Bfin3712|CDS|CDS	7.9	1.0	36.0	J	COG0198	Ribosomal protein L24
Dfor1281|CDS|CDS	7.8	1.0	35.6	J	COG0256	Ribosomal protein L18
BactD14440|CDS|CDS	7.8	1.0	35.5	J	COG0080	Ribosomal protein L11
Bxyl1696|CDS|CDS	7.8	1.0	35.5	J	COG0080	Ribosomal protein L11
Buni2324|CDS|CDS	11.6	1.5	35.2	J	COG0264	Translation elongation factor Ts
Cbol4974|CDS|CDS	7.7	1.0	34.8	J	COG0290	Translation initiation factor 3 (IF-3)
TS29Rum13747|CDS|CDS	15.3	2.0	34.6	J	COG0051	Ribosomal protein S10
TS29Rum14233|CDS|CDS	53.1	7.0	34.4	J	COG0049	Ribosomal protein S7
Buni1601|CDS|CDS	7.5	1.0	34.0	J	COG0290	Translation initiation factor 3 (IF-3)
TS29Par888|CDS|CDS	15.0	2.0	34.0	J	COG0333	Ribosomal protein L32
TS29Rum13734|CDS|CDS	37.0	5.0	33.6	J	COG0199	Ribosomal protein S14
Csym4102|CDS|CDS	22.0	3.0	33.3	J	COG0050	GTPases - translation elongation factors
BactD12041|CDS|CDS	5.8	0.8	33.3	J	COG0480	Translation elongation factors (GTPases)
TS28Fae20653|CDS|CDS	14.7	2.0	33.3	J	COG0480	Translation elongation factors (GTPases)
Msmi740267|CDS|CDS	6.2	0.9	32.7	J	COG0081	Ribosomal protein L1
Dlon0201|CDS|CDS	7.2	1.0	32.5	J	COG0522	Ribosomal protein S4 and related proteins
TS28Fae10960|CDS|CDS	9.5	1.3	32.3	J	COG0238	Ribosomal protein S18
TS28Bac6108|CDS|CDS	2.3	0.3	31.8	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Ccom0484|CDS|CDS	7.0	1.0	31.8	J	COG0203	Ribosomal protein L17
TS28Fae05863|CDS|CDS	7.0	1.0	31.8	J	COG0480	Translation elongation factors (GTPases)
TS28Fae13722|CDS|CDS	3.5	0.5	31.8	J	COG0097	Ribosomal protein L6P/L9E
Cste1008|CDS|CDS	7.0	1.0	31.8	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
TS29Rum06183|CDS|CDS	7.0	1.0	31.8	J	COG2868	Predicted ribosomal protein
TS28Met0975|CDS|CDS	3.5	0.5	31.8	J	COG0185	Ribosomal protein S19
Cmet0169|CDS|CDS	7.0	1.0	31.8	J	COG0480	Translation elongation factors (GTPases)
Bcap2264|CDS|CDS	7.0	1.0	31.8	J	COG0093	Ribosomal protein L14
Msmi741036|CDS|CDS	3.5	0.5	31.8	J	COG0185	Ribosomal protein S19
Msmi750644|CDS|CDS	3.5	0.5	31.8	J	COG0185	Ribosomal protein S19
Bcap3099|CDS|CDS	7.0	1.0	31.8	J	COG0267	Ribosomal protein L33
Bxyl1680|CDS|CDS	14.0	2.0	31.8	J	COG0091	Ribosomal protein L22
BactD14455|CDS|CDS	14.0	2.0	31.8	J	COG0091	Ribosomal protein L22
BactD14463|CDS|CDS	27.9	4.0	31.6	J	COG0097	Ribosomal protein L6P/L9E
TS28Clo00190|CDS|CDS	13.7	2.0	31.1	J	COG0052	Ribosomal protein S2
Bste2294|CDS|CDS	13.6	2.0	30.9	J	COG0091	Ribosomal protein L22
TS29Rum21002|CDS|CDS	27.0	4.0	30.6	J	COG0198	Ribosomal protein L24
Buni0631|CDS|CDS	7.8	1.2	30.5	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
CspM6212581|CDS|CDS	13.3	2.0	30.1	J	COG0050	GTPases - translation elongation factors
Robe1730|CDS|CDS	13.3	2.0	30.1	J	COG0088	Ribosomal protein L4
TS28Fae22844|CDS|CDS	16.5	2.5	30.0	J	COG0088	Ribosomal protein L4
Ehal0625|CDS|CDS	16.3	2.5	29.6	J	COG0050	GTPases - translation elongation factors
TS28Eub5491|CDS|CDS	16.3	2.5	29.6	J	COG0050	GTPases - translation elongation factors
TS28Fae07804|CDS|CDS	6.5	1.0	29.5	J	COG0359	Ribosomal protein L9
TS28Fae01963|CDS|CDS	12.8	2.0	29.1	J	COG0048	Ribosomal protein S12
Rtor0507|CDS|CDS	3.2	0.5	28.8	J	COG0200	Ribosomal protein L15
TS29Bac03521|CDS|CDS	6.3	1.0	28.8	J	COG0130	Pseudouridine synthase
Bxyl2755|CDS|CDS	6.3	1.0	28.7	J	COG0103	Ribosomal protein S9
Bxyl1679|CDS|CDS	11.1	1.8	28.5	J	COG0092	Ribosomal protein S3
TS28Rum13634|CDS|CDS	18.8	3.0	28.5	J	COG0233	Ribosome recycling factor
Buni1580|CDS|CDS	35.1	5.7	28.1	J	COG0173	Aspartyl-tRNA synthetase
Csym4103|CDS|CDS	12.1	2.0	27.5	J	COG0480	Translation elongation factors (GTPases)
TS29Bac11453|CDS|CDS	87.2	14.5	27.3	J	COG0050	GTPases - translation elongation factors
Robe1841|CDS|CDS	2.0	0.3	27.2	J	COG0184	Ribosomal protein S15P/S13E
TS29Rum10660|CDS|CDS	2.0	0.3	27.2	J	COG0184	Ribosomal protein S15P/S13E
Bxyl2065|CDS|CDS	2.0	0.3	27.2	J	COG0495	Leucyl-tRNA synthetase
TS28Met0812|CDS|CDS	1.5	0.3	27.2	J	COG0103	Ribosomal protein S9
TS28Rum12100|CDS|CDS	3.0	0.5	27.2	J	COG0042	tRNA-dihydrouridine synthase
TS29Bac06690|CDS|CDS	3.0	0.5	27.2	J	COG0100	Ribosomal protein S11
TS28Col1452|CDS|CDS	12.0	2.0	27.2	J	COG0092	Ribosomal protein S3
TS28Fae21266|CDS|CDS	3.0	0.5	27.2	J	COG0050	GTPases - translation elongation factors
Dlon0347|CDS|CDS	6.0	1.0	27.2	J	COG0184	Ribosomal protein S15P/S13E
TS28Fae18624|CDS|CDS	3.0	0.5	27.2	J	COG0244	Ribosomal protein L10
Msmi750605|CDS|CDS	1.5	0.3	27.2	J	COG0103	Ribosomal protein S9
Rlac1587|CDS|CDS	6.0	1.0	27.2	J	COG0228	Ribosomal protein S16
TS28Rum15986|CDS|CDS	6.0	1.0	27.2	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)
Msmi741073|CDS|CDS	1.5	0.3	27.2	J	COG0103	Ribosomal protein S9

TS28Fae03931|CDS|CDS	18.0	3.0	27.2	J	COG0144|COG3270	tRNA and rRNA cytosine-C5-methylases|Uncharacterized conserved protein
Bova0792|CDS|CDS	4.5	0.8	27.0	J	COG0264	Translation elongation factor Ts
Begg2627|CDS|CDS	4.0	0.7	26.9	J	COG0090	Ribosomal protein L2
Bste2310|CDS|CDS	11.5	2.0	26.2	J	COG0080	Ribosomal protein L11
Bryfor3830|CDS|CDS	17.2	3.0	26.0	J	COG0480	Translation elongation factors (GTPases)
Csym4104|CDS|CDS	5.7	1.0	25.9	J	COG0049	Ribosomal protein S7
TS28Ali1618|CDS|CDS	5.7	1.0	25.7	J	COG0441	Threonyl-tRNA synthetase
TS28Rum13882|CDS|CDS	8.5	1.5	25.7	J	COG0102	Ribosomal protein L13
TS29Fae06981|CDS|CDS	2.8	0.5	25.7	J	COG0264	Translation elongation factor Ts
TS28Rum15336|CDS|CDS	11.3	2.0	25.7	J	COG0254	Ribosomal protein L31
TS28Fae20654|CDS|CDS	33.7	6.0	25.5	J	COG0050	GTPases - translation elongation factors
Bfin3713|CDS|CDS	3.7	0.7	25.2	J	COG0094	Ribosomal protein L5
Caer1979|CDS|CDS	5.5	1.0	25.0	J	COG0197	Ribosomal protein L16/L10E
Aput0546|CDS|CDS	11.0	2.0	25.0	J	COG0090	Ribosomal protein L2
Dlon0189|CDS|CDS	5.5	1.0	25.0	J	COG0097	Ribosomal protein L6P/L9E
Casp6320|CDS|CDS	5.5	1.0	25.0	J	COG0267	Ribosomal protein L33
TS29Rum08033|CDS|CDS	11.0	2.0	25.0	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)
Bxyl1699|CDS|CDS	36.4	6.7	24.8	J	COG0050	GTPases - translation elongation factors
Bryfor3831|CDS|CDS	16.2	3.0	24.5	J	COG0050	GTPases - translation elongation factors
Bxyl0455|CDS|CDS	1.8	0.3	24.3	J	COG0173	Aspartyl-tRNA synthetase
TS28Bac1897|CDS|CDS	5.3	1.0	24.2	J	COG0143	Methionyl-tRNA synthetase
Rgna2525|CDS|CDS	5.3	1.0	24.2	J	COG0094	Ribosomal protein L5
Dlon1162|CDS|CDS	5.3	1.0	24.2	J	COG0222	Ribosomal protein L7/L12
Robe1468|CDS|CDS	15.9	3.0	24.0	J	COG0828	Ribosomal protein S21
TS28Rum11482|CDS|CDS	37.0	7.0	24.0	J	COG0198	Ribosomal protein L24
FpraM2122622|CDS|CDS	10.5	2.0	23.8	J	COG0566	rRNA methylases
Cbol5446|CDS|CDS	10.5	2.0	23.8	J	COG0087	Ribosomal protein L3
TS29Bac09457|CDS|CDS	21.0	4.0	23.8	J	COG0185	Ribosomal protein S19
Casp5594|CDS|CDS	10.3	2.0	23.5	J	COG0211	Ribosomal protein L27
Dfor1292|CDS|CDS	10.3	2.0	23.3	J	COG0091	Ribosomal protein L22
Bxyl1664|CDS|CDS	10.2	2.0	23.2	J	COG0024	Methionine aminopeptidase
TS29Rum16474|CDS|CDS	28.0	5.5	23.1	J	COG0211	Ribosomal protein L27
Cbol5409|CDS|CDS	10.0	2.0	22.7	J	COG0102	Ribosomal protein L13
Dlon0181|CDS|CDS	5.0	1.0	22.7	J	COG0197	Ribosomal protein L16/L10E
TS28Eub5772|CDS|CDS	2.5	0.5	22.7	J	COG1841	Ribosomal protein L30/L7E
TS28Dor1580|CDS|CDS	2.5	0.5	22.7	J	COG0200	Ribosomal protein L15
Ehal1406|CDS|CDS	2.5	0.5	22.7	J	COG1841	Ribosomal protein L30/L7E
TS28Col1442|CDS|CDS	5.0	1.0	22.7	J	COG0256	Ribosomal protein L18
TS29Rum13321|CDS|CDS	5.0	1.0	22.7	J	COG0292	Ribosomal protein L20
Dlon0193|CDS|CDS	2.5	0.5	22.7	J	COG0200	Ribosomal protein L15
Rgna1846|CDS|CDS	2.5	0.5	22.7	J	COG0211	Ribosomal protein L27
TS28Eub8305|CDS|CDS	5.0	1.0	22.7	J	COG0197	Ribosomal protein L16/L10E
TS28Clo02719|CDS|CDS	10.0	2.0	22.7	J	COG0088	Ribosomal protein L4
TS28Rum16023|CDS|CDS	43.5	8.7	22.7	J	COG0102	Ribosomal protein L13
Acac3102|CDS|CDS	5.0	1.0	22.7	J	COG0094	Ribosomal protein L5
Acol1127|CDS|CDS	5.0	1.0	22.7	J	COG0480	Translation elongation factors (GTPases)
Caer1218|CDS|CDS	2.5	0.5	22.7	J	COG0098	Ribosomal protein S5
Rumhyd2193|CDS|CDS	5.0	1.0	22.7	J	COG2890|COG3872	Methylase of polypeptide chain release factors|Predicted metal-dependent enzyme
TS29Dor1582|CDS|CDS	2.5	0.5	22.7	J	COG0211	Ribosomal protein L27
TS28Fae01161|CDS|CDS	2.5	0.5	22.7	J	COG0291	Ribosomal protein L35
Cbol2237|CDS|CDS	29.9	6.0	22.6	J	COG0050	GTPases - translation elongation factors
BactD14441|CDS|CDS	19.7	4.0	22.4	J	COG0081	Ribosomal protein L1
Bxyl1695|CDS|CDS	19.7	4.0	22.4	J	COG0081	Ribosomal protein L1
TS28Rum15875|CDS|CDS	29.4	6.0	22.3	J	COG0087	Ribosomal protein L3
TS29Rum13735|CDS|CDS	12.2	2.5	22.1	J	COG0094	Ribosomal protein L5
TS29Rum13738|CDS|CDS	24.1	5.0	21.9	J	COG0255	Ribosomal protein L29
TS29Bac07881|CDS|CDS	3.2	0.7	21.8	J	COG0539	Ribosomal protein S1
BactD14469|CDS|CDS	11.7	2.5	21.3	J	COG0024	Methionine aminopeptidase
Csci0801|CDS|CDS	4.7	1.0	21.2	J	COG0049	Ribosomal protein S7
TS28Eub8310|CDS|CDS	2.3	0.5	21.2	J	COG0097	Ribosomal protein L6P/L9E
TS28Fae10286|CDS|CDS	9.3	2.0	21.2	J	COG0233	Ribosome recycling factor
Rgna1209|CDS|CDS	2.3	0.5	21.2	J	COG0360	Ribosomal protein S6
RintL13584|CDS|CDS	9.3	2.0	21.0	J	COG0081	Ribosomal protein L1
TS28Rum15874|CDS|CDS	32.3	7.0	20.9	J	COG0088	Ribosomal protein L4
Aput0543|CDS|CDS	32.0	7.0	20.8	J	COG0480	Translation elongation factors (GTPases)
Bhan0425|CDS|CDS	4.5	1.0	20.4	J	COG0094	Ribosomal protein L5
TS28Eub4402|CDS|CDS	4.5	1.0	20.4	J	COG0228	Ribosomal protein S16
Aput1877|CDS|CDS	9.0	2.0	20.4	J	COG2264	Ribosomal protein L11 methylase
TS29Col1653|CDS|CDS	9.0	2.0	20.4	J	COG0097	Ribosomal protein L6P/L9E
Rtor0519|CDS|CDS	4.5	1.0	20.4	J	COG0197	Ribosomal protein L16/L10E
Dfor0348|CDS|CDS	9.0	2.0	20.4	J	COG0360	Ribosomal protein S6
Cste0999|CDS|CDS	9.0	2.0	20.4	J	COG0081	Ribosomal protein L1
TS28Rum00103|CDS|CDS	9.0	2.0	20.4	J	COG0099	Ribosomal protein S13
Aput0547|CDS|CDS	9.0	2.0	20.4	J	COG0186	Ribosomal protein S17
Bfin3715|CDS|CDS	4.5	1.0	20.2	J	COG0096	Ribosomal protein S8
Buni0614|CDS|CDS	57.9	13.0	20.2	J	COG0092	Ribosomal protein S3
TS28Rum11472|CDS|CDS	15.5	3.5	20.1	J	COG0024	Methionine aminopeptidase
TS28Dor0002|CDS|CDS	8.8	2.0	19.9	J	COG0091	Ribosomal protein L22
TS28Eub7689|CDS|CDS	56.1	13.0	19.6	J	COG0049	Ribosomal protein S7
Dfor1048|CDS|CDS	17.2	4.0	19.6	J	COG0050	GTPases - translation elongation factors
TS28Rum00003|CDS|CDS	6.5	1.5	19.5	J	COG0256	Ribosomal protein L18
Robe1745|CDS|CDS	6.5	1.5	19.5	J	COG0256	Ribosomal protein L18
Bova0748|CDS|CDS	4.3	1.0	19.4	J	COG0088	Ribosomal protein L4
Msmi740266|CDS|CDS	5.0	1.2	19.4	J	COG0244	Ribosomal protein L10
Msmi751414|CDS|CDS	5.0	1.2	19.4	J	COG0244	Ribosomal protein L10
BactD13208|CDS|CDS	4.3	1.0	19.3	J	COG0441	Threonyl-tRNA synthetase
TS29Bif3778|CDS|CDS	1.1	0.3	19.2	J	COG0185	Ribosomal protein S19
TS28Bif0836|CDS|CDS	1.1	0.3	19.2	J	COG0185	Ribosomal protein S19
BactD13209|CDS|CDS	6.7	1.6	19.1	J	COG0290	Translation initiation factor 3 (IF-3)
Bova1291|CDS|CDS	6.7	1.6	19.1	J	COG0290	Translation initiation factor 3 (IF-3)
BactD11537|CDS|CDS	2.8	0.7	19.1	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
TS29Met0847|CDS|CDS	4.2	1.0	19.1	J	COG0097	Ribosomal protein L6P/L9E
Bova1401|CDS|CDS	10.4	2.5	19.0	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29RumUnc1196|CDS|CDS	25.0	6.0	18.9	J	COG0290	Translation initiation factor 3 (IF-3)
TS29Rum13737|CDS|CDS	75.0	18.0	18.9	J	COG0186	Ribosomal protein S17

TS29RumUnc1162|CDS|CDS	29.0	7.0	18.8	J	COG3743|COG0261	Uncharacterized conserved protein|Ribosomal protein L21
Bxyl1675|CDS|CDS	4.1	1.0	18.7	J	COG0093	Ribosomal protein L14
Bcac3587|CDS|CDS	1.4	0.3	18.6	J	COG0211	Ribosomal protein L27
TS28Fae22588|CDS|CDS	40.7	10.0	18.5	J	COG0255	Ribosomal protein L29
Bova0742|CDS|CDS	4.0	1.0	18.3	J	COG0024	Methionine aminopeptidase
Svar0549|CDS|CDS	12.0	3.0	18.2	J	COG0480	Translation elongation factors (GTPases)
TS28Rum00104|CDS|CDS	4.0	1.0	18.2	J	COG0100	Ribosomal protein S11
Svar0403|CDS|CDS	4.0	1.0	18.2	J	COG0080	Ribosomal protein L11
TS28Dor1478|CDS|CDS	4.0	1.0	18.2	J	COG0267	Ribosomal protein L33
Csci1697|CDS|CDS	2.0	0.5	18.2	J	COG0254	Ribosomal protein L31
Dlon0182|CDS|CDS	4.0	1.0	18.2	J	COG0255	Ribosomal protein L29
Cste0078|CDS|CDS	4.0	1.0	18.2	J	COG0480	Translation elongation factors (GTPases)
TS28Col1430|CDS|CDS	8.0	2.0	18.2	J	COG0100	Ribosomal protein S11
Cbol5441|CDS|CDS	4.0	1.0	18.2	J	COG0091	Ribosomal protein L22
Casp0940|CDS|CDS	4.0	1.0	18.2	J	COG0257	Ribosomal protein L36
TS28Rum10760|CDS|CDS	4.0	1.0	18.2	J	COG0480	Translation elongation factors (GTPases)
TS28Fae13718|CDS|CDS	12.0	3.0	18.2	J	COG0200	Ribosomal protein L15
Msmi750611|CDS|CDS	1.0	0.3	18.2	J	COG0099	Ribosomal protein S13
TS29Col0504|CDS|CDS	2.0	0.5	18.2	J	COG0199	Ribosomal protein S14
TS28Rum14857|CDS|CDS	4.0	1.0	18.2	J	COG1189	Predicted rRNA methylase
Rgna2513|CDS|CDS	4.0	1.0	18.2	J	COG0257	Ribosomal protein L36
Bcac2368|CDS|CDS	4.0	1.0	18.1	J	COG0227	Ribosomal protein L28
Bxyl1682|CDS|CDS	13.8	3.5	17.8	J	COG0090	Ribosomal protein L2
TS28Rum08848|CDS|CDS	11.8	3.0	17.8	J	COG0090	Ribosomal protein L2
Rgna2535|CDS|CDS	7.8	2.0	17.8	J	COG0089	Ribosomal protein L23
Robe3802|CDS|CDS	15.5	4.0	17.6	J	COG0099	Ribosomal protein S13
Bste2280|CDS|CDS	3.9	1.0	17.6	J	COG0200	Ribosomal protein L15
Bfin1190|CDS|CDS	6.4	1.7	17.4	J	COG0539	Ribosomal protein S1
TS29Bac02139|CDS|CDS	1.9	0.5	17.3	J	COG0539	Ribosomal protein S1
Rumhyd1580|CDS|CDS	19.0	5.0	17.2	J	COG0050	GTPases - translation elongation factors
Rgna1515|CDS|CDS	34.1	9.0	17.2	J	COG0050	GTPases - translation elongation factors
Bint1670|CDS|CDS	3.8	1.0	17.2	J	COG0222	Ribosomal protein L7/L12
TS29Rum17167|CDS|CDS	45.3	12.0	17.1	J	COG0360	Ribosomal protein S6
Bxyl0972|CDS|CDS	9.5	2.5	17.0	J	COG0480	Translation elongation factors (GTPases)
Cste0994|CDS|CDS	7.5	2.0	16.9	J	COG0050	GTPases - translation elongation factors
Buni0608|CDS|CDS	13.0	3.5	16.9	J	COG0024	Methionine aminopeptidase
BactD24191|CDS|CDS	3.7	1.0	16.7	J	COG0539	Ribosomal protein S1
Cbol5942|CDS|CDS	11.0	3.0	16.6	J	COG1544	Ribosome-associated protein Y (PSrp-1)
Dfor1297|CDS|CDS	7.2	2.0	16.3	J	COG0087	Ribosomal protein L3
TS29Clo0314|CDS|CDS	18.0	5.0	16.3	J	COG0009	Putative translation factor (SUA5)
TS29RumUnc0852|CDS|CDS	75.5	21.0	16.3	J	COG0050	GTPases - translation elongation factors
Bxyl1661|CDS|CDS	3.6	1.0	16.3	J	COG0100	Ribosomal protein S11
Chyl2252|CDS|CDS	7.1	2.0	16.2	J	COG0480	Translation elongation factors (GTPases)
TS29Rum15322|CDS|CDS	17.8	5.0	16.1	J	COG0211	Ribosomal protein L27
TS29Rum03453|CDS|CDS	14.0	4.0	15.9	J	COG0828	Ribosomal protein S21
TS28Bac2659|CDS|CDS	2.3	0.7	15.9	J	COG0525	Valyl-tRNA synthetase
TS28Bac4345|CDS|CDS	4.7	1.3	15.9	J	COG0180	Tryptophanyl-tRNA synthetase
Rtor2165|CDS|CDS	3.5	1.0	15.9	J	COG0184	Ribosomal protein S15P/S13E
Chir2104|CDS|CDS	3.5	1.0	15.9	J	COG0050	GTPases - translation elongation factors
Bcap2268|CDS|CDS	3.5	1.0	15.9	J	COG0096	Ribosomal protein S8
TS28Bac4689|CDS|CDS	2.3	0.7	15.9	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Ccom0299|CDS|CDS	20.7	6.0	15.7	J	COG0050	GTPases - translation elongation factors
BactD20044|CDS|CDS	3.4	1.0	15.6	J	COG0090	Ribosomal protein L2
Bova0747|CDS|CDS	3.4	1.0	15.6	J	COG0090	Ribosomal protein L2
Acac2828|CDS|CDS	17.1	5.0	15.5	J	COG0050	GTPases - translation elongation factors
TS28Met0777|CDS|CDS	0.9	0.3	15.4	J	COG1841	Ribosomal protein L30/L7E
Msmi741053|CDS|CDS	0.9	0.3	15.4	J	COG1841	Ribosomal protein L30/L7E
TS28Rum08197|CDS|CDS	1.7	0.5	15.4	J	COG0080	Ribosomal protein L11
Rtor0296|CDS|CDS	1.7	0.5	15.4	J	COG0080	Ribosomal protein L11
Rtor0520|CDS|CDS	3.4	1.0	15.4	J	COG0092	Ribosomal protein S3
TS28Met0759|CDS|CDS	2.3	0.7	15.3	J	COG5257	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)
BWH20067|CDS|CDS	1.7	0.5	15.3	J	COG0186	Ribosomal protein S17
TS28Ali0073|CDS|CDS	3.3	1.0	15.1	J	COG0291	Ribosomal protein L35
Cbol5283|CDS|CDS	10.0	3.0	15.1	J	COG2264	Ribosomal protein L11 methylase
Eeli1002|CDS|CDS	5.0	1.5	15.1	J	COG0480	Translation elongation factors (GTPases)
Rgna0577|CDS|CDS	8.3	2.5	15.1	J	COG0290	Translation initiation factor 3 (IF-3)
BactD20780|CDS|CDS	3.3	1.0	15.1	J	COG0343	Queuine/archaeosine tRNA-ribosyltransferase
Dlon1158|CDS|CDS	3.3	1.0	15.1	J	COG0081	Ribosomal protein L1
TS28Eub0671|CDS|CDS	1.7	0.5	15.1	J	COG0103	Ribosomal protein S9
Ehal0508|CDS|CDS	1.7	0.5	15.1	J	COG0103	Ribosomal protein S9
TS29Bac02529|CDS|CDS	6.6	2.0	15.0	J	COG0238	Ribosomal protein S18
Bste2288|CDS|CDS	9.9	3.0	15.0	J	COG0198	Ribosomal protein L24
Rlac2126|CDS|CDS	29.6	9.0	15.0	J	COG0050	GTPases - translation elongation factors
Bste2308|CDS|CDS	3.3	1.0	14.9	J	COG0244	Ribosomal protein L10
TS29Fae04369|CDS|CDS	23.0	7.0	14.9	J	COG0255	Ribosomal protein L29
TS28Rum00088|CDS|CDS	3.3	1.0	14.8	J	COG0522	Ribosomal protein S4 and related proteins
Dlon0191|CDS|CDS	3.3	1.0	14.8	J	COG0098	Ribosomal protein S5
TS29Bac09460|CDS|CDS	19.5	6.0	14.7	J	COG0088	Ribosomal protein L4
Bxyl1676|CDS|CDS	4.8	1.5	14.5	J	COG0186	Ribosomal protein S17
Msmi740893|CDS|CDS	3.2	1.0	14.5	J	COG5256	Translation elongation factor EF-1alpha (GTPase)
Rtor0546|CDS|CDS	12.8	4.0	14.5	J	COG0050	GTPases - translation elongation factors
Robe1740|CDS|CDS	19.0	6.0	14.4	J	COG0198	Ribosomal protein L24
Bcap2652|CDS|CDS	12.6	4.0	14.3	J	COG0050	GTPases - translation elongation factors
TS29Clo1420|CDS|CDS	11.0	3.5	14.3	J	COG0267	Ribosomal protein L33
Bste2301|CDS|CDS	6.3	2.0	14.3	J	COG0480	Translation elongation factors (GTPases)
Buni2043|CDS|CDS	12.5	4.0	14.2	J	COG0172	Seryl-tRNA synthetase
TS29Dor1077|CDS|CDS	25.0	8.0	14.2	J	COG0101	Pseudouridylate synthase
Begg2623|CDS|CDS	21.9	7.0	14.2	J	COG0197	Ribosomal protein L16/L10E
BactD10526|CDS|CDS	9.3	3.0	14.1	J	COG0343	Queuine/archaeosine tRNA-ribosyltransferase
TS28Met1809|CDS|CDS	4.7	1.5	14.1	J	COG0244	Ribosomal protein L10
TS28Col1460|CDS|CDS	12.3	4.0	14.0	J	COG0051	Ribosomal protein S10
Robe3195|CDS|CDS	3.1	1.0	14.0	J	COG0103	Ribosomal protein S9
BactD14443|CDS|CDS	5.6	1.8	14.0	J	COG0222	Ribosomal protein L7/L12
Cnex0780|CDS|CDS	6.1	2.0	13.9	J	COG0480	Translation elongation factors (GTPases)
Robe3352|CDS|CDS	3.0	1.0	13.8	J	COG0292	Ribosomal protein L20
Msmi740440|CDS|CDS	1.0	0.3	13.6	J	COG0060	Isoleucyl-tRNA synthetase

TS28Eub3732|CDS|CDS	1.5	0.5	13.6	J	COG0186	Ribosomal protein S17
CspM6210512|CDS|CDS	3.0	1.0	13.6	J	COG0222	Ribosomal protein L7/L12
Chyl2587|CDS|CDS	3.0	1.0	13.6	J	COG0009	Putative translation factor (SUA5)
Caer1213|CDS|CDS	1.5	0.5	13.6	J	COG0094	Ribosomal protein L5
Cspi1174|CDS|CDS	3.0	1.0	13.6	J	COG0094	Ribosomal protein L5
RintL11234|CDS|CDS	3.0	1.0	13.6	J	COG0233	Ribosome recycling factor
Acac0404|CDS|CDS	3.0	1.0	13.6	J	COG0215	Cysteinyl-tRNA synthetase
Acol3298|CDS|CDS	3.0	1.0	13.6	J	COG0621	2-methylthioadenine synthetase
TS28Col1459|CDS|CDS	3.0	1.0	13.6	J	COG0087	Ribosomal protein L3
TS28Rum06712|CDS|CDS	1.5	0.5	13.6	J	COG0254	Ribosomal protein L31
TS28Rum08934|CDS|CDS	3.0	1.0	13.6	J	COG0173	Aspartyl-tRNA synthetase
TS28Rum15334|CDS|CDS	3.0	1.0	13.6	J	COG2890|COG3872	Methylase of polypeptide chain release factors|Predicted metal-dependent enzyme
CspM6213073|CDS|CDS	3.0	1.0	13.6	J	COG0184	Ribosomal protein S15P/S13E
TS28Clo03785|CDS|CDS	3.0	1.0	13.6	J	COG0495	Leucyl-tRNA synthetase
Casp3650|CDS|CDS	6.0	2.0	13.6	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29Rum21000|CDS|CDS	6.0	2.0	13.6	J	COG0199	Ribosomal protein S14
Bhan0161|CDS|CDS	3.0	1.0	13.6	J	COG0222	Ribosomal protein L7/L12
Msmi741072|CDS|CDS	0.8	0.3	13.6	J	COG0102|COG0103	Ribosomal protein L13|Ribosomal protein S9
Dlon0477|CDS|CDS	1.5	0.5	13.6	J	COG0360	Ribosomal protein S6
Acac3116|CDS|CDS	3.0	1.0	13.6	J	COG0100	Ribosomal protein S11
Aput1243|CDS|CDS	15.0	5.0	13.6	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
BDI1432|CDS|acetyltransferase	3.0	1.0	13.6	J	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins
Msmi750606|CDS|CDS	0.8	0.3	13.6	J	COG0102|COG0103	Ribosomal protein L13|Ribosomal protein S9
TS28Eub2928|CDS|CDS	3.0	1.0	13.6	J	COG0088	Ribosomal protein L4
Dfor0679|CDS|CDS	3.0	1.0	13.6	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS28Eub0835|CDS|CDS	3.0	1.0	13.6	J	COG0052	Ribosomal protein S2
TS29Fae07124|CDS|CDS	3.0	1.0	13.6	J	COG0099	Ribosomal protein S13
TS28Rum02498|CDS|CDS	1.5	0.5	13.6	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases
TS28Eub8303|CDS|CDS	1.5	0.5	13.6	J	COG0091	Ribosomal protein L22
TS29Fae02038|CDS|CDS	3.0	1.0	13.6	J	COG0480	Translation elongation factors (GTPases)
Msmi750131|CDS|CDS	1.5	0.5	13.6	J	COG1097	RNA-binding protein Rrp4 and related proteins (contain S1 domain and KH domain)
Aput0545|CDS|CDS	3.0	1.0	13.6	J	COG0089	Ribosomal protein L23
Rtor0508|CDS|CDS	1.5	0.5	13.6	J	COG1841	Ribosomal protein L30/L7E
Ehal1398|CDS|CDS	1.5	0.5	13.6	J	COG0186	Ribosomal protein S17
TS28Dor0199|CDS|CDS	1.5	0.5	13.6	J	COG0360	Ribosomal protein S6
TS28Eub8309|CDS|CDS	3.0	1.0	13.6	J	COG0199	Ribosomal protein S14
Casp0948|CDS|CDS	3.0	1.0	13.6	J	COG0098	Ribosomal protein S5
TS28Rum12913|CDS|CDS	3.0	1.0	13.6	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)
TS29Par346|CDS|CDS	6.0	2.0	13.6	J	COG1186	Protein chain release factor B
TS28Rum10131|CDS|CDS	1.5	0.5	13.6	J	COG1841	Ribosomal protein L30/L7E
Acac3258|CDS|CDS	6.0	2.0	13.6	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
TS29Bac03357|CDS|CDS	1.5	0.5	13.6	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Robe2994|CDS|CDS	1.5	0.5	13.6	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
Buni0869|CDS|CDS	3.0	1.0	13.6	J	COG0124	Histidyl-tRNA synthetase
Dfor1295|CDS|CDS	6.0	2.0	13.6	J	COG0089	Ribosomal protein L23
TS28Met0811|CDS|CDS	0.8	0.3	13.6	J	COG0102|COG0103	Ribosomal protein L13|Ribosomal protein S9
Acac2792|CDS|CDS	3.0	1.0	13.6	J	COG0081	Ribosomal protein L1
TS28Fae14973|CDS|CDS	4.5	1.5	13.6	J	COG0264	Translation elongation factor Ts
Rgna0725|CDS|CDS	9.0	3.0	13.6	J	COG0102	Ribosomal protein L13
TS29Clo3379|CDS|CDS	9.0	3.0	13.6	J	COG0096	Ribosomal protein S8
TS29Bac03383|CDS|CDS	14.9	5.0	13.5	J	COG0335	Ribosomal protein L19
TS28Bif0827|CDS|CDS	3.7	1.3	13.4	J	COG0199	Ribosomal protein S14
TS29Bif3787|CDS|CDS	3.7	1.3	13.4	J	COG0199	Ribosomal protein S14
Bxyl1687|CDS|CDS	15.7	5.3	13.4	J	COG0480	Translation elongation factors (GTPases)
BactD14457|CDS|CDS	8.8	3.0	13.3	J	COG0197	Ribosomal protein L16/L10E
Bxyl1678|CDS|CDS	8.8	3.0	13.3	J	COG0197	Ribosomal protein L16/L10E
TS29Bac09453|CDS|CDS	8.8	3.0	13.3	J	COG0197	Ribosomal protein L16/L10E
Bcat1281|CDS|CDS	0.7	0.3	13.3	J	COG0050	GTPases - translation elongation factors
Rtor2123|CDS|CDS	5.8	2.0	13.2	J	COG0211	Ribosomal protein L27
TS28Fae18887|CDS|CDS	62.2	21.5	13.1	J	COG0480	Translation elongation factors (GTPases)
TS28Fae17754|CDS|CDS	4.3	1.5	13.1	J	COG0184	Ribosomal protein S15P/S13E
Bxyl3165|CDS|CDS	4.3	1.5	13.1	J	COG3743|COG0261	Uncharacterized conserved protein|Ribosomal protein L21
BactD12745|CDS|CDS	4.3	1.5	13.1	J	COG3743|COG0261	Uncharacterized conserved protein|Ribosomal protein L21
Caer1926|CDS|CDS	17.2	6.0	13.0	J	COG0050	GTPases - translation elongation factors
Bste2309|CDS|CDS	2.9	1.0	13.0	J	COG0081	Ribosomal protein L1
TS28Fae22837|CDS|CDS	16.7	5.8	13.0	J	COG0255	Ribosomal protein L29
TS29Fae05292|CDS|CDS	16.7	5.8	13.0	J	COG0255	Ribosomal protein L29
BactD11553|CDS|CDS	1.7	0.6	13.0	J	COG0264	Translation elongation factor Ts
Msmi750166|CDS|CDS	2.9	1.0	12.9	J	COG1358	Ribosomal protein HS6-type (S12/L30/L7a)
TS29Rum13740|CDS|CDS	91.0	32.0	12.9	J	COG0092	Ribosomal protein S3
TS28Fae00364|CDS|CDS	4.3	1.5	12.9	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Bfin1667|CDS|CDS	5.1	1.8	12.7	J	COG0222	Ribosomal protein L7/L12
Buni1537|CDS|CDS	7.0	2.5	12.7	J	COG0621	2-methylthioadenine synthetase
Aput0475|CDS|CDS	14.0	5.0	12.7	J	COG0809	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)
BactD20041|CDS|CDS	5.6	2.0	12.7	J	COG0480	Translation elongation factors (GTPases)
Bova3923|CDS|CDS	5.6	2.0	12.6	J	COG0525	Valyl-tRNA synthetase
Rtor0525|CDS|CDS	11.1	4.0	12.6	J	COG0088	Ribosomal protein L4
TS29Bac05586|CDS|CDS	8.3	3.0	12.5	J	COG0227	Ribosomal protein L28
Buni1535|CDS|CDS	8.3	3.0	12.5	J	COG0227	Ribosomal protein L28
TS28Fae20865|CDS|CDS	67.4	24.5	12.5	J	COG0050	GTPases - translation elongation factors
TS29Fae07576|CDS|CDS	11.0	4.0	12.5	J	COG0333	Ribosomal protein L32
BactD11129|CDS|CDS	5.5	2.0	12.4	J	COG0335	Ribosomal protein L19
TS29Rum16828|CDS|CDS	80.7	29.5	12.4	J	COG1544	Ribosome-associated protein Y (PSrp-1)
TS29Bac09462|CDS|CDS	19.1	7.0	12.4	J	COG0051	Ribosomal protein S10
TS29Bif1366|CDS|CDS	1.4	0.5	12.4	J	COG0185	Ribosomal protein S19
TS28Bif3994|CDS|CDS	1.4	0.5	12.4	J	COG0185	Ribosomal protein S19
TS29Bac03348|CDS|CDS	31.8	11.7	12.4	J	COG0050	GTPases - translation elongation factors
TS28Fae22095|CDS|CDS	16.3	6.0	12.4	J	COG0244	Ribosomal protein L10
TS28Fae22833|CDS|CDS	9.5	3.5	12.3	J	COG0094	Ribosomal protein L5
Bova2660|CDS|CDS	2.7	1.0	12.3	J	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)
Buni0229|CDS|CDS	29.7	11.0	12.2	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
Dfor1282|CDS|CDS	8.1	3.0	12.2	J	COG0097	Ribosomal protein L6P/L9E

TS29Fae04377|CDS|CDS	35.0	13.0	12.2	J	COG0256	Ribosomal protein L18
BactD14471|CDS|CDS	5.8	2.2	12.2	J	COG0099	Ribosomal protein S13
Bxyl1662|CDS|CDS	5.8	2.2	12.2	J	COG0099	Ribosomal protein S13
TS29Bac11677|CDS|CDS	5.8	2.2	12.2	J	COG0099	Ribosomal protein S13
BactD10953|CDS|CDS	2.7	1.0	12.2	J	COG0254	Ribosomal protein L31
Bxyl4302|CDS|CDS	2.7	1.0	12.2	J	COG0254	Ribosomal protein L31
TS29Rum18651|CDS|CDS	40.1	15.0	12.1	J	COG0230	Ribosomal protein L34
Cbol3498|CDS|CDS	2.7	1.0	12.1	J	COG0261	Ribosomal protein L21
Robe0463|CDS|CDS	8.0	3.0	12.1	J	COG2868	Predicted ribosomal protein
TS29Rum17165|CDS|CDS	12.0	4.5	12.1	J	COG0238	Ribosomal protein S18
TS29Bac09464|CDS|CDS	13.3	5.0	12.1	J	COG0048	Ribosomal protein S12
Caer1974|CDS|CDS	1.3	0.5	12.1	J	COG0089	Ribosomal protein L23
Csci2147|CDS|CDS	1.3	0.5	12.1	J	COG0099	Ribosomal protein S13
Msmi741035|CDS|CDS	0.5	0.2	12.1	J	COG0090	Ribosomal protein L2
TS29Bac09450|CDS|CDS	13.2	5.0	12.0	J	COG0093	Ribosomal protein L14
Bxyl3415|CDS|CDS	6.6	2.5	11.9	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)
TS29Rum21005|CDS|CDS	18.3	7.0	11.9	J	COG0091	Ribosomal protein L22
TS29Bac11674|CDS|CDS	11.7	4.5	11.8	J	COG0024	Methionine aminopeptidase
Cbol5435|CDS|CDS	13.0	5.0	11.8	J	COG0198	Ribosomal protein L24
TS28Rum10132|CDS|CDS	6.5	2.5	11.8	J	COG0098	Ribosomal protein S5
Caer1975|CDS|CDS	6.5	2.5	11.8	J	COG0090	Ribosomal protein L2
TS29Dor0119|CDS|CDS	13.0	5.0	11.8	J	COG0203	Ribosomal protein L17
Cbol5939|CDS|CDS	13.0	5.0	11.8	J	COG1186	Protein chain release factor B
TS29Met0155|CDS|CDS	5.2	2.0	11.8	J	COG1534|COG2023	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein|RNase P subunit RPR2
TS29Rum02975|CDS|CDS	5.2	2.0	11.8	J	COG0049	Ribosomal protein S7
TS28Rum00134|CDS|CDS	20.8	8.0	11.8	J	COG0522	Ribosomal protein S4 and related proteins
TS29Rum20255|CDS|CDS	33.6	13.0	11.7	J	COG0828	Ribosomal protein S21
Bxyl2674|CDS|CDS	2.6	1.0	11.7	J	COG0423	Glycyl-tRNA synthetase (class II)
Begg2625|CDS|CDS	15.4	6.0	11.6	J	COG0091	Ribosomal protein L22
TS29Bac11569|CDS|CDS	5.1	2.0	11.6	J	COG0335	Ribosomal protein L19
TS28Bac0178|CDS|CDS	4.7	1.8	11.6	J	COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases
Bthe3731273|CDS|CDS	0.6	0.3	11.5	J	COG0361	Translation initiation factor 1 (IF-1)
Bthe7330389|CDS|CDS	0.6	0.3	11.5	J	COG0361	Translation initiation factor 1 (IF-1)
Bova3915|CDS|CDS	5.1	2.0	11.5	J	COG0539	Ribosomal protein S1
Robe1742|CDS|CDS	2.5	1.0	11.5	J	COG0199	Ribosomal protein S14
TS28Fae20938|CDS|CDS	7.6	3.0	11.5	J	COG0081	Ribosomal protein L1
Bxyl4315|CDS|CDS	0.8	0.3	11.3	J	COG4108	Peptide chain release factor RF-3
Cnex0779|CDS|CDS	5.0	2.0	11.3	J	COG0049	Ribosomal protein S7
Cnex2193|CDS|CDS	2.5	1.0	11.3	J	COG0291	Ribosomal protein L35
TS28Eub5749|CDS|CDS	5.0	2.0	11.3	J	COG0081	Ribosomal protein L1
TS28Dor2168|CDS|CDS	2.5	1.0	11.3	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
Ehal0628|CDS|CDS	2.5	1.0	11.3	J	COG0048	Ribosomal protein S12
Dfor1285|CDS|CDS	5.0	2.0	11.3	J	COG0094	Ribosomal protein L5
Caer0966|CDS|CDS	2.5	1.0	11.3	J	COG0102	Ribosomal protein L13
Msmi741079|CDS|CDS	1.3	0.5	11.3	J	COG0052	Ribosomal protein S2
Caer0941|CDS|CDS	2.5	1.0	11.3	J	COG0012	Predicted GTPase, probable translation factor
TS29Rum01567|CDS|CDS	5.0	2.0	11.3	J	COG0215	Cysteinyl-tRNA synthetase
TS29Bac10926|CDS|CDS	20.0	8.0	11.3	J	COG0184	Ribosomal protein S15P/S13E
TS28Clo08945|CDS|CDS	5.0	2.0	11.3	J	COG0324	tRNA delta(2)-isopentenylpyrophosphate transferase
Dfor1280|CDS|CDS	5.0	2.0	11.3	J	COG0098	Ribosomal protein S5
TS28Fae22819|CDS|CDS	5.0	2.0	11.3	J	COG0257	Ribosomal protein L36
Csym1952|CDS|CDS	2.5	1.0	11.3	J	COG0052	Ribosomal protein S2
Csci2157|CDS|CDS	5.0	2.0	11.3	J	COG0256	Ribosomal protein L18
Aput0079|CDS|CDS	7.5	3.0	11.3	J	COG0144|COG3270	tRNA and rRNA cytosine-C5-methylases|Uncharacterized conserved protein
TS29Rum13732|CDS|CDS	63.7	25.5	11.3	J	COG0097	Ribosomal protein L6P/L9E
Cbol5437|CDS|CDS	7.5	3.0	11.3	J	COG0186	Ribosomal protein S17
Msmi741545|CDS|CDS	3.1	1.3	11.3	J	COG0050|COG3276|COG5257	GTPases - translation elongation factors|Selenocysteine-specific translation elongation factor|Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)
TS28Rum02469|CDS|CDS	5.0	2.0	11.3	J	COG0050	GTPases - translation elongation factors
TS28Bac6009|CDS|CDS	8.2	3.3	11.2	J	COG0480	Translation elongation factors (GTPases)
TS29Bac11320|CDS|CDS	19.7	8.0	11.2	J	COG0102	Ribosomal protein L13
TS29Rum14232|CDS|CDS	7.2	3.0	10.9	J	COG0048	Ribosomal protein S12
Msmi741054|CDS|CDS	1.2	0.5	10.9	J	COG0200	Ribosomal protein L15
Csci0840|CDS|CDS	1.2	0.5	10.9	J	COG0080	Ribosomal protein L11
TS28Rum10530|CDS|CDS	6.0	2.5	10.9	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
TS28Dor1588|CDS|CDS	7.2	3.0	10.8	J	COG0522	Ribosomal protein S4 and related proteins
Bxyl1478|CDS|CDS	11.9	5.0	10.8	J	COG0292	Ribosomal protein L20
Rgna2511|CDS|CDS	4.7	2.0	10.7	J	COG0100	Ribosomal protein S11
BactD23545|CDS|CDS	5.3	2.3	10.7	J	COG0290	Translation initiation factor 3 (IF-3)
Bste2290|CDS|CDS	9.4	4.0	10.7	J	COG0186	Ribosomal protein S17
BactD14454|CDS|CDS	18.8	8.0	10.7	J	COG0185	Ribosomal protein S19
Buni0616|CDS|CDS	16.9	7.2	10.7	J	COG0090	Ribosomal protein L2
TS29Rum17009|CDS|CDS	63.1	27.0	10.6	J	COG0049	Ribosomal protein S7
CspL21100|CDS|CDS	7.0	3.0	10.6	J	COG0050	GTPases - translation elongation factors
Caer0634|CDS|CDS	7.0	3.0	10.6	J	COG0211	Ribosomal protein L27
TS29Fae04386|CDS|CDS	7.0	3.0	10.6	J	COG0257	Ribosomal protein L36
Cbol6231|CDS|CDS	9.3	4.0	10.6	J	COG0222	Ribosomal protein L7/L12
Bxyl0484|CDS|CDS	2.3	1.0	10.6	J	COG0343	Queuine/archaeosine tRNA-ribosyltransferase
Csym4210|CDS|CDS	2.3	1.0	10.6	J	COG0256	Ribosomal protein L18
Buni2581|CDS|CDS	14.8	6.3	10.6	J	COG0480	Translation elongation factors (GTPases)
TS28Fae22840|CDS|CDS	5.8	2.5	10.4	J	COG0091	Ribosomal protein L22
BactD20481|CDS|CDS	1.1	0.5	10.4	J	COG0073|COG0072	EMAP domain|Phenylalanyl-tRNA synthetase beta subunit
TS29Bac07466|CDS|CDS	8.0	3.5	10.4	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
Msmi741037|CDS|CDS	1.7	0.8	10.3	J	COG0091	Ribosomal protein L22
BactD12039|CDS|CDS	1.7	0.8	10.3	J	COG0480	Translation elongation factors (GTPases)
TS28Met0974|CDS|CDS	1.7	0.8	10.3	J	COG0091	Ribosomal protein L22
Rtor0548|CDS|CDS	4.5	2.0	10.3	J	COG0049	Ribosomal protein S7
TS28Rum14509|CDS|CDS	12.4	5.5	10.2	J	COG0184	Ribosomal protein S15P/S13E
TS29Rum19937|CDS|CDS	12.4	5.5	10.2	J	COG0184	Ribosomal protein S15P/S13E
TS29Rum11337|CDS|CDS	4.5	2.0	10.2	J	COG0173	Aspartyl-tRNA synthetase
Cbol5436|CDS|CDS	4.5	2.0	10.2	J	COG0093	Ribosomal protein L14
TS28Col1446|CDS|CDS	4.5	2.0	10.2	J	COG0094	Ribosomal protein L5

Robe3803|CDS|CDS	11.2	5.0	10.2	J	COG0100	Ribosomal protein S11
TS29Rum17218|CDS|CDS	7.8	3.5	10.2	J	COG0227	Ribosomal protein L28
TS28Rum14884|CDS|CDS	7.8	3.5	10.2	J	COG0227	Ribosomal protein L28
TS28Rum14514|CDS|CDS	17.8	8.0	10.1	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29Rum21168|CDS|CDS	105.0	47.5	10.0	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)
TS29Col0513|CDS|CDS	0.5	23.0	0.1	J	COG0024	Methionine aminopeptidase
Cnex3328|CDS|CDS	0.1	3.1	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Bif3831|CDS|CDS	1.6	74.5	0.1	J	COG0172	Seryl-tRNA synthetase
RintL13310|CDS|CDS	0.1	3.2	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Rum16878|CDS|CDS	1.0	48.0	0.1	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
TS29RumUnc0086|CDS|CDS	2.0	96.0	0.1	J	COG0173	Aspartyl-tRNA synthetase
TS29Bif3328|CDS|CDS	0.8	36.6	0.1	J	COG0162	Tyrosyl-tRNA synthetase
TS29Bif3761|CDS|CDS	0.5	24.4	0.1	J	COG0102	Ribosomal protein L13
TS28Bif0864|CDS|CDS	0.5	24.4	0.1	J	COG0102	Ribosomal protein L13
TS28Fae22788|CDS|CDS	0.5	24.5	0.1	J	COG0621	2-methylthioadenine synthetase
TS29Col1050|CDS|CDS	0.5	26.0	0.1	J	COG0441	Threonyl-tRNA synthetase
TS29Col1254|CDS|CDS	1.0	52.0	0.1	J	COG4108	Peptide chain release factor RF-3
TS29Col0853|CDS|CDS	1.0	53.0	0.1	J	COG0018	Arginyl-tRNA synthetase
TS29Col1724|CDS|CDS	0.5	26.5	0.1	J	COG0264	Translation elongation factor Ts
TS28Bif4917|CDS|CDS	0.5	26.5	0.1	J	COG0242	N-formylmethionyl-tRNA deformylase
TS29Bif3482|CDS|CDS	0.5	26.5	0.1	J	COG0242	N-formylmethionyl-tRNA deformylase
Robe3326|CDS|CDS	0.2	11.0	0.1	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
TS28Bif2061|CDS|CDS	0.8	46.5	0.1	J	COG0018	Arginyl-tRNA synthetase
TS29Col1679|CDS|CDS	0.5	28.0	0.1	J	COG0621	2-methylthioadenine synthetase
Ccom1270|CDS|CDS	0.3	14.0	0.1	J	COG1190	Lysyl-tRNA synthetase (class II)
TS29Col1113|CDS|CDS	1.0	56.0	0.1	J	COG0173	Aspartyl-tRNA synthetase
TS28Fae01734|CDS|CDS	0.5	28.0	0.1	J	COG0594	RNase P protein component
TS29Rum12540|CDS|CDS	1.0	57.0	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Bif0190|CDS|CDS	0.8	43.2	0.1	J	COG0064	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)
TS29Bif3726|CDS|CDS	2.2	126.7	0.1	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
TS29Fae00174|CDS|CDS	0.8	48.0	0.1	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
TS29Bif1379|CDS|CDS	0.2	13.0	0.1	J	COG0098	Ribosomal protein S5
TS28Bif1917|CDS|CDS	0.3	14.8	0.1	J	COG0441	Threonyl-tRNA synthetase
Bpse1165|CDS|CDS	0.3	19.7	0.1	J	COG1530	Ribonucleases G and E
TS29Rum20529|CDS|CDS	1.0	60.0	0.1	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
TS28Bif4800|CDS|CDS	0.3	15.2	0.1	J	COG0048	Ribosomal protein S12
TS29Bif3378|CDS|CDS	0.3	15.2	0.1	J	COG0048	Ribosomal protein S12
TS29Bif4099|CDS|CDS	1.7	101.8	0.1	J	COG0480	Translation elongation factors (GTPases)
TS28Bif0647|CDS|CDS	0.5	28.4	0.1	J	COG0024	Methionine aminopeptidase
TS29Bif3938|CDS|CDS	0.5	28.4	0.1	J	COG0024	Methionine aminopeptidase
TS29Rum19839|CDS|CDS	0.5	32.0	0.1	J	COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases
Csci3178|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
Edol0293|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
Clep2037|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
Bhan1170|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Clo4568|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
Rgna3445|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
Robe2636|CDS|CDS	0.1	4.4	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Bif3934|CDS|CDS	1.0	66.8	0.1	J	COG0442	Prolyl-tRNA synthetase
TS29Bif3567|CDS|CDS	1.7	112.5	0.1	J	COG0143	Methionyl-tRNA synthetase
TS29Bif2069|CDS|CDS	0.3	17.1	0.1	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29Met0199|CDS|CDS	0.4	28.0	0.1	J	COG0060|COG0525|COG0495	Isoleucyl-tRNA synthetase|Valyl-tRNA synthetase|Leucyl-tRNA synthetase
TS29Rum15211|CDS|CDS	0.5	35.0	0.1	J	COG0564	Pseudouridylate synthases, 23S RNA-specific
TS29Bif2700|CDS|CDS	0.3	17.8	0.1	J	COG0264	Translation elongation factor Ts
TS28Bif1987|CDS|CDS	0.3	17.8	0.1	J	COG0264	Translation elongation factor Ts
TS28Fae20099|CDS|CDS	0.5	36.0	0.1	J	COG0060	Isoleucyl-tRNA synthetase
TS28Bif0652|CDS|CDS	1.0	77.8	0.1	J	COG0442	Prolyl-tRNA synthetase
Bthe3732590|CDS|CDS	0.2	14.7	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Bif3025|CDS|CDS	0.8	59.7	0.1	J	COG0012	Predicted GTPase, probable translation factor
TS29Rum13828|CDS|CDS	0.5	43.5	0.1	J	COG0144|COG3270	tRNA and rRNA cytosine-C5-methylases|Uncharacterized conserved protein
TS29Bif1520|CDS|CDS	0.3	22.1	0.1	J	COG0442	Prolyl-tRNA synthetase
Svar2455|CDS|CDS	1.0	87.2	0.1	J	COG0480	Translation elongation factors (GTPases)
Ccom2219|CDS|CDS	1.0	87.2	0.1	J	COG0480	Translation elongation factors (GTPases)
Cmet2527|CDS|CDS	1.0	87.2	0.1	J	COG0480	Translation elongation factors (GTPases)
CspM6211935|CDS|CDS	1.0	87.2	0.1	J	COG0480	Translation elongation factors (GTPases)
TS29Bif0825|CDS|CDS	0.3	23.3	0.0	J	COG0336|COG4752	tRNA-(guanine-N1)-methyltransferase|Uncharacterized protein conserved in bacteria
TS28Bif0460|CDS|CDS	0.3	23.3	0.0	J	COG0336|COG4752	tRNA-(guanine-N1)-methyltransferase|Uncharacterized protein conserved in bacteria
Dfor1337|CDS|CDS	0.1	14.0	0.0	J	COG0525	Valyl-tRNA synthetase
Dfor0369|CDS|CDS	0.3	24.5	0.0	J	COG1190	Lysyl-tRNA synthetase (class II)
TS29Fae00886|CDS|CDS	0.5	49.0	0.0	J	COG0482	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain
TS28Bif1123|CDS|CDS	0.5	49.3	0.0	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
Bsp1160235|CDS|CDS	0.3	26.3	0.0	J	COG0480	Translation elongation factors (GTPases)
TS28Bif4153|CDS|CDS	0.3	26.1	0.0	J	COG0442	Prolyl-tRNA synthetase
TS28Fae10791|CDS|CDS	0.3	26.5	0.0	J	COG0012	Predicted GTPase, probable translation factor
TS29Bif3762|CDS|CDS	0.1	15.3	0.0	J	COG0103	Ribosomal protein S9
TS29Bif2797|CDS|CDS	1.3	134.6	0.0	J	COG0441	Threonyl-tRNA synthetase
Acac2285|CDS|CDS	0.1	7.7	0.0	J	COG0480	Translation elongation factors (GTPases)
TS28Bif4388|CDS|CDS	0.5	58.8	0.0	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
TS29Bif0456|CDS|CDS	0.5	58.8	0.0	J	COG0030	Dimethyladenosine transferase (rRNA methylation)
TS29Rum16537|CDS|CDS	0.5	60.5	0.0	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
TS28Bif0903|CDS|CDS	0.2	24.5	0.0	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
TS29Bif3639|CDS|CDS	0.8	106.5	0.0	J	COG0018	Arginyl-tRNA synthetase
TS28Bif0662|CDS|CDS	0.3	33.3	0.0	J	COG0009	Putative translation factor (SUA5)
TS29Fae00305|CDS|CDS	0.5	70.5	0.0	J	COG0144|COG3270	tRNA and rRNA cytosine-C5-methylases|Uncharacterized conserved protein
TS29Bif4038|CDS|CDS	0.5	71.7	0.0	J	COG0124	Histidyl-tRNA synthetase
TS29Bif1289|CDS|CDS	0.5	73.0	0.0	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
TS29Bif0640|CDS|CDS	0.5	73.3	0.0	J	COG0008	Glutamyl- and glutaminyl-tRNA synthetases
TS29Fae03432|CDS|CDS	0.5	86.5	0.0	J	COG0042	tRNA-dihydrouridine synthase

TS28Bif4914|CDS|CDS	0.3	43.6	0.0	J	COG1186	Protein chain release factor B
TS29Bif3479|CDS|CDS	0.3	43.6	0.0	J	COG1186	Protein chain release factor B
TS29Bif3327|CDS|CDS	0.5	99.8	0.0	J	COG0532	Translation initiation factor 2 (IF-2; GTPase)
TS29Bif3848|CDS|CDS	0.3	59.8	0.0	J	COG1190|COG2898	Lysyl-tRNA synthetase (class II)|Uncharacterized conserved protein
TS28Bif0755|CDS|CDS	0.3	59.8	0.0	J	COG1190|COG2898	Lysyl-tRNA synthetase (class II)|Uncharacterized conserved protein
Bxyl3345|CDS|CDS	6.1	2.5	11.0	J|E|K|L	COG0454|COG1670|COG2818|COG2320|COG0456|COG0346	Histone acetyltransferase HPA2 and related acetyltransferases|Acetyltransferases, including N-acetylases of ribosomal proteins|3-methyladenine DNA glycosylase|Uncharacterized conserved protein|Acetyltransferases|Lactoylglutathione lyase and related lyases
Csci0722|CDS|CDS	8.0	2.0	18.2	J|F	COG0572|COG0441	Uridine kinase|Threonyl-tRNA synthetase
BactD11169|CDS|CDS	8.0	3.5	10.4	J|F	COG0572|COG0441	Uridine kinase|Threonyl-tRNA synthetase
Bpse0475|CDS|CDS	2.0	0.5	18.2	J|K|L	COG0513	Superfamily II DNA and RNA helicases
TS28Met0755|CDS|CDS	3.8	1.1	16.1	J|L	COG0532|COG1372	Translation initiation factor 2 (IF-2; GTPase)|Intein/homing endonuclease
BactD10461|CDS|CDS	8.5	2.5	15.4	J|L	COG1670|COG2818|COG2320	Acetyltransferases, including N-acetylases of ribosomal proteins|3-methyladenine DNA glycosylase|Uncharacterized conserved protein
BDI1477|CDS|acetyltransferase	5.0	2.0	11.3	J|L	COG1670|COG2818|COG2320	Acetyltransferases, including N-acetylases of ribosomal proteins|3-methyladenine DNA glycosylase|Uncharacterized conserved protein
TS29Bac03896|CDS|CDS	1.0	47.0	0.1	J|L	COG1112|COG0539	Superfamily I DNA and RNA helicases and helicase subunits|Ribosomal protein S1
BDI1691|CDS|phosphoglucomutase	10.0	4.0	11.3	J|M|G	COG1208|COG1210|COG1109	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)|UDP-glucose pyrophosphorylase|Phosphomannomutase
Bcap1540|CDS|CDS	17.0	1.0	77.2	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
Acac3518|CDS|CDS	7.3	1.0	33.3	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
CspM6210271|CDS|CDS	7.0	1.0	31.8	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
Ehal1349|CDS|CDS	6.8	1.5	20.7	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
FpraM2122358|CDS|CDS	83.4	34.0	11.1	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
Robe1488|CDS|CDS	26.2	11.5	10.3	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
Cbol1182|CDS|CDS	20.0	9.0	10.1	J|M|I	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
BactD14439|CDS|CDS	13.2	0.3	180.3	K	COG0250	Transcription antiterminator
Buni0213|CDS|CDS	15.7	1.0	71.1	K	COG0195	Transcription elongation factor
TS28Rum14419|CDS|CDS	7.8	0.5	71.1	K	COG1609	Transcriptional regulators
TS29Bac11680|CDS|CDS	7.2	0.5	65.6	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
Robe0625|CDS|CDS	76.2	6.0	57.6	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Rum10463|CDS|CDS	12.0	1.0	54.5	K	COG1420	Transcriptional regulator of heat shock gene
Caer1004|CDS|CDS	11.0	1.0	49.9	K	COG1609	Transcriptional regulators
TS28Fae13861|CDS|CDS	5.5	0.5	49.9	K	COG0195	Transcription elongation factor
Bxyl1979|CDS|CDS	2.8	0.3	49.9	K	COG0557	Exoribonuclease R
Cbol2921|CDS|CDS	10.7	1.0	48.4	K	COG1278	Cold shock proteins
Bxyl2502|CDS|CDS	2.7	0.3	37.3	K	COG0195	Transcription elongation factor
Bfin1666|CDS|CDS	3.8	0.5	34.2	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
Bxyl1659|CDS|CDS	7.5	1.0	34.1	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
DpigATC0212|CDS|CDS	7.5	1.0	34.0	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
TS28Rum16432|CDS|CDS	7.5	1.0	34.0	K	COG1959	Predicted transcriptional regulator
TS29Rum04952|CDS|CDS	4.7	0.7	31.8	K	COG0250	Transcription antiterminator
TS29Bac07474|CDS|CDS	6.8	1.0	30.6	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bova0437|CDS|CDS	3.3	0.5	29.9	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
BactD21826|CDS|CDS	3.3	0.5	29.9	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
FpraM2121830|CDS|CDS	6.6	1.0	29.9	K	COG1420	Transcriptional regulator of heat shock gene

TS28Fae18996|CDS|CDS	6.5	1.0	29.5	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bthe3732368|CDS|CDS	9.3	1.5	28.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bfin0906|CDS|CDS	9.3	1.5	28.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bthe7331684|CDS|CDS	9.3	1.5	28.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
BactD12633|CDS|CDS	9.3	1.5	28.0	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
ShigspD91146|CDS|CDS	6.0	1.0	27.2	K	COG1414	Transcriptional regulator
CspM6210742|CDS|CDS	3.0	0.5	27.2	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
BactD24488|CDS|CDS	5.4	1.0	24.5	K	COG1475	Predicted transcriptional regulators
Robe1907|CDS|CDS	15.8	3.0	23.8	K	COG1278	Cold shock proteins
Buni1628|CDS|CDS	1.7	0.3	22.7	K	COG2183	Transcriptional accessory protein
Rumhyd1096|CDS|CDS	5.0	1.0	22.7	K	COG1609	Transcriptional regulators
RintL12661|CDS|CDS	5.0	1.0	22.7	K	COG1158	Transcription termination factor
BactD20038|CDS|CDS	7.4	1.5	22.5	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
Bova1640|CDS|CDS	2.5	0.5	22.2	K	COG0846	NAD-dependent protein deacetylases, SIR2 family
Bxyl3700|CDS|CDS	9.8	2.0	22.1	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Bova0752|CDS|CDS	13.5	2.8	21.6	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS28Fae19034|CDS|CDS	1.6	0.3	21.6	K	COG0782	Transcription elongation factor
Aput2177|CDS|CDS	4.7	1.0	21.2	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
Msmi751317|CDS|CDS	1.1	0.3	20.0	K	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB
Casp1823|CDS|CDS	4.0	1.0	18.2	K	COG0583	Transcriptional regulator
Cbol1615|CDS|CDS	4.0	1.0	18.2	K	COG2186|COG1802	Transcriptional regulators|Transcriptional regulators
TS29Bac05129|CDS|CDS	36.0	9.0	18.2	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
TS28Fae21805|CDS|CDS	1.3	0.3	18.2	K	COG0846	NAD-dependent protein deacetylases, SIR2 family
Bxyl3927|CDS|CDS	4.6	1.2	18.0	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
Cbol2781|CDS|CDS	11.0	3.0	16.6	K	COG2186	Transcriptional regulators
Rtor0295|CDS|CDS	3.5	1.0	15.9	K	COG0250	Transcription antiterminator
TS29Par551|CDS|CDS	10.5	3.0	15.9	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Rum08196|CDS|CDS	3.5	1.0	15.9	K	COG0250	Transcription antiterminator
Robe3026|CDS|CDS	8.5	2.5	15.4	K	COG4465	Pleiotropic transcriptional repressor
Bova0739|CDS|CDS	6.3	2.0	14.2	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS29Bac03346|CDS|CDS	17.9	5.8	13.9	K	COG0250	Transcription antiterminator
Bxyl1697|CDS|CDS	17.9	5.8	13.9	K	COG0250	Transcription antiterminator
Bxyl1691|CDS|CDS	17.3	5.7	13.9	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS29Rum14790|CDS|CDS	1.5	0.5	13.6	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS29Clo3724|CDS|CDS	1.0	0.3	13.6	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
ShigspD90056|CDS|CDS	3.0	1.0	13.6	K	COG1309	Transcriptional regulator
Robe0356|CDS|CDS	3.0	1.0	13.6	K	COG0557	Exoribonuclease R
Hfil0357|CDS|CDS	6.0	2.0	13.6	K	COG0557	Exoribonuclease R
Cbol5958|CDS|CDS	3.0	1.0	13.6	K	COG1609	Transcriptional regulators
Bthe3731478|CDS|CDS	3.0	1.0	13.6	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Acac3486|CDS|CDS	3.0	1.0	13.6	K	COG3711|COG3933	Transcriptional antiterminator|Transcriptional antiterminator
Dlon2751|CDS|CDS	3.0	1.0	13.6	K	COG1158	Transcription termination factor
TS28Dor2360|CDS|CDS	1.5	0.5	13.6	K	COG0250	Transcription antiterminator
Casp4805|CDS|CDS	3.0	1.0	13.6	K	COG2188	Transcriptional regulators
Dfor3178|CDS|CDS	3.0	1.0	13.6	K	COG1316	Transcriptional regulator
TS28Rum06224|CDS|CDS	1.5	0.5	13.6	K	COG0195	Transcription elongation factor
Dlon1156|CDS|CDS	1.5	0.5	13.6	K	COG0250	Transcription antiterminator
TS28Clo03068|CDS|CDS	12.0	4.0	13.6	K	COG1420	Transcriptional regulator of heat shock gene
TS28Clo01612|CDS|CDS	3.0	1.0	13.6	K	COG2183	Transcriptional accessory protein
TS28Bac5421|CDS|CDS	1.5	0.5	13.6	K	COG1733	Predicted transcriptional regulators
TS28Ali2077|CDS|CDS	3.0	1.0	13.6	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS28Rum14517|CDS|CDS	18.0	6.0	13.6	K	COG0195	Transcription elongation factor
TS29Bac07269|CDS|CDS	21.6	7.5	13.1	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
Bthe7335410|CDS|CDS	3.5	1.3	12.7	K	COG1158	Transcription termination factor
TS28Clo05718|CDS|CDS	11.0	4.0	12.5	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Fae10763|CDS|CDS	23.1	8.5	12.3	K	COG1420	Transcriptional regulator of heat shock gene
Buni0623|CDS|CDS	89.8	33.5	12.2	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
BactD13771|CDS|CDS	3.6	1.3	12.2	K	COG0195	Transcription elongation factor
BactD13503|CDS|CDS	2.6	1.0	12.0	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
Dfor1153|CDS|CDS	10.5	4.0	11.9	K	COG0250	Transcription antiterminator
Aput1109|CDS|CDS	21.0	8.0	11.9	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS28Fae17996|CDS|CDS	2.6	1.0	11.7	K	COG0195	Transcription elongation factor
Begg2652|CDS|CDS	15.3	6.0	11.5	K	COG0250	Transcription antiterminator
FpraM2120253|CDS|CDS	70.3	28.0	11.4	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS28Fae08669|CDS|CDS	2.5	1.0	11.3	K	COG1609	Transcriptional regulators
TS28Fae18648|CDS|CDS	2.5	1.0	11.3	K	COG1396	Predicted transcriptional regulators
Cbol6589|CDS|CDS	5.0	2.0	11.3	K	COG2186	Transcriptional regulators
TS29Bac04442|CDS|CDS	5.0	2.0	11.3	K	COG0789	Predicted transcriptional regulators
TS29Bac02015|CDS|CDS	5.0	2.0	11.3	K	COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Rtor0136|CDS|CDS	7.5	3.0	11.3	K	COG1396	Predicted transcriptional regulators
Bcac1758|CDS|CDS	1.2	0.5	11.3	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
Msmi741542|CDS|CDS	0.8	0.3	10.9	K	COG1095	DNA-directed RNA polymerase, subunit E'
Msmi750175|CDS|CDS	0.8	0.3	10.9	K	COG1095	DNA-directed RNA polymerase, subunit E'
TS28Met1211|CDS|CDS	0.6	0.3	10.9	K	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB
Buni3063|CDS|CDS	2.8	1.2	10.7	K	COG1508	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog
BactD14444|CDS|CDS	15.2	6.5	10.6	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS28Eub0216|CDS|CDS	3.5	1.5	10.6	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
TS28Rum00133|CDS|CDS	34.5	15.0	10.4	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
TS28Fae21836|CDS|CDS	6.5	2.8	10.4	K	COG2186|COG1802	Transcriptional regulators|Transcriptional regulators
TS28Met0883|CDS|CDS	1.5	0.7	10.2	K	COG0195	Transcription elongation factor
Msmi740887|CDS|CDS	1.5	0.7	10.2	K	COG0195	Transcription elongation factor
Msmi750797|CDS|CDS	1.5	0.7	10.2	K	COG0195	Transcription elongation factor
Clep0604|CDS|CDS	6.3	2.8	10.1	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
Robe2662|CDS|CDS	0.3	12.2	0.1	K	COG3655	Predicted transcriptional regulator
TS29Fae09850|CDS|CDS	1.5	68.3	0.1	K	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen
TS29Fae04404|CDS|CDS	1.0	46.0	0.1	K	COG0195	Transcription elongation factor
TS29Col0092|CDS|CDS	0.5	23.0	0.1	K	COG0782	Transcription elongation factor
TS29Fae06652|CDS|CDS	0.5	23.0	0.1	K	COG1475	Predicted transcriptional regulators
TS29Rum19594|CDS|CDS	1.0	48.0	0.1	K	COG2207	AraC-type DNA-binding domain-containing proteins
TS29Rum00367|CDS|CDS	1.0	48.0	0.1	K	COG0583	Transcriptional regulator
Dfor0448|CDS|CDS	0.1	5.5	0.1	K	COG0583	Transcriptional regulator
TS29Rum16863|CDS|CDS	0.5	25.0	0.1	K	COG0454	Histone acetyltransferase HPA2 and related acetyltransferases

TS29Rum13581|CDS|CDS	0.5	28.0	0.1	K	COG0568|COG1191	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)|DNA-directed RNA polymerase specialized sigma subunit
TS29Rum01249|CDS|CDS	0.5	29.0	0.1	K	COG0454	Histone acetyltransferase HPA2 and related acetyltransferases
TS28Bif4627|CDS|CDS	0.3	15.8	0.1	K	COG1316	Transcriptional regulator
BactD12821|CDS|CDS	0.1	8.0	0.1	K	COG1521	Putative transcriptional regulator, homolog of Bvg accessory factor
TS29Fae09975|CDS|CDS	0.5	33.5	0.1	K	COG1321	Mn-dependent transcriptional regulator
TS29Bif3502|CDS|CDS	2.2	149.3	0.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
TS29Bif3221|CDS|CDS	0.3	17.4	0.1	K	COG1316	Transcriptional regulator
TS29Bif2544|CDS|CDS	0.7	48.4	0.1	K	COG0568	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
TS28Bif4941|CDS|CDS	2.2	158.3	0.1	K	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit
Bpse1724|CDS|CDS	0.3	24.5	0.1	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS29Rum16786|CDS|CDS	0.5	37.5	0.1	K	COG1609	Transcriptional regulators
TS29Bif3226|CDS|CDS	0.3	19.0	0.1	K	COG0782	Transcription elongation factor
TS28Bif4632|CDS|CDS	0.3	19.0	0.1	K	COG0782	Transcription elongation factor
TS29Rum20239|CDS|CDS	1.0	77.0	0.1	K	COG1293	Predicted RNA-binding protein homologous to eukaryotic snRNP
Robe2731|CDS|CDS	0.1	9.8	0.1	K	COG0583	Transcriptional regulator
TS29Rum13704|CDS|CDS	0.5	44.5	0.1	K	COG0583	Transcriptional regulator
TS29Bif2367|CDS|CDS	0.8	72.3	0.0	K	COG1414	Transcriptional regulator
TS29Bif3800|CDS|CDS	0.5	49.3	0.0	K	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit
Ehal2096|CDS|CDS	0.1	11.2	0.0	K	COG0583	Transcriptional regulator
TS29Rum20808|CDS|CDS	0.5	52.0	0.0	K	COG4189	Predicted transcriptional regulator
Dfor3096|CDS|CDS	0.3	28.0	0.0	K	COG3655	Predicted transcriptional regulator
TS29Fae09118|CDS|CDS	0.5	54.5	0.0	K	COG2188	Transcriptional regulators
TS28Bif0944|CDS|CDS	0.5	56.4	0.0	K	COG1414	Transcriptional regulator
TS29Bif2366|CDS|CDS	0.5	56.4	0.0	K	COG1414	Transcriptional regulator
TS29Bif0573|CDS|CDS	0.3	32.6	0.0	K	COG1609	Transcriptional regulators
TS28Bif1207|CDS|CDS	0.3	32.6	0.0	K	COG1609	Transcriptional regulators
Ccom0524|CDS|CDS	0.1	18.0	0.0	K	COG0583	Transcriptional regulator
TS29Bif0465|CDS|CDS	0.5	82.5	0.0	K	COG1475	Predicted transcriptional regulators
TS29Fae08964|CDS|CDS	0.3	55.0	0.0	K	COG2188	Transcriptional regulators
TS28Bif1198|CDS|CDS	0.3	42.5	0.0	K	COG1609	Transcriptional regulators
TS29Bif4136|CDS|CDS	0.3	43.2	0.0	K	COG1609	Transcriptional regulators
TS28Bif5008|CDS|CDS	0.3	43.2	0.0	K	COG1609	Transcriptional regulators
TS29Fae06037|CDS|CDS	0.5	87.5	0.0	K	COG1609	Transcriptional regulators
TS29Rum11457|CDS|CDS	0.5	110.0	0.0	K	COG2909	ATP-dependent transcriptional regulator
TS29Rum11584|CDS|CDS	0.2	44.5	0.0	K	COG0846	NAD-dependent protein deacetylases, SIR2 family
TS29Bif0377|CDS|CDS	0.3	93.5	0.0	K	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit
TS29Bif0579|CDS|CDS	0.3	81.5	0.0	K	COG1609	Transcriptional regulators
TS29Bif3615|CDS|CDS	0.3	104.3	0.0	K	COG1414	Transcriptional regulator
Buni0316|CDS|CDS	9.7	1.0	44.2	K|G	COG1940	Transcriptional regulator/sugar kinase
BDI1657|CDS|ribokinase	4.0	1.0	18.2	K|G	COG1609|COG0524|COG1349|COG2771	Transcriptional regulators|Sugar kinases, ribokinase family|Transcriptional regulators of sugar metabolism|DNA-binding HTH domain-containing proteins
Cbol4822|CDS|CDS	15.0	4.0	17.0	K|G	COG2376|COG2390	Dihydroxyacetone kinase|Transcriptional regulator, contains sigma factor-related N-terminal domain
Rgna0964|CDS|CDS	1.5	0.5	13.6	K|G	COG1349	Transcriptional regulators of sugar metabolism
Cbol2158|CDS|CDS	3.0	1.0	13.6	K|G	COG1940	Transcriptional regulator/sugar kinase
BactD21070|CDS|CDS	2.5	1.0	11.3	K|G	COG1940	Transcriptional regulator/sugar kinase
Robe3270|CDS|CDS	8.5	3.5	11.0	K|G	COG1349	Transcriptional regulators of sugar metabolism
Ehal1017|CDS|CDS	3.5	1.5	10.6	K|G	COG2376|COG2390	Dihydroxyacetone kinase|Transcriptional regulator, contains sigma factor-related N-terminal domain
TS28Clo06356|CDS|CDS	7.0	3.0	10.6	K|H	COG0340|COG1654	Biotin-(acetyl-CoA carboxylase) ligase|Biotin operon repressor
TS28Fae19466|CDS|CDS	0.5	52.0	0.0	K|H	COG0351|COG0352|COG1992|COG0819	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase|Thiamine monophosphate synthase|Uncharacterized conserved protein|Putative transcription activator
TS29Bac11801|CDS|CDS	0.3	12.0	0.1	K|J|L	COG0513	Superfamily II DNA and RNA helicases
Casp3410|CDS|CDS	3.0	1.0	13.6	K|L	COG0553|COG4279	Superfamily II DNA/RNA helicases, SNF2 family|Uncharacterized conserved protein
TS28Clo04581|CDS|CDS	3.0	1.0	13.6	K|L	COG1595|COG2255	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog|Holliday junction resolvasome, helicase subunit
TS28Met0885|CDS|CDS	1.8	0.7	11.9	K|L	COG0086|COG1372	DNA-directed RNA polymerase, beta' subunit/160 kD subunit|Intein/homing endonuclease
TS29Bac10519|CDS|CDS	3.0	140.0	0.1	K|L	COG4646	DNA methylase
TS29Rum21230|CDS|CDS	1.0	46.7	0.1	K|L	COG4646	DNA methylase
Robe2639|CDS|CDS	3.0	144.5	0.1	K|L	COG4646	DNA methylase
FpraM2121389|CDS|CDS	3.0	145.0	0.1	K|L	COG4646	DNA methylase
TS29Fae03658|CDS|CDS	0.5	26.0	0.1	K|L	COG1200	RecG-like helicase
TS29Fae10411|CDS|CDS	3.0	159.5	0.1	K|L	COG4646	DNA methylase
TS29Bif3302|CDS|CDS	2.2	123.7	0.1	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
TS28Bif4704|CDS|CDS	2.2	123.7	0.1	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
TS28Eub6362|CDS|CDS	3.8	228.8	0.1	K|L	COG4646	DNA methylase
Dfor3055|CDS|CDS	6.5	397.9	0.1	K|L	COG4646	DNA methylase
TS29RumUnc1595|CDS|CDS	2.0	135.0	0.1	K|L	COG1197	Transcription-repair coupling factor (superfamily II helicase)
TS28Fae22501|CDS|CDS	1.0	72.0	0.1	K|L	COG4646	DNA methylase
TS29Rum11733|CDS|CDS	4.0	359.5	0.1	K|L	COG4646	DNA methylase
TS29Bif0823|CDS|CDS	0.9	92.5	0.0	K|L	COG1200	RecG-like helicase
Hfil2119|CDS|CDS	1.0	102.4	0.0	K|L	COG4646	DNA methylase
TS29Fae00379|CDS|CDS	1.0	139.0	0.0	K|L	COG1199	Rad3-related DNA helicases
TS28Bif0462|CDS|CDS	0.5	70.8	0.0	K|L	COG1200	RecG-like helicase
Cnex1513|CDS|CDS	1.0	151.0	0.0	K|L	COG4646	DNA methylase
Ccom0363|CDS|CDS	0.3	51.7	0.0	K|L	COG4646	DNA methylase
TS29Dor2220|CDS|CDS	0.5	106.0	0.0	K|L	COG2176|COG1199	DNA polymerase III, alpha subunit (gram-positive type)|Rad3-related DNA helicases
TS29Bif2118|CDS|CDS	0.3	81.8	0.0	K|L	COG0553|COG4279	Superfamily II DNA/RNA helicases, SNF2 family|Uncharacterized conserved protein
TS28Rum06767|CDS|CDS	3.0	0.3	40.9	K|L|T	COG0515	Serine/threonine protein kinase
TS28Rum01136|CDS|CDS	16.2	3.5	21.0	K|L|T	COG0515|COG2815|COG5616|COG0631|COG2319|COG3899	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Predicted integral membrane protein|Serine/threonine protein phosphatase|FOG: WD40 repeat|Predicted ATPase
TS29Rum13694|CDS|CDS	1.0	90.0	0.1	K|L|T	COG4886|COG4252|COG0515|COG2815|COG1357|COG0631|COG2319|COG3899|COG1716|COG5635	Leucine-rich repeat (LRR) protein|Predicted transmembrane sensor domain|Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Uncharacterized low-complexity proteins|Serine/threonine protein phosphatase|FOG: WD40 repeat|Predicted ATPase|FOG: FHA domain|Predicted NTPase (NACHT family)
TS28Bif4495|CDS|CDS	0.8	69.5	0.0	K|L|T	COG0515|COG2815|COG3899	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Predicted ATPase

TS29Fae05647|CDS|CDS	1.0	96.0	0.0	K|L|T	COG0515|COG2815|COG3899	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Predicted ATPase
TS28Bif4494|CDS|CDS	0.3	69.3	0.0	K|L|T	COG3391|COG0515|COG2815|COG5616|COG3899	Uncharacterized conserved protein|Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Predicted integral membrane protein|Predicted ATPase
TS29Bif0525|CDS|CDS	0.3	71.3	0.0	K|L|T	COG0515|COG2815|COG3899	Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Predicted ATPase
TS28Rum16414|CDS|CDS	5.0	0.5	45.4	K|L|V	COG4096|COG3886|COG1061	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Predicted HKD family nuclease|DNA or RNA helicases of superfamily II
TS28Eub7322|CDS|CDS	0.5	24.0	0.1	K|L|V	COG4096|COG3886|COG1061	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Predicted HKD family nuclease|DNA or RNA helicases of superfamily II
TS29Fae03478|CDS|CDS	4.0	250.0	0.1	K|L|V	COG4096|COG3886|COG1061	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Predicted HKD family nuclease|DNA or RNA helicases of superfamily II
TS29Rum20052|CDS|CDS	0.5	61.0	0.0	K|L|V	COG4096|COG3886|COG1061	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Predicted HKD family nuclease|DNA or RNA helicases of superfamily II
FpraM2121013|CDS|CDS	4.3	1.0	19.7	K|M|G	COG4464|COG1316	Capsular polysaccharide biosynthesis protein|Transcriptional regulator
TS28Dor1748|CDS|CDS	238.0	2.0	540.2	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Rum01137|CDS|CDS	11.0	0.5	99.9	K|T	COG0789|COG0631	Predicted transcriptional regulators|Serine/threonine protein phosphatase
TS28Rum10489|CDS|CDS	6.0	0.5	54.5	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Fae03017|CDS|CDS	9.0	1.0	40.9	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Bif1322|CDS|CDS	7.0	1.0	31.8	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Fae10784|CDS|CDS	40.0	7.0	25.9	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Clo0809|CDS|CDS	15.0	3.0	22.7	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS28Fae14042|CDS|CDS	11.5	2.3	22.4	K|T	COG3604|COG4624	Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains|Iron only hydrogenase large subunit, C-terminal domain
TS29Rum07087|CDS|CDS	10.0	3.0	15.1	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28RumUnc0141|CDS|CDS	3.0	1.0	13.6	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Rum03656|CDS|CDS	3.0	1.0	13.6	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS28Col0012|CDS|CDS	3.0	1.0	13.6	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS28Eub0060|CDS|CDS	3.0	1.0	13.6	K|T	COG3604|COG5564	Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains|Predicted TIM-barrel enzyme, possibly a dioxygenase
TS28Fae22647|CDS|CDS	2.5	1.0	11.3	K|T	COG4753|COG3279	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator of the LytR/AlgR family
TS28Rum12330|CDS|CDS	20.0	8.0	11.3	K|T	COG2770|COG4252|COG3437|COG2206	FOG: HAMP domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|HD-GYP domain
TS28Fae21039|CDS|CDS	21.5	9.0	10.8	K|T	COG1974|COG2932	SOS-response transcriptional repressors (RecA-mediated autopeptidases)|Predicted transcriptional regulator
TS29Bac02534|CDS|CDS	37.6	16.0	10.7	K|T	COG0642|COG5002|COG2202|COG2770|COG2203|COG3437|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Osmosensitive K+ channel histidine kinase
TS28Rum11325|CDS|CDS	7.0	3.0	10.6	K|T	COG0745|COG0784|COG3706|COG3707	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|FOG: CheY-like receiver|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulator with putative antiterminator output domain
TS28Fae15090|CDS|CDS	0.5	24.5	0.1	K|T	COG0789|COG0631	Predicted transcriptional regulators|Serine/threonine protein phosphatase
TS29Rum20340|CDS|CDS	1.0	50.0	0.1	K|T	COG4753|COG2207|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS28Fae21327|CDS|CDS	0.7	35.0	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS29Col1822|CDS|CDS	1.5	80.0	0.1	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS29Fae05517|CDS|CDS	1.0	54.0	0.1	K|T	COG4753|COG3279	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator of the LytR/AlgR family
TS28Rum01910|CDS|CDS	0.3	14.0	0.1	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS29Fae09631|CDS|CDS	1.0	59.0	0.1	K|T	COG4585|COG2197	Signal transduction histidine kinase|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain
TS29Fae08798|CDS|CDS	0.3	21.0	0.1	K|T	COG2770|COG4252|COG3437|COG2206	FOG: HAMP domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|HD-GYP domain
TS28Rum13916|CDS|CDS	1.0	64.0	0.1	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Rum16916|CDS|CDS	1.5	98.0	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS29Fae03363|CDS|CDS	1.0	69.0	0.1	K|T	COG3279	Response regulator of the LytR/AlgR family
TS29Rum16573|CDS|CDS	1.0	70.0	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS29Rum00191|CDS|CDS	0.5	37.0	0.1	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Bif3212|CDS|CDS	0.3	19.5	0.1	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Rum00186|CDS|CDS	0.3	24.0	0.1	K|T	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
TS29Rum16549|CDS|CDS	1.0	86.0	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein

TS29Bac05460|CDS|CDS	0.3	29.5	0.1	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS29Fae05594|CDS|CDS	1.0	114.5	0.0	K|T	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
TS29Fae10051|CDS|CDS	1.0	117.0	0.0	K|T	COG4753|COG2207|COG4936|COG4977	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Predicted sensor domain|Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain
TS29Fae06785|CDS|CDS	0.7	91.0	0.0	K|T	COG3275|COG2972|COG4936|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain|Predicted cobalamin binding protein
TS29Fae07228|CDS|CDS	1.0	141.0	0.0	K|T	COG3275|COG2972|COG4936	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted sensor domain
TS29Col0151|CDS|CDS	0.5	77.0	0.0	K|T	COG2770|COG4252|COG3437|COG2206	FOG: HAMP domain|Predicted transmembrane sensor domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|HD-GYP domain
TS29Fae07402|CDS|CDS	197.0	6.0	149.1	L	COG0350	Methylated DNA-protein cysteine methyltransferase
TS28Fae15389|CDS|CDS	42.8	1.5	129.4	L	COG0776	Bacterial nucleoid DNA-binding protein
Caer1102|CDS|CDS	5.5	0.3	74.9	L	COG3547	Transposase and inactivated derivatives
TS28Fae02025|CDS|CDS	23.5	1.5	71.1	L	COG0776	Bacterial nucleoid DNA-binding protein
Bple2878|CDS|CDS	10.1	0.7	68.7	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Bthe7331652|CDS|CDS	5.9	0.5	53.7	L	COG3436	Transposase and inactivated derivatives
TS28Col0361|CDS|CDS	11.0	1.0	49.9	L	COG0497	ATPase involved in DNA repair
TS29Bac08102|CDS|CDS	41.0	4.0	46.5	L	COG0776	Bacterial nucleoid DNA-binding protein
ShigspD91210|CDS|CDS	5.0	0.5	45.4	L	COG0178	Excinuclease ATPase subunit
TS28Clo09221|CDS|CDS	47.7	5.0	43.3	L	COG2812	DNA polymerase III, gamma/tau subunits
TS28Rum14944|CDS|CDS	9.5	1.0	43.1	L	COG0272	NAD-dependent DNA ligase (contains BRCT domain type II)
TS28Clo10370|CDS|CDS	8.0	1.0	36.3	L	COG0270	Site-specific DNA methylase
Bryfor0301|CDS|CDS	12.0	1.5	36.3	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Bthe7335644|CDS|CDS	2.3	0.3	31.8	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Bcac1992|CDS|CDS	3.5	0.5	31.8	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
TS29Bac09910|CDS|CDS	2.3	0.3	30.6	L	COG0776	Bacterial nucleoid DNA-binding protein
TS28Rum15890|CDS|CDS	6.5	1.0	29.5	L	COG0629	Single-stranded DNA-binding protein
BactD20034|CDS|CDS	13.0	2.0	29.4	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
TS28Bac4655|CDS|CDS	5.3	0.8	29.1	L	COG0497	ATPase involved in DNA repair
TS29Bac11232|CDS|CDS	7.3	1.2	28.5	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Bova0241|CDS|CDS	6.2	1.0	28.1	L	COG0514	Superfamily II DNA helicase
TS29Par798|CDS|CDS	3.0	0.5	27.2	L	COG1372|COG0468	Intein/homing endonuclease|RecA/RadA recombinase
Msmi751024|CDS|CDS	1.2	0.2	27.2	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
TS28Clo05057|CDS|CDS	6.0	1.0	27.2	L	COG0305	Replicative DNA helicase
Acod0610|CDS|CDS	6.0	1.0	27.2	L	COG1643	HrpA-like helicases
Cmit1568|CDS|CDS	11.0	2.0	25.0	L	COG3547	Transposase and inactivated derivatives
Even0454|CDS|CDS	1.8	0.3	25.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum01721|CDS|CDS	27.0	5.0	24.5	L	COG0629	Single-stranded DNA-binding protein
Bthe7335545|CDS|CDS	7.8	1.5	23.5	L	COG0116|COG1092	Predicted N6-adenine-specific DNA methylase|Predicted SAM-dependent methyltransferases
Bova3913|CDS|CDS	2.5	0.5	22.7	L	COG3344	Retron-type reverse transcriptase
BactD24194|CDS|CDS	2.5	0.5	22.7	L	COG3344	Retron-type reverse transcriptase
TS29Bac06951|CDS|CDS	5.0	1.0	22.7	L	COG3449	DNA gyrase inhibitor
TS28Fae16374|CDS|CDS	10.0	2.0	22.7	L	COG0419	ATPase involved in DNA repair
TS28Bac2303|CDS|CDS	3.3	0.7	22.7	L	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes
TS28Bac2095|CDS|CDS	1.7	0.3	22.7	L	COG1573	Uracil-DNA glycosylase
Buni0980|CDS|CDS	1.7	0.3	22.7	L	COG1573	Uracil-DNA glycosylase
Bxyl1700|CDS|CDS	9.4	2.0	21.4	L	COG4974	Site-specific recombinase XerD
Buni3576|CDS|CDS	4.5	1.0	20.4	L	COG0468	RecA/RadA recombinase
TS28Rum05048|CDS|CDS	4.5	1.0	20.4	L	COG3344|COG1518|COG1468	Retron-type reverse transcriptase|Uncharacterized protein predicted to be involved in DNA repair|RecB family exonuclease
Aput0978|CDS|CDS	9.0	2.0	20.4	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
Bxyl1701|CDS|CDS	4.3	1.0	19.4	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
Buni0861|CDS|CDS	8.5	2.0	19.3	L	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes
CspSS20429|CDS|CDS	2.0	0.5	18.2	L	COG0675	Transposase and inactivated derivatives
Bfra31120412|CDS|CDS	4.0	1.0	18.2	L	COG0514	Superfamily II DNA helicase
Caer0012|CDS|CDS	2.0	0.5	18.2	L	COG0593	ATPase involved in DNA replication initiation
ShigspD92610|CDS|CDS	2.0	0.5	18.2	L	COG2255	Holliday junction resolvasome, helicase subunit
TS29Bac11451|CDS|CDS	52.5	14.0	17.0	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
BactD10140|CDS|CDS	5.6	1.5	16.9	L	COG3436	Transposase and inactivated derivatives
Aput0249|CDS|CDS	5.5	1.5	16.6	L	COG0272	NAD-dependent DNA ligase (contains BRCT domain type II)
Buni1782|CDS|CDS	1.8	0.5	16.6	L	COG0708	Exonuclease III
Bxyl2519|CDS|CDS	5.3	1.5	16.1	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
TS29Bac11452|CDS|CDS	24.0	7.0	15.6	L	COG4974	Site-specific recombinase XerD
Buni3017|CDS|CDS	13.6	4.0	15.5	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Bxyl4353|CDS|CDS	1.1	0.3	15.4	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
Bpse1603|CDS|CDS	3.3	1.0	15.1	L	COG4974|COG4973	Site-specific recombinase XerD|Site-specific recombinase XerC
TS29Bac03350|CDS|CDS	13.1	4.0	14.8	L	COG4974	Site-specific recombinase XerD
Buni2885|CDS|CDS	4.3	1.3	14.8	L	COG0587	DNA polymerase III, alpha subunit
TS28Rum00945|CDS|CDS	6.5	2.0	14.8	L	COG2812	DNA polymerase III, gamma/tau subunits
TS28Bac4342|CDS|CDS	2.0	0.7	13.6	L	COG0323	DNA mismatch repair enzyme (predicted ATPase)
BactD13464|CDS|CDS	1.0	0.3	13.6	L	COG1074	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)
TS29Rum03743|CDS|CDS	1.0	0.3	13.6	L	COG0177	Predicted EndoIII-related endonuclease
TS28Bac2186|CDS|CDS	1.0	0.3	13.6	L	COG0178	Excinuclease ATPase subunit
Buni0443|CDS|CDS	1.0	0.3	13.6	L	COG0556	Helicase subunit of the DNA excision repair complex
BactD12341|CDS|CDS	1.0	0.3	13.6	L	COG0497	ATPase involved in DNA repair
Buni0436|CDS|CDS	1.0	0.3	13.6	L	COG0178	Excinuclease ATPase subunit
TS28Rum05868|CDS|CDS	1.0	0.3	13.6	L	COG0177	Predicted EndoIII-related endonuclease
Buni3546|CDS|CDS	1.5	0.5	13.6	L	COG0249|COG1193	Mismatch repair ATPase (MutS family)|Mismatch repair ATPase (MutS family)
CspM6211169|CDS|CDS	3.0	1.0	13.6	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
TS29Bac08566|CDS|CDS	3.0	1.0	13.6	L	COG0816	Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)
Cspi0976|CDS|CDS	3.0	1.0	13.6	L	COG2801	Transposase and inactivated derivatives
Dlon2379|CDS|CDS	1.5	0.5	13.6	L	COG0358	DNA primase (bacterial type)

Aput0305|CDS|CDS	3.0	1.0	13.6	L	COG0178	Excinuclease ATPase subunit
CspSS20428|CDS|CDS	3.0	1.0	13.6	L	COG1943	Transposase and inactivated derivatives
TS28EntUnc069|CDS|CDS	3.0	1.0	13.6	L	COG0629	Single-stranded DNA-binding protein
Acol2493|CDS|CDS	3.0	1.0	13.6	L	COG0249	Mismatch repair ATPase (MutS family)
RintL11896|CDS|CDS	3.0	1.0	13.6	L	COG0468	RecA/RadA recombinase
RintL13053|CDS|CDS	3.0	1.0	13.6	L	COG3663	G:T/U mismatch-specific DNA glycosylase
Bthe3734439|CDS|CDS	5.9	2.0	13.4	L	COG3436	Transposase and inactivated derivatives
TS29Bac10352|CDS|CDS	3.0	1.0	13.4	L	COG1372|COG0187	Intein/homing endonuclease|Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Buni3407|CDS|CDS	5.3	1.8	13.2	L	COG0497	ATPase involved in DNA repair
Bxyl3451|CDS|CDS	5.8	2.0	13.1	L	COG0514	Superfamily II DNA helicase
ShigspD90986|CDS|CDS	2.8	1.0	12.9	L	COG2812	DNA polymerase III, gamma/tau subunits
TS29RumUnc1254|CDS|CDS	66.0	23.5	12.8	L	COG0629	Single-stranded DNA-binding protein
Bxyl3976|CDS|CDS	4.2	1.5	12.7	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
Bxyl2046|CDS|CDS	2.2	0.8	12.5	L	COG0249	Mismatch repair ATPase (MutS family)
TS28Met1400|CDS|CDS	1.2	0.5	12.1	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
Msmi740652|CDS|CDS	1.2	0.5	12.1	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
Caer0878|CDS|CDS	1.3	0.5	12.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
Cnex3141|CDS|CDS	1.8	0.7	11.9	L	COG3335	Transposase and inactivated derivatives
Bthe3732898|CDS|CDS	1.7	0.7	11.8	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Bxyl0421|CDS|CDS	3.8	1.5	11.4	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
Msmi740593|CDS|CDS	1.3	0.5	11.3	L	COG0608	Single-stranded DNA-specific exonuclease
Cbol5308|CDS|CDS	5.0	2.0	11.3	L	COG0514	Superfamily II DNA helicase
TS29Fae02317|CDS|CDS	5.0	2.0	11.3	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS28Rum03483|CDS|CDS	2.5	1.0	11.3	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
Eeli2670|CDS|CDS	0.3	0.1	11.3	L	COG1533	DNA repair photolyase
Bxyl0247|CDS|CDS	3.7	1.5	11.1	L	COG0514|COG0507	Superfamily II DNA helicase|ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
Rlac0757|CDS|CDS	1.5	0.6	11.0	L	COG1533	DNA repair photolyase
TS28Fae10273|CDS|CDS	14.5	6.0	11.0	L	COG0629	Single-stranded DNA-binding protein
Dlon0415|CDS|CDS	2.0	0.8	10.9	L	COG2255	Holliday junction resolvasome, helicase subunit
TS29Bac01275|CDS|CDS	38.3	16.0	10.9	L	COG0514	Superfamily II DNA helicase
Aput0457|CDS|CDS	19.0	8.0	10.8	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase
Bfin0523|CDS|CDS	1.2	0.5	10.6	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS28Bac5038|CDS|CDS	2.3	1.0	10.6	L	COG0514	Superfamily II DNA helicase
Csci2796|CDS|CDS	2.3	1.0	10.6	L	COG0210	Superfamily I DNA and RNA helicases
TS28Rum16265|CDS|CDS	4.5	2.0	10.2	L	COG2176	DNA polymerase III, alpha subunit (gram-positive type)
Bxyl3883|CDS|CDS	3.3	1.5	10.1	L	COG0419	ATPase involved in DNA repair
TS29Fae05603|CDS|CDS	25.5	11.5	10.1	L	COG0776	Bacterial nucleoid DNA-binding protein
TS29Rum20668|CDS|CDS	0.5	23.0	0.1	L	COG0353	Recombinational DNA repair protein (RecF pathway)
Rtor1856|CDS|CDS	0.3	15.4	0.1	L	COG2801	Transposase and inactivated derivatives
Msmi741062|CDS|CDS	0.3	11.7	0.1	L	COG0551|COG0210|COG1599	Zn-finger domain associated with topoisomerase type I|Superfamily I DNA and RNA helicases|Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins
TS29Bac00474|CDS|CDS	0.5	23.5	0.1	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
BactD10695|CDS|CDS	0.5	23.5	0.1	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
TS29Fae09842|CDS|CDS	2.0	94.5	0.1	L	COG0358	DNA primase (bacterial type)
TS28Rum15978|CDS|CDS	0.6	27.8	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
FpraM2121415|CDS|CDS	0.3	15.0	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Rum13416|CDS|CDS	0.5	24.0	0.1	L	COG0350|COG2315|COG3695|COG1515	Methylated DNA-protein cysteine methyltransferase|Uncharacterized protein conserved in bacteria|Predicted methylated DNA-protein cysteine methyltransferase|Deoxyinosine 3'endonuclease (endonuclease V)
FpraM2121445|CDS|CDS	2.0	96.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Fae00292|CDS|CDS	0.5	24.0	0.1	L	COG0817	Holliday junction resolvasome, endonuclease subunit
TS29Bac11814|CDS|CDS	0.2	8.1	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS29Rum11531|CDS|CDS	1.0	48.5	0.1	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
TS29Fae01387|CDS|CDS	2.2	107.0	0.1	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
TS29Fae03922|CDS|CDS	0.7	32.5	0.1	L	COG0272	NAD-dependent DNA ligase (contains BRCT domain type II)
TS29Fae06170|CDS|CDS	2.3	114.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Ccom1150|CDS|CDS	1.0	49.0	0.1	L	COG3666	Transposase and inactivated derivatives
TS29Bif1093|CDS|CDS	1.0	49.0	0.1	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
TS29Rum19564|CDS|CDS	0.6	29.5	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum11913|CDS|CDS	1.0	51.0	0.1	L	COG3547	Transposase and inactivated derivatives
TS29Rum18395|CDS|CDS	1.0	51.0	0.1	L	COG3344	Retron-type reverse transcriptase
TS29Fae07024|CDS|CDS	1.5	77.5	0.1	L	COG0270	Site-specific DNA methylase
CspSS21647|CDS|CDS	0.2	8.7	0.1	L	COG0582	Integrase
CspSS21128|CDS|CDS	0.1	4.3	0.1	L	COG3344	Retron-type reverse transcriptase
TS28Rum01606|CDS|CDS	0.3	13.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum19153|CDS|CDS	0.3	13.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Bac11684|CDS|CDS	0.3	17.3	0.1	L	COG0249	Mismatch repair ATPase (MutS family)
TS29Rum15532|CDS|CDS	1.0	53.0	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Rum20776|CDS|CDS	1.0	53.0	0.1	L	COG0177	Predicted EndoIII-related endonuclease
TS29Rum00845|CDS|CDS	2.0	107.0	0.1	L	COG0322	Nuclease subunit of the excinuclease complex
TS29Bif3624|CDS|CDS	1.5	80.7	0.1	L	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes
TS29Fae07925|CDS|CDS	0.3	18.0	0.1	L	COG1484	DNA replication protein
TS29Rum01844|CDS|CDS	0.3	18.4	0.1	L	COG2801	Transposase and inactivated derivatives
TS28Fae20136|CDS|CDS	1.0	55.5	0.1	L	COG0587	DNA polymerase III, alpha subunit
TS29Bac10257|CDS|CDS	0.3	14.0	0.1	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
TS29Col1861|CDS|CDS	0.5	28.0	0.1	L	COG0353	Recombinational DNA repair protein (RecF pathway)
TS29Fae01483|CDS|CDS	1.0	57.0	0.1	L	COG0863	DNA modification methylase
TS28Bif0895|CDS|CDS	2.8	156.8	0.1	L	COG1112	Superfamily I DNA and RNA helicases and helicase subunits
TS29Fae01391|CDS|CDS	1.2	68.5	0.1	L	COG1533	DNA repair photolyase
TS29Par830|CDS|CDS	0.5	29.0	0.1	L	COG4227	Antirestriction protein
TS29Rum21195|CDS|CDS	1.0	58.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
BactD10428|CDS|CDS	0.5	29.0	0.1	L	COG4227	Antirestriction protein
TS29Fae03430|CDS|CDS	2.0	117.5	0.1	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS29Rum15534|CDS|CDS	2.0	119.0	0.1	L	COG0587	DNA polymerase III, alpha subunit
Bcro1279|CDS|CDS	0.3	18.7	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
Cste0814|CDS|CDS	0.2	12.0	0.1	L	COG4584	Transposase and inactivated derivatives

Cnex1210|CDS|CDS	0.3	18.7	0.1	L	COG1533	DNA repair photolyase
TS28Bif5349|CDS|CDS	0.8	46.7	0.1	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS28Bif4152|CDS|CDS	0.3	20.8	0.1	L	COG0514|COG0507	Superfamily II DNA helicase|ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Bif1519|CDS|CDS	0.3	20.8	0.1	L	COG0514|COG0507	Superfamily II DNA helicase|ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Bif2295|CDS|CDS	1.5	94.2	0.1	L	COG1643	HrpA-like helicases
TS29Bif3732|CDS|CDS	2.8	172.8	0.1	L	COG1112	Superfamily I DNA and RNA helicases and helicase subunits
TS29RumUnc0143|CDS|CDS	1.0	63.0	0.1	L	COG2189	Adenine specific DNA methylase Mod
TS29Bif2351|CDS|CDS	0.5	31.5	0.1	L	COG0210|COG1379	Superfamily I DNA and RNA helicases|Uncharacterized conserved protein
Csci0105|CDS|CDS	1.3	81.1	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum17228|CDS|CDS	0.5	32.0	0.1	L	COG2255	Holliday junction resolvasome, helicase subunit
Robe3542|CDS|CDS	0.3	16.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
FpraM2121397|CDS|CDS	3.0	194.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum20324|CDS|CDS	1.3	81.0	0.1	L	COG5421	Transposase
TS29Bac00703|CDS|CDS	1.0	65.0	0.1	L	COG3547	Transposase and inactivated derivatives
Bxyl1638|CDS|CDS	1.0	65.0	0.1	L	COG3547	Transposase and inactivated derivatives
Acol1045|CDS|CDS	0.7	44.3	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Col1496|CDS|CDS	0.5	33.0	0.1	L	COG2812|COG0470	DNA polymerase III, gamma/tau subunits|ATPase involved in DNA replication
TS29Rum13830|CDS|CDS	2.5	167.5	0.1	L	COG3857	ATP-dependent nuclease, subunit B
TS29Rum19567|CDS|CDS	0.5	33.5	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Fae08597|CDS|CDS	0.5	34.0	0.1	L	COG0708	Exonuclease III
TS29Rum16540|CDS|CDS	1.5	105.0	0.1	L	COG0210	Superfamily I DNA and RNA helicases
TS29Col1287|CDS|CDS	1.3	93.5	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS28Fae21437|CDS|CDS	0.3	23.5	0.1	L	COG0582	Integrase
TS29Col1238|CDS|CDS	1.0	72.0	0.1	L	COG0178	Excinuclease ATPase subunit
FpraM2121954|CDS|CDS	0.5	36.0	0.1	L	COG0587	DNA polymerase III, alpha subunit
Rbro1703|CDS|CDS	0.4	28.8	0.1	L	COG3935	Putative primosome component and related proteins
TS29Rum19546|CDS|CDS	1.0	73.0	0.1	L	COG3547	Transposase and inactivated derivatives
Cbol3905|CDS|CDS	0.4	29.5	0.1	L	COG3935	Putative primosome component and related proteins
TS29Fae00119|CDS|CDS	1.0	74.5	0.1	L	COG0272	NAD-dependent DNA ligase (contains BRCT domain type II)
TS29RumUnc1198|CDS|CDS	1.0	76.0	0.1	L	COG3857	ATP-dependent nuclease, subunit B
TS29Col1585|CDS|CDS	0.5	38.0	0.1	L	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)
Dfor3087|CDS|CDS	0.3	24.3	0.1	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Rum21205|CDS|CDS	0.5	39.3	0.1	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair
TS29Bif0669|CDS|CDS	0.8	60.4	0.1	L	COG1372|COG0305	Intein/homing endonuclease|Replicative DNA helicase
TS28Bif1084|CDS|CDS	0.8	60.4	0.1	L	COG1372|COG0305	Intein/homing endonuclease|Replicative DNA helicase
TS29Bac10496|CDS|CDS	1.0	81.0	0.1	L	COG4227	Antirestriction protein
TS29Fae01385|CDS|CDS	1.0	82.0	0.1	L	COG2256|COG2110	ATPase related to the helicase subunit of the Holliday junction resolvase|Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1
TS29Fae01431|CDS|CDS	2.0	164.0	0.1	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Begg1044|CDS|CDS	0.2	13.8	0.1	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS28Bif4427|CDS|CDS	0.2	14.2	0.1	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS28Bif4598|CDS|CDS	0.3	21.7	0.1	L	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes
TS29Bif3199|CDS|CDS	0.3	21.7	0.1	L	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes
Casp0340|CDS|CDS	0.5	43.5	0.1	L	COG0582	Integrase
TS29Rum00228|CDS|CDS	1.0	87.5	0.1	L	COG0587	DNA polymerase III, alpha subunit
TS29RumUnc0815|CDS|CDS	1.0	88.0	0.1	L	COG0587	DNA polymerase III, alpha subunit
Ccom0764|CDS|CDS	0.2	17.9	0.1	L	COG0358	DNA primase (bacterial type)
TS28Fae12194|CDS|CDS	0.5	45.0	0.1	L	COG0210|COG1074|COG2887	Superfamily I DNA and RNA helicases|ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)|RecB family exonuclease
FpraM2122522|CDS|CDS	0.5	45.4	0.0	L	COG1484	DNA replication protein
TS29Bif0764|CDS|CDS	1.0	91.0	0.0	L	COG3344	Retron-type reverse transcriptase
Rtor0134|CDS|CDS	0.3	30.3	0.0	L	COG3328	Transposase and inactivated derivatives
Rtor0268|CDS|CDS	0.3	30.3	0.0	L	COG3328	Transposase and inactivated derivatives
CspM6211315|CDS|CDS	0.3	30.7	0.0	L	COG3935	Putative primosome component and related proteins
TS29Fae07197|CDS|CDS	1.0	92.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum11630|CDS|CDS	1.0	93.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Bif0534|CDS|CDS	2.0	186.3	0.0	L	COG3464	Transposase and inactivated derivatives
RintL13796|CDS|CDS	0.3	26.8	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Bxyl2351|CDS|CDS	0.1	13.5	0.0	L	COG3436	Transposase and inactivated derivatives
Svar2340|CDS|CDS	1.0	94.7	0.0	L	COG0358	DNA primase (bacterial type)
TS29Fae00497|CDS|CDS	1.5	144.5	0.0	L	COG0249	Mismatch repair ATPase (MutS family)
TS29Rum17721|CDS|CDS	1.0	96.5	0.0	L	COG2826	Transposase and inactivated derivatives, IS30 family
TS28Rum11517|CDS|CDS	0.3	32.3	0.0	L	COG3328	Transposase and inactivated derivatives
TS28Bif4927|CDS|CDS	2.3	223.9	0.0	L	COG0210|COG2887	Superfamily I DNA and RNA helicases|RecB family exonuclease
TS29Bif3491|CDS|CDS	2.3	223.9	0.0	L	COG0210|COG2887	Superfamily I DNA and RNA helicases|RecB family exonuclease
TS29Bif3202|CDS|CDS	1.7	166.1	0.0	L	COG0556	Helicase subunit of the DNA excision repair complex
TS29Fae09862|CDS|CDS	1.0	100.0	0.0	L	COG0582	Integrase
FpraM2120450|CDS|CDS	0.3	25.1	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Fae03202|CDS|CDS	1.0	101.0	0.0	L	COG2801	Transposase and inactivated derivatives
TS29Fae09088|CDS|CDS	1.0	102.5	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Bcap3493|CDS|CDS	0.1	9.3	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Bif3071|CDS|CDS	0.3	34.3	0.0	L	COG3436	Transposase and inactivated derivatives
Ceut1170|CDS|CDS	0.9	91.0	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
Bcap2324|CDS|CDS	0.8	90.9	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Ceut1811|CDS|CDS	1.0	105.0	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29RumUnc0157|CDS|CDS	0.3	37.4	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Bif3492|CDS|CDS	1.5	168.8	0.0	L	COG2887	RecB family exonuclease
TS28Bif4928|CDS|CDS	1.5	168.8	0.0	L	COG2887	RecB family exonuclease
TS29Fae01430|CDS|CDS	1.0	113.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Bif2815|CDS|CDS	1.0	113.5	0.0	L	COG1204|COG4581|COG1202	Superfamily II helicase|Superfamily II RNA helicase|Superfamily II helicase, archaea-specific
TS29Rum16681|CDS|CDS	0.6	68.0	0.0	L	COG5421	Transposase
TS29RumUnc0158|CDS|CDS	0.3	39.5	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Fae00212|CDS|CDS	0.5	60.5	0.0	L	COG0497	ATPase involved in DNA repair
Ccom2074|CDS|CDS	0.5	59.3	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Fae01429|CDS|CDS	1.0	126.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs

Ccom0010|CDS|CDS	0.8	96.3	0.0	L	COG0675	Transposase and inactivated derivatives
Hfil2883|CDS|CDS	0.5	64.3	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Col0751|CDS|CDS	0.5	67.0	0.0	L	COG0322	Nuclease subunit of the excinuclease complex
CspM6211302|CDS|CDS	0.1	19.3	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Fae08666|CDS|CDS	1.0	137.0	0.0	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
Acol1043|CDS|CDS	0.2	23.1	0.0	L	COG1484	DNA replication protein
TS29Fae06183|CDS|CDS	1.5	220.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum13789|CDS|CDS	0.5	74.0	0.0	L	COG2826	Transposase and inactivated derivatives, IS30 family
TS29Bif3097|CDS|CDS	0.8	112.0	0.0	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains
TS29Fae08189|CDS|CDS	1.0	149.5	0.0	L	COG0210|COG1074	Superfamily I DNA and RNA helicases|ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)
Csci0106|CDS|CDS	0.2	25.1	0.0	L	COG1484	DNA replication protein
Robe2622|CDS|CDS	0.3	50.3	0.0	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Robe0878|CDS|CDS	0.3	50.3	0.0	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
Robe3717|CDS|CDS	0.3	50.3	0.0	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS29Fae03779|CDS|CDS	0.5	80.0	0.0	L	COG5377	Phage-related protein, predicted endonuclease
TS28Fae11460|CDS|CDS	1.0	166.0	0.0	L	COG3344	Retron-type reverse transcriptase
TS29Bif3995|CDS|CDS	1.0	170.5	0.0	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase
Cbol3901|CDS|CDS	0.3	57.0	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Fae05812|CDS|CDS	0.5	87.5	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Rum00526|CDS|CDS	0.3	59.5	0.0	L	COG3666	Transposase and inactivated derivatives
TS28Bif1893|CDS|CDS	0.3	59.5	0.0	L	COG1204|COG4581	Superfamily II helicase|Superfamily II RNA helicase
TS29Bif0981|CDS|CDS	0.6	115.3	0.0	L	COG1372|COG0188	Intein/homing endonuclease|Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
RintL12726|CDS|CDS	0.4	67.4	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
Rtor0214|CDS|CDS	0.2	30.3	0.0	L	COG2946	Putative phage replication protein RstA
Robe3718|CDS|CDS	0.3	63.3	0.0	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
Robe2623|CDS|CDS	0.3	63.3	0.0	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
Robe0879|CDS|CDS	0.3	63.3	0.0	L	COG4974|COG0582|COG4973	Site-specific recombinase XerD|Integrase|Site-specific recombinase XerC
Csci0107|CDS|CDS	0.3	65.3	0.0	L	COG3935	Putative primosome component and related proteins
Acol1042|CDS|CDS	0.3	65.3	0.0	L	COG3935	Putative primosome component and related proteins
TS29Fae00720|CDS|CDS	0.5	99.5	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Bif2528|CDS|CDS	0.5	102.4	0.0	L	COG0468	RecA/RadA recombinase
TS29Fae09082|CDS|CDS	0.3	52.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS28Bif5320|CDS|CDS	0.3	53.8	0.0	L	COG0270	Site-specific DNA methylase
TS29Bif0549|CDS|CDS	0.3	53.8	0.0	L	COG0270	Site-specific DNA methylase
TS28Bif5104|CDS|CDS	0.3	57.8	0.0	L	COG1204|COG4581	Superfamily II helicase|Superfamily II RNA helicase
CspM6211314|CDS|CDS	0.2	43.0	0.0	L	COG1484	DNA replication protein
TS28Bif5101|CDS|CDS	0.3	64.7	0.0	L	COG2256	ATPase related to the helicase subunit of the Holliday junction resolvase
TS29Bif4054|CDS|CDS	0.3	64.7	0.0	L	COG2256	ATPase related to the helicase subunit of the Holliday junction resolvase
CspSS21813|CDS|CDS	0.2	45.3	0.0	L	COG2946	Putative phage replication protein RstA
TS29Fae01424|CDS|CDS	0.3	100.0	0.0	L	COG1961	Site-specific recombinases, DNA invertase Pin homologs
TS29Bif0475|CDS|CDS	0.5	151.2	0.0	L	COG1195	Recombinational DNA repair ATPase (RecF pathway)
FpraM2122493|CDS|CDS	0.1	28.4	0.0	L	COG0507	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member
TS29Bif0477|CDS|CDS	0.6	231.8	0.0	L	COG0187	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
TS29Bif0478|CDS|CDS	0.3	121.3	0.0	L	COG1372|COG0188	Intein/homing endonuclease|Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
Robe0877|CDS|CDS	0.3	102.8	0.0	L	COG0582	Integrase
Robe3716|CDS|CDS	0.3	102.8	0.0	L	COG0582	Integrase
Robe2621|CDS|CDS	0.3	102.8	0.0	L	COG0582	Integrase
TS29Fae09860|CDS|CDS	0.3	103.0	0.0	L	COG4974|COG0582	Site-specific recombinase XerD|Integrase
TS29Bif2550|CDS|CDS	0.3	114.3	0.0	L	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
TS29Bif0610|CDS|CDS	0.6	276.6	0.0	L	COG2812	DNA polymerase III, gamma/tau subunits
TS28Bif4428|CDS|CDS	0.1	80.9	0.0	L	COG1372|COG0188	Intein/homing endonuclease|Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit
Even0584|CDS|CDS	0.2	141.1	0.0	L	COG0358	DNA primase (bacterial type)
TS29Bif4053|CDS|CDS	0.3	207.3	0.0	L	COG1204|COG4581	Superfamily II helicase|Superfamily II RNA helicase
Casp0359|CDS|CDS	5.0	1.5	15.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Rum02179|CDS|CDS	1.5	0.5	13.6	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Rum20503|CDS|CDS	1.5	108.0	0.1	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Rum19622|CDS|CDS	0.7	63.5	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Rum18715|CDS|CDS	1.3	136.3	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS28Fae14717|CDS|CDS	0.3	39.7	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Fae08918|CDS|CDS	0.3	41.5	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Svar2339|CDS|CDS	0.2	25.3	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
TS29Bif2593|CDS|CDS	1.0	150.0	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Rgna0696|CDS|CDS	0.2	39.9	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
Edol0075|CDS|CDS	0.2	56.8	0.0	L|B	COG0550|COG0551|COG5531	Topoisomerase IA|Zn-finger domain associated with topoisomerase type I|SWIB-domain-containing proteins implicated in chromatin remodeling
BactD12937|CDS|CDS	4.3	0.3	57.9	L|D	COG0419|COG1196	ATPase involved in DNA repair|Chromosome segregation ATPases
Bfin1435|CDS|CDS	4.3	1.0	19.3	L|D	COG0419|COG1196	ATPase involved in DNA repair|Chromosome segregation ATPases
Buni1744|CDS|CDS	25.0	4.0	28.4	L|H	COG0494|COG1235|COG0321	NTP pyrophosphohydrolases including oxidative damage repair enzymes|Metal dependent hydrolases of the beta-lactamase superfamily I|Lipoate-protein ligase B
BactD11639|CDS|CDS	2.3	0.3	42.4	L|I	COG0494|COG1443	NTP pyrophosphohydrolases including oxidative damage repair enzymes|Isopentenyldiphosphate isomerase
Bova3491|CDS|CDS	1.0	0.3	18.2	L|I	COG0494|COG1443	NTP pyrophosphohydrolases including oxidative damage repair enzymes|Isopentenyldiphosphate isomerase
Ehal1725|CDS|CDS	0.4	17.9	0.1	L|U	COG1961|COG2948|COG3293	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components|Transposase and inactivated derivatives

FpraM2121413|CDS|CDS	1.3	61.0	0.1	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
Robe2672|CDS|CDS	3.0	139.7	0.1	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
Rlac1242|CDS|CDS	0.1	7.8	0.1	L|U	COG1961|COG2948|COG3293	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components|Transposase and inactivated derivatives
Rtor1326|CDS|CDS	1.0	81.7	0.1	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
TS29Fae03372|CDS|CDS	2.0	184.0	0.0	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
TS29Rum18376|CDS|CDS	0.3	23.8	0.0	L|U	COG1961|COG2948|COG3293	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components|Transposase and inactivated derivatives
Rgna3503|CDS|CDS	0.1	24.3	0.0	L|U	COG1961|COG2948|COG3293	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components|Transposase and inactivated derivatives
Cnex1121|CDS|CDS	0.1	24.3	0.0	L|U	COG1961|COG2948|COG3293	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components|Transposase and inactivated derivatives
FpraM2122467|CDS|CDS	0.5	86.0	0.0	L|U	COG1961|COG2948	Site-specific recombinases, DNA invertase Pin homologs|Type IV secretory pathway, VirB10 components
CspM6211944|CDS|CDS	1.0	295.8	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
Acol2738|CDS|CDS	1.0	347.8	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
Dlon1325|CDS|CDS	0.4	134.5	0.0	L|U	COG3505|COG1961	Type IV secretory pathway, VirD4 components|Site-specific recombinases, DNA invertase Pin homologs
TS28Eub8187|CDS|CDS	7.0	2.5	12.7	L|V	COG1131|COG3666|COG4152|COG4586	ABC-type multidrug transport system, ATPase component|Transposase and inactivated derivatives|ABC-type uncharacterized transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component
TS29Bif2990|CDS|CDS	0.5	51.2	0.0	L|V	COG1131|COG3666	ABC-type multidrug transport system, ATPase component|Transposase and inactivated derivatives
Dfor0353|CDS|CDS	281.0	3.0	425.2	M	COG1087	UDP-glucose 4-epimerase
Buni0727|CDS|CDS	50.5	1.5	152.8	M	COG1887	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC
Bfra31123865|CDS|CDS	19.5	0.6	151.5	M	COG3209	Rhs family protein
TS29Par381|CDS|CDS	26.5	1.0	120.3	M	COG1664	Integral membrane protein CcmA involved in cell shape determination
Caer0911|CDS|CDS	26.0	1.0	118.0	M	COG1388|COG0791	FOG: LysM repeat|Cell wall-associated hydrolases (invasion-associated proteins)
BactD13204|CDS|CDS	8.6	0.3	116.7	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS28Fae18454|CDS|CDS	12.0	0.5	109.0	M	COG0438	Glycosyltransferase
Buni1596|CDS|CDS	10.8	0.5	98.4	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS29Bac03642|CDS|CDS	10.0	0.5	90.8	M	COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes
Acac3081|CDS|CDS	18.0	1.0	81.7	M	COG0794	Predicted sugar phosphate isomerase involved in capsule formation
TS28Rum15589|CDS|CDS	7.5	0.5	68.1	M	COG3773	Cell wall hydrolyses involved in spore germination
TS28Bac1101|CDS|CDS	4.3	0.3	59.0	M	COG0793	Periplasmic protease
Buni3092|CDS|CDS	4.3	0.3	59.0	M	COG0793	Periplasmic protease
Bxyl4005|CDS|CDS	5.7	0.5	51.5	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS28Rum14452|CDS|CDS	9.5	1.0	43.1	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
TS28Fae02811|CDS|CDS	16.0	2.0	36.3	M	COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily
TS28Fae12113|CDS|CDS	4.0	0.5	36.3	M	COG0438	Glycosyltransferase
TS28Bac6034|CDS|CDS	2.7	0.3	36.3	M	COG1043	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase
Buni0765|CDS|CDS	2.7	0.3	36.3	M	COG1043	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase
Dlon1846|CDS|CDS	3.5	0.5	31.8	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Aput1465|CDS|CDS	14.0	2.0	31.8	M	COG1004	Predicted UDP-glucose 6-dehydrogenase
TS28Fae17534|CDS|CDS	3.5	0.5	31.8	M	COG1346|COG1380	Putative effector of murein hydrolase|Putative effector of murein hydrolase LrgA
TS28Rum16477|CDS|CDS	10.3	1.5	31.0	M	COG1087	UDP-glucose 4-epimerase
TS28Fae10727|CDS|CDS	3.3	0.5	30.3	M	COG3757	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
TS28Bac4748|CDS|CDS	3.3	0.5	30.3	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
BactD13908|CDS|CDS	2.2	0.3	30.0	M	COG0794	Predicted sugar phosphate isomerase involved in capsule formation
Buni3001|CDS|CDS	2.2	0.3	29.5	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Bac2244|CDS|CDS	2.2	0.3	29.5	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS29Bac03657|CDS|CDS	6.5	1.0	29.5	M	COG4775	Outer membrane protein/protective antigen OMA87
Buni2105|CDS|CDS	12.5	2.0	28.4	M	COG1087	UDP-glucose 4-epimerase
TS28Bac5564|CDS|CDS	4.0	0.7	27.2	M	COG4948	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily
TS29Bac02721|CDS|CDS	74.0	13.0	25.8	M	COG3209	Rhs family protein
Bxyl1472|CDS|CDS	21.6	3.8	25.5	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Aput1907|CDS|CDS	11.0	2.0	25.0	M	COG0793	Periplasmic protease
TS28Fae08672|CDS|CDS	11.0	2.0	25.0	M	COG3764	Sortase (surface protein transpeptidase)
TS28Fae08674|CDS|CDS	27.0	5.0	24.5	M	COG4932	Predicted outer membrane protein
Bxyl2539|CDS|CDS	2.7	0.5	24.2	M	COG0773	UDP-N-acetylmuramate-alanine ligase
TS29Bac06795|CDS|CDS	2.7	0.5	24.2	M	COG1043	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase
BactD23550|CDS|CDS	5.2	1.0	23.8	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
BactD13371|CDS|CDS	10.2	2.0	23.2	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS28Rum04443|CDS|CDS	1.7	0.3	22.7	M	COG3883|COG0791	Uncharacterized protein conserved in bacteria|Cell wall-associated hydrolases (invasion-associated proteins)
Bthe7335556|CDS|CDS	1.7	0.3	22.7	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Col0487|CDS|CDS	5.0	1.0	22.7	M	COG0796	Glutamate racemase
TS28Fae16438|CDS|CDS	5.0	1.0	22.7	M	COG5434	Endopolygalacturonase
TS28Fae01996|CDS|CDS	2.5	0.5	22.7	M	COG0438|COG0463|COG1543	Glycosyltransferase|Glycosyltransferases involved in cell wall biogenesis|Uncharacterized conserved protein
Bthe3733491|CDS|CDS	12.1	2.6	21.3	M	COG3209	Rhs family protein
TS28Bac5428|CDS|CDS	1.5	0.3	20.4	M	COG0773	UDP-N-acetylmuramate-alanine ligase
Caer0379|CDS|CDS	4.5	1.0	20.4	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Bac3217|CDS|CDS	6.0	1.3	20.4	M	COG0769|COG0770	UDP-N-acetylmuramyl tripeptide synthase|UDP-N-acetylmuramyl pentapeptide synthase
Buni1477|CDS|CDS	4.3	1.0	19.7	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS28Met1177|CDS|CDS	3.6	0.8	19.5	M	COG1210	UDP-glucose pyrophosphorylase
BactD11310|CDS|CDS	1.3	0.3	18.2	M	COG1209	dTDP-glucose pyrophosphorylase
ShigspD90537|CDS|CDS	2.0	0.5	18.2	M	COG1087	UDP-glucose 4-epimerase
TS28Ali0459|CDS|CDS	4.0	1.0	18.2	M	COG4775	Outer membrane protein/protective antigen OMA87

BactD20657|CDS|CDS	2.0	0.5	18.2	M	COG0744|COG5009	Membrane carboxypeptidase (penicillin-binding protein)|Membrane carboxypeptidase/penicillin-binding protein
Casp3572|CDS|CDS	4.0	1.0	18.2	M	COG1686	D-alanyl-D-alanine carboxypeptidase
Ccom0922|CDS|CDS	8.0	2.0	18.2	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
RintL12189|CDS|CDS	4.0	1.0	18.2	M	COG0845	Membrane-fusion protein
Aput0950|CDS|CDS	4.0	1.0	18.2	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
b0759|CDS|UDP-galactose-4-epimerase	2.0	0.5	18.2	M	COG1087	UDP-glucose 4-epimerase
Dlon2639|CDS|CDS	2.0	0.5	18.2	M	COG0707	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
Bxyl1067|CDS|CDS	2.7	0.7	18.2	M	COG3049	Penicillin V acylase and related amidases
BactD11915|CDS|CDS	2.7	0.7	18.2	M	COG3049	Penicillin V acylase and related amidases
BactD22517|CDS|CDS	9.0	2.3	17.5	M	COG3209	Rhs family protein
Bthe3733495|CDS|CDS	50.0	13.2	17.2	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
Aput1467|CDS|CDS	11.0	3.0	16.6	M	COG1091	dTDP-4-dehydrorhamnose reductase
Buni1406|CDS|CDS	3.5	1.0	15.9	M	COG1215	Glycosyltransferases, probably involved in cell wall biogenesis
TS28Bac2239|CDS|CDS	3.5	1.0	15.9	M	COG0438|COG1543	Glycosyltransferase|Uncharacterized conserved protein
TS28Bif4864|CDS|CDS	1.8	0.5	15.9	M	COG0787|COG0802	Alanine racemase|Predicted ATPase or kinase
Cbol2247|CDS|CDS	7.0	2.0	15.9	M	COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes
TS28Rum11795|CDS|CDS	7.0	2.0	15.9	M	COG2148|COG0707	Sugar transferases involved in lipopolysaccharide synthesis|UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
Buni1330|CDS|CDS	2.3	0.7	15.9	M	COG0463|COG2246	Glycosyltransferases involved in cell wall biogenesis|Predicted membrane protein
TS28Bac1301|CDS|CDS	2.3	0.7	15.9	M	COG0463|COG2246	Glycosyltransferases involved in cell wall biogenesis|Predicted membrane protein
TS28Fae00348|CDS|CDS	8.5	2.5	15.4	M	COG0517|COG0399	FOG: CBS domain|Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis
Bova3011|CDS|CDS	3.4	1.0	15.3	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
BactD20408|CDS|CDS	5.0	1.5	15.1	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
Rtor1960|CDS|CDS	5.0	1.5	15.1	M	COG3764	Sortase (surface protein transpeptidase)
TS28Rum07177|CDS|CDS	5.0	1.5	15.1	M	COG3764	Sortase (surface protein transpeptidase)
TS28Rum09521|CDS|CDS	1.7	0.5	15.1	M	COG0845	Membrane-fusion protein
TS29Bac03581|CDS|CDS	24.2	7.3	15.0	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS29Bac08589|CDS|CDS	32.5	10.0	14.8	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
FpraM2120556|CDS|CDS	6.2	2.0	14.0	M	COG4886|COG4932	Leucine-rich repeat (LRR) protein|Predicted outer membrane protein
TS28Eub4771|CDS|CDS	1.0	0.3	13.6	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
Rbro1448|CDS|CDS	1.0	0.3	13.6	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
TS28Bac4161|CDS|CDS	1.0	0.3	13.6	M	COG3049	Penicillin V acylase and related amidases
BactD11309|CDS|CDS	1.0	0.3	13.6	M	COG1088	dTDP-D-glucose 4,6-dehydratase
Buni3008|CDS|CDS	1.0	0.3	13.6	M	COG0773	UDP-N-acetylmuramate-alanine ligase
TS28Fae10280|CDS|CDS	4.0	1.3	13.6	M	COG0750	Predicted membrane-associated Zn-dependent proteases 1
TS29Fae05751|CDS|CDS	4.0	1.3	13.6	M	COG0750	Predicted membrane-associated Zn-dependent proteases 1
Csci1066|CDS|CDS	3.0	1.0	13.6	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
Bcap2672|CDS|CDS	3.0	1.0	13.6	M	COG0463|COG2246	Glycosyltransferases involved in cell wall biogenesis|Predicted membrane protein
Bova2815|CDS|CDS	3.0	1.0	13.6	M	COG1388|COG0739	FOG: LysM repeat|Membrane proteins related to metalloendopeptidases
RintL12454|CDS|CDS	3.0	1.0	13.6	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
Bcap0706|CDS|CDS	3.0	1.0	13.6	M	COG1922|COG2148	Teichoic acid biosynthesis proteins|Sugar transferases involved in lipopolysaccharide synthesis
TS29Bac08801|CDS|CDS	3.0	1.0	13.6	M	COG0739	Membrane proteins related to metalloendopeptidases
TS28Rum13006|CDS|CDS	3.0	1.0	13.6	M	COG0845	Membrane-fusion protein
ShigspD91330|CDS|CDS	3.0	1.0	13.6	M	COG0773	UDP-N-acetylmuramate-alanine ligase
Ccom1964|CDS|CDS	3.0	1.0	13.6	M	COG0769|COG0770	UDP-N-acetylmuramyl tripeptide synthase|UDP-N-acetylmuramyl pentapeptide synthase
TS28Fae03437|CDS|CDS	3.0	1.0	13.6	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
TS28Fae22537|CDS|CDS	3.0	1.0	13.6	M	COG1088	dTDP-D-glucose 4,6-dehydratase
RintL11515|CDS|CDS	3.0	1.0	13.6	M	COG0463|COG1887|COG1216	Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Predicted glycosyltransferases
Buni3002|CDS|CDS	7.0	2.3	13.6	M	COG0769|COG0770	UDP-N-acetylmuramyl tripeptide synthase|UDP-N-acetylmuramyl pentapeptide synthase
Buni1697|CDS|CDS	13.3	4.5	13.4	M	COG0845	Membrane-fusion protein
Bfra31123864|CDS|CDS	25.0	8.5	13.3	M	COG3209|COG5276	Rhs family protein|Uncharacterized conserved protein
Rgna3058|CDS|CDS	8.5	3.0	12.9	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Aput1897|CDS|CDS	17.0	6.0	12.9	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS29Bac05145|CDS|CDS	22.2	8.0	12.6	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS28Rum01499|CDS|CDS	23.0	8.5	12.3	M	COG0845	Membrane-fusion protein
TS29Par279|CDS|CDS	4.0	1.5	12.1	M	COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes
BactD22211|CDS|CDS	1.3	0.5	12.1	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
Bova1669|CDS|CDS	4.3	1.7	11.8	M	COG1087	UDP-glucose 4-epimerase
BactD23345|CDS|CDS	1.7	0.7	11.3	M	COG0357	Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division
Cbol0545|CDS|CDS	5.0	2.0	11.3	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Rum16310|CDS|CDS	2.5	1.0	11.3	M	COG0463|COG1216|COG1887|COG3754	Glycosyltransferases involved in cell wall biogenesis|Predicted glycosyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis protein
Even1783|CDS|CDS	5.0	2.0	11.3	M	COG5498	Predicted glycosyl hydrolase
Buni0590|CDS|CDS	2.5	1.0	11.3	M	COG0845	Membrane-fusion protein
Clep2070|CDS|CDS	1.7	0.7	11.3	M	COG1088	dTDP-D-glucose 4,6-dehydratase
TS28Rum14458|CDS|CDS	32.1	13.3	10.9	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Rum14451|CDS|CDS	10.5	4.5	10.6	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase
Cbol4143|CDS|CDS	7.0	3.0	10.6	M	COG1876	D-alanyl-D-alanine carboxypeptidase
Buni1800|CDS|CDS	3.5	1.5	10.6	M	COG3858|COG1215	Predicted glycosyl hydrolase|Glycosyltransferases, probably involved in cell wall biogenesis
ShigspD90212|CDS|CDS	3.5	1.5	10.6	M	COG1209	dTDP-glucose pyrophosphorylase
TS28Fae18682|CDS|CDS	3.5	1.5	10.6	M	COG1696	Predicted membrane protein involved in D-alanine export
Robe1118|CDS|CDS	1.2	0.5	10.6	M	COG0845	Membrane-fusion protein
Clep1094|CDS|CDS	2.3	1.0	10.6	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
Bxyl1425|CDS|CDS	2.3	1.0	10.6	M	COG1596	Periplasmic protein involved in polysaccharide export

TS28Clo08359|CDS|CDS	2.3	1.0	10.6	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase
BactD13168|CDS|CDS	2.3	1.0	10.6	M	COG1596	Periplasmic protein involved in polysaccharide export
Msmi740177|CDS|CDS	0.8	0.3	10.2	M	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
Cnex0258|CDS|CDS	9.0	4.0	10.2	M	COG0481	Membrane GTPase LepA
Bxyl4354|CDS|CDS	2.2	1.0	10.1	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS29Bac02766|CDS|CDS	20.0	9.0	10.1	M	COG1970	Large-conductance mechanosensitive channel
TS28Rum14888|CDS|CDS	21.0	9.5	10.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS29Fae01172|CDS|CDS	2.0	91.5	0.1	M	COG5434	Endopolygalacturonase
TS29Fae08277|CDS|CDS	1.5	69.5	0.1	M	COG3757|COG5263	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|FOG: Glucan-binding domain (YG repeat)
TS29Bac07785|CDS|CDS	0.3	15.5	0.1	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Eub7067|CDS|CDS	1.3	62.0	0.1	M	COG4932	Predicted outer membrane protein
TS29Bac08778|CDS|CDS	0.3	15.7	0.1	M	COG0845	Membrane-fusion protein
TS29Bif3408|CDS|CDS	2.0	94.5	0.1	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS28Fae08969|CDS|CDS	0.5	24.0	0.1	M	COG1091	dTDP-4-dehydrorhamnose reductase
TS29Fae00697|CDS|CDS	1.0	48.0	0.1	M	COG0707	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
TS29Rum21239|CDS|CDS	3.9	187.0	0.1	M	COG4932	Predicted outer membrane protein
TS29RumUnc0709|CDS|CDS	1.0	50.0	0.1	M	COG0739|COG3883|COG2951|COG0791	Membrane proteins related to metalloendopeptidases|Uncharacterized protein conserved in bacteria|Membrane-bound lytic murein transglycosylase B|Cell wall-associated hydrolases (invasion-associated proteins)
TS28Rum02251|CDS|CDS	1.5	75.5	0.1	M	COG4932	Predicted outer membrane protein
TS29Bac00439|CDS|CDS	0.3	16.8	0.1	M	COG1696	Predicted membrane protein involved in D-alanine export
TS28Bif5294|CDS|CDS	1.2	59.0	0.1	M	COG1088	dTDP-D-glucose 4,6-dehydratase
TS29Bif0922|CDS|CDS	1.2	59.0	0.1	M	COG1088	dTDP-D-glucose 4,6-dehydratase
TS29Rum11714|CDS|CDS	2.0	101.5	0.1	M	COG0741|COG3757	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
Ccom1804|CDS|CDS	0.3	12.8	0.1	M	COG4932	Predicted outer membrane protein
TS29RumUnc1441|CDS|CDS	1.5	76.5	0.1	M	COG4932	Predicted outer membrane protein
TS29Bif2467|CDS|CDS	1.3	63.9	0.1	M	COG0769|COG0770	UDP-N-acetylmuramyl tripeptide synthase|UDP-N-acetylmuramyl pentapeptide synthase
TS29Bac09108|CDS|CDS	0.3	13.0	0.1	M	COG0739|COG3883|COG5412|COG0791	Membrane proteins related to metalloendopeptidases|Uncharacterized protein conserved in bacteria|Phage-related protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Fae05357|CDS|CDS	0.5	26.0	0.1	M	COG0796	Glutamate racemase
TS29Fae08641|CDS|CDS	1.0	52.5	0.1	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
TS29RumUnc1680|CDS|CDS	1.0	53.0	0.1	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS29Bif3436|CDS|CDS	1.8	93.5	0.1	M	COG0787|COG0802	Alanine racemase|Predicted ATPase or kinase
Caer1588|CDS|CDS	1.0	54.0	0.1	M	COG1209	dTDP-glucose pyrophosphorylase
TS28Fae16711|CDS|CDS	0.5	27.0	0.1	M	COG1686	D-alanyl-D-alanine carboxypeptidase
TS29Fae08152|CDS|CDS	1.5	81.0	0.1	M	COG0787	Alanine racemase
TS29Bac01443|CDS|CDS	0.1	6.0	0.1	M	COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Bpse0004|CDS|CDS	0.3	18.2	0.1	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS28Bif5291|CDS|CDS	1.0	57.5	0.1	M	COG1209	dTDP-glucose pyrophosphorylase
TS29Bif0924|CDS|CDS	1.0	57.5	0.1	M	COG1209	dTDP-glucose pyrophosphorylase
TS28Bif3454|CDS|CDS	0.3	14.5	0.1	M	COG0770	UDP-N-acetylmuramyl pentapeptide synthase
TS29Fae03175|CDS|CDS	1.5	87.0	0.1	M	COG0438	Glycosyltransferase
TS29Fae08564|CDS|CDS	1.5	87.0	0.1	M	COG0769|COG0770	UDP-N-acetylmuramyl tripeptide synthase|UDP-N-acetylmuramyl pentapeptide synthase
TS29Bif2272|CDS|CDS	0.5	29.0	0.1	M	COG0773	UDP-N-acetylmuramate-alanine ligase
TS29Bif0622|CDS|CDS	1.5	88.5	0.1	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS28Bif1145|CDS|CDS	1.5	88.5	0.1	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS29RumUnc1673|CDS|CDS	1.0	60.0	0.1	M	COG1368	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily
TS28Fae21403|CDS|CDS	0.5	30.5	0.1	M	COG1089	GDP-D-mannose dehydratase
TS29Col0684|CDS|CDS	0.5	31.0	0.1	M	COG0812	UDP-N-acetylmuramate dehydrogenase
TS29Bif1539|CDS|CDS	0.3	20.7	0.1	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS29Fae07271|CDS|CDS	9.0	564.3	0.1	M	COG4932	Predicted outer membrane protein
TS29Fae10170|CDS|CDS	1.0	63.0	0.1	M	COG1004	Predicted UDP-glucose 6-dehydrogenase
TS28Rum14365|CDS|CDS	0.5	32.5	0.1	M	COG1696	Predicted membrane protein involved in D-alanine export
TS28Rum11600|CDS|CDS	0.5	32.7	0.1	M	COG4932	Predicted outer membrane protein
Clep1819|CDS|CDS	0.2	11.0	0.1	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
TS29Rum20806|CDS|CDS	1.0	68.0	0.1	M	COG3940|COG5520	Predicted beta-xylosidase|O-Glycosyl hydrolase
TS29Fae09858|CDS|CDS	1.0	70.0	0.1	M	COG1876	D-alanyl-D-alanine carboxypeptidase
TS29Rum00488|CDS|CDS	0.5	35.5	0.1	M	COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes
TS29Col0670|CDS|CDS	0.5	37.0	0.1	M	COG3409	Putative peptidoglycan-binding domain-containing protein
TS29Bif1172|CDS|CDS	1.0	77.7	0.1	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS29Fae08522|CDS|CDS	1.5	117.5	0.1	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS29Bac04286|CDS|CDS	0.3	27.0	0.1	M	COG0438|COG1216	Glycosyltransferase|Predicted glycosyltransferases
CspSS23032|CDS|CDS	0.3	20.3	0.1	M	COG4932	Predicted outer membrane protein
TS29Fae08263|CDS|CDS	0.5	41.3	0.1	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
TS29Rum16612|CDS|CDS	1.0	84.0	0.1	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS29Rum02620|CDS|CDS	0.2	17.0	0.1	M	COG1088	dTDP-D-glucose 4,6-dehydratase
TS29Fae06331|CDS|CDS	0.5	43.0	0.1	M	COG1083	CMP-N-acetylneuraminic acid synthetase
TS29Rum17185|CDS|CDS	0.5	44.5	0.1	M	COG1696	Predicted membrane protein involved in D-alanine export
TS29Bif3383|CDS|CDS	1.0	92.7	0.0	M	COG0438	Glycosyltransferase
TS29Rum20318|CDS|CDS	0.5	50.0	0.0	M	COG0562	UDP-galactopyranose mutase
TS28Bif4905|CDS|CDS	0.5	50.3	0.0	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
Ehal1311|CDS|CDS	0.3	35.5	0.0	M	COG3049	Penicillin V acylase and related amidases
TS28Fae18189|CDS|CDS	0.3	35.5	0.0	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis
TS28Dor2628|CDS|CDS	2.0	217.3	0.0	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
TS29Bif0923|CDS|CDS	1.0	109.0	0.0	M	COG1091|COG1898	dTDP-4-dehydrorhamnose reductase|dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes
Robe2641|CDS|CDS	1.0	110.2	0.0	M	COG4932	Predicted outer membrane protein

TS29Fae09122|CDS|CDS	1.0	112.2	0.0	M	COG0739|COG3883|COG2951|COG0791	Membrane proteins related to metalloendopeptidases|Uncharacterized protein conserved in bacteria|Membrane-bound lytic murein transglycosylase B|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Rum21218|CDS|CDS	0.3	37.7	0.0	M	COG1686	D-alanyl-D-alanine carboxypeptidase
TS29Dor2226|CDS|CDS	2.0	229.3	0.0	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
CspM6211847|CDS|CDS	0.2	25.5	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
Cnex2289|CDS|CDS	0.2	25.5	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
Dfor2036|CDS|CDS	0.2	25.5	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
Ceut2220|CDS|CDS	0.2	25.5	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
Rbro1720|CDS|CDS	0.2	25.5	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Rum04257|CDS|CDS	0.3	30.0	0.0	M	COG1087	UDP-glucose 4-epimerase
TS29Rum00441|CDS|CDS	3.0	362.0	0.0	M	COG4886|COG3209|COG5276	Leucine-rich repeat (LRR) protein|Rhs family protein|Uncharacterized conserved protein
Ccom1803|CDS|CDS	0.3	30.2	0.0	M	COG4932	Predicted outer membrane protein
TS28Eub6359|CDS|CDS	0.3	41.0	0.0	M	COG0741|COG3757	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
TS29Rum21227|CDS|CDS	0.3	41.0	0.0	M	COG0741|COG3757	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)
Acac2248|CDS|CDS	0.2	27.0	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
TS28Rum11599|CDS|CDS	0.5	64.5	0.0	M	COG4932	Predicted outer membrane protein
TS28Bif5307|CDS|CDS	1.0	129.5	0.0	M	COG2148|COG0707	Sugar transferases involved in lipopolysaccharide synthesis|UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase
CspSS20003|CDS|CDS	0.3	33.5	0.0	M	COG4932	Predicted outer membrane protein
TS29Bif3514|CDS|CDS	0.5	78.1	0.0	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS28Bif4472|CDS|CDS	0.3	54.7	0.0	M	COG3409	Putative peptidoglycan-binding domain-containing protein
TS29Rum15667|CDS|CDS	1.0	167.0	0.0	M	COG5283|COG0741	Phage-related tail protein|Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)
Csci3148|CDS|CDS	0.1	15.3	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
Acol2776|CDS|CDS	0.1	15.5	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Bif3866|CDS|CDS	0.5	86.3	0.0	M	COG1087	UDP-glucose 4-epimerase
Cbol3084|CDS|CDS	0.1	15.9	0.0	M	COG0741|COG3757|COG0791	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)|Lyzozyme M1 (1,4-beta-N-acetylmuramidase)|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Bif0527|CDS|CDS	0.5	88.0	0.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Bif4496|CDS|CDS	0.5	88.0	0.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS29Bif3469|CDS|CDS	0.5	92.3	0.0	M	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
TS28Bif4957|CDS|CDS	0.5	95.1	0.0	M	COG5009|COG0744	Membrane carboxypeptidase/penicillin-binding protein|Membrane carboxypeptidase (penicillin-binding protein)
TS29Rum19621|CDS|CDS	1.2	221.8	0.0	M	COG4932	Predicted outer membrane protein
TS29RumUnc1573|CDS|CDS	1.0	218.0	0.0	M	COG4932|COG0739	Predicted outer membrane protein|Membrane proteins related to metalloendopeptidases
TS28Rum13909|CDS|CDS	0.3	82.5	0.0	M	COG4932	Predicted outer membrane protein
Dlon1668|CDS|CDS	0.3	84.5	0.0	M	COG4932	Predicted outer membrane protein
TS29Bif3594|CDS|CDS	0.5	127.0	0.0	M	COG0463	Glycosyltransferases involved in cell wall biogenesis
TS29Bif2829|CDS|CDS	0.2	51.5	0.0	M	COG0682	Prolipoprotein diacylglyceryltransferase
TS29Bif3079|CDS|CDS	0.3	80.6	0.0	M	COG1207	N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)
TS29Bif2420|CDS|CDS	0.3	98.5	0.0	M	COG0770	UDP-N-acetylmuramyl pentapeptide synthase
TS29Bif3129|CDS|CDS	1.0	476.0	0.0	M	COG4932	Predicted outer membrane protein
TS29Bif0506|CDS|CDS	0.3	178.0	0.0	M	COG3409	Putative peptidoglycan-binding domain-containing protein
TS29Bif2418|CDS|CDS	0.3	142.8	0.0	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2
TS28Fae15061|CDS|CDS	4.0	1.0	18.2	M|D	COG3206|COG0489|COG3944|COG2148	Uncharacterized protein involved in exopolysaccharide biosynthesis|ATPases involved in chromosome partitioning|Capsular polysaccharide biosynthesis protein|Sugar transferases involved in lipopolysaccharide synthesis
Buni2991|CDS|CDS	2.7	1.2	10.4	M|D	COG0739|COG4942	Membrane proteins related to metalloendopeptidases|Membrane-bound metallopeptidase
TS28Bac1582|CDS|CDS	2.7	1.2	10.4	M|D	COG0739|COG4942	Membrane proteins related to metalloendopeptidases|Membrane-bound metallopeptidase
TS29Bif0926|CDS|CDS	0.8	75.0	0.1	M|D	COG3206|COG0489|COG3944|COG2148	Uncharacterized protein involved in exopolysaccharide biosynthesis|ATPases involved in chromosome partitioning|Capsular polysaccharide biosynthesis protein|Sugar transferases involved in lipopolysaccharide synthesis
TS28Bif5289|CDS|CDS	0.8	110.0	0.0	M|D	COG3206|COG0489|COG3944|COG2148	Uncharacterized protein involved in exopolysaccharide biosynthesis|ATPases involved in chromosome partitioning|Capsular polysaccharide biosynthesis protein|Sugar transferases involved in lipopolysaccharide synthesis
BLD0562|CDS|Glycosyltransferase	2.3	0.3	40.9	M|G	COG0438|COG1543|COG0561|COG0297	Glycosyltransferase|Uncharacterized conserved protein|Predicted hydrolases of the HAD superfamily|Glycogen synthase
BactD10924|CDS|CDS	5.3	1.0	23.9	M|G	COG0438|COG0058	Glycosyltransferase|Glucan phosphorylase

Cbol4450|CDS|CDS	9.0	2.0	20.4	M|G	COG0451	Nucleoside-diphosphate-sugar epimerases
Buni1607|CDS|CDS	2.0	0.7	13.6	M|G	COG1086	Predicted nucleoside-diphosphate sugar epimerases
Bste1255|CDS|CDS	7.9	3.3	10.8	M|G	COG0438|COG0058	Glycosyltransferase|Glucan phosphorylase
BFych463854|CDS|glycosyltransferase	1.5	0.5	13.6	M|I	COG0463|COG1887|COG1216|COG1835	Glycosyltransferases involved in cell wall biogenesis|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Predicted glycosyltransferases|Predicted acyltransferases
TS29Fae09887|CDS|CDS	0.5	62.5	0.0	M|I	COG0463|COG1216|COG1835|COG1887|COG3754	Glycosyltransferases involved in cell wall biogenesis|Predicted glycosyltransferases|Predicted acyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis protein
TS28Eub1969|CDS|CDS	6.8	2.5	12.4	M|I|J	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
TS29Rum20296|CDS|CDS	114.5	46.5	11.2	M|I|J	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
TS29Bif3204|CDS|CDS	1.6	82.6	0.1	M|I|J	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
TS28Bif4604|CDS|CDS	0.7	38.3	0.1	M|I|J	COG0539|COG0761	Ribosomal protein S1|Penicillin tolerance protein
TS29Rum07198|CDS|CDS	1.0	0.3	13.6	M|J	COG0110|COG1208	Acetyltransferase (isoleucine patch superfamily)|Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)
TS28Fae12337|CDS|CDS	5.2	1.0	23.5	M|T	COG0739|COG3883|COG3103|COG0791	Membrane proteins related to metalloendopeptidases|Uncharacterized protein conserved in bacteria|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Rum19363|CDS|CDS	1.3	62.5	0.1	M|T	COG3409|COG1388|COG3883|COG3103|COG0791	Putative peptidoglycan-binding domain-containing protein|FOG: LysM repeat|Uncharacterized protein conserved in bacteria|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Rum21247|CDS|CDS	1.0	52.5	0.1	M|T	COG0739|COG3409|COG1388|COG3883|COG2951|COG5412|COG3103|COG0791	Membrane proteins related to metalloendopeptidases|Putative peptidoglycan-binding domain-containing protein|FOG: LysM repeat|Uncharacterized protein conserved in bacteria|Membrane-bound lytic murein transglycosylase B|Phage-related protein|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS29Fae06489|CDS|CDS	0.3	22.8	0.0	M|T	COG3409|COG1388|COG3883|COG3103|COG0791	Putative peptidoglycan-binding domain-containing protein|FOG: LysM repeat|Uncharacterized protein conserved in bacteria|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
TS28Fae00439|CDS|CDS	0.3	29.3	0.0	M|T	COG3409|COG1388|COG3883|COG3103|COG0791	Putative peptidoglycan-binding domain-containing protein|FOG: LysM repeat|Uncharacterized protein conserved in bacteria|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
Buni0764|CDS|CDS	4.4	0.5	40.1	M|U	COG1538	Outer membrane protein
TS28Fae10606|CDS|CDS	0.3	85.0	0.0	M|U|T	COG3409|COG1388|COG3451|COG3883|COG3103|COG0791	Putative peptidoglycan-binding domain-containing protein|FOG: LysM repeat|Type IV secretory pathway, VirB4 components|Uncharacterized protein conserved in bacteria|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)
Casp6307|CDS|CDS	6.0	1.0	27.2	N	COG5492	Bacterial surface proteins containing Ig-like domains
RintL10672|CDS|CDS	4.0	1.0	18.2	N	COG1843|COG1749|COG4786	Flagellar hook capping protein|Flagellar hook protein FlgE|Flagellar basal body rod protein
Cbol5448|CDS|CDS	12.0	3.0	18.2	N	COG5492|COG5263	Bacterial surface proteins containing Ig-like domains|FOG: Glucan-binding domain (YG repeat)
RintL11106|CDS|CDS	4.0	1.0	18.2	N	COG1344	Flagellin and related hook-associated proteins
TS28Clo03935|CDS|CDS	17.0	5.0	15.4	N	COG5492	Bacterial surface proteins containing Ig-like domains
TS29Rum12393|CDS|CDS	1.0	51.0	0.1	N	COG3225	ABC-type uncharacterized transport system involved in gliding motility, auxiliary component
TS29Fae04131|CDS|CDS	0.3	18.0	0.1	N	COG5651	PPE-repeat proteins
TS29Rum11623|CDS|CDS	1.0	65.0	0.1	N	COG5651	PPE-repeat proteins
TS29Met0283|CDS|CDS	0.3	26.0	0.1	N	COG5651	PPE-repeat proteins
TS28Dor2601|CDS|CDS	10.5	2.0	23.8	N|C|L|U	COG1156|COG1372|COG1157|COG0056	Archaeal/vacuolar-type H+-ATPase subunit B|Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|F0F1-type ATP synthase, alpha subunit
TS28Met1777|CDS|CDS	4.9	1.0	23.2	N|C|L|U	COG1156|COG1372|COG1157|COG0055	Archaeal/vacuolar-type H+-ATPase subunit B|Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|F0F1-type ATP synthase, beta subunit
TS29Par214|CDS|CDS	11.0	2.5	20.0	N|C|L|U	COG1156|COG1372|COG1157|COG0056	Archaeal/vacuolar-type H+-ATPase subunit B|Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|F0F1-type ATP synthase, alpha subunit
TS28Rum07611|CDS|CDS	7.5	2.5	13.6	N|C|L|U	COG1372|COG1157|COG1155|COG0055	Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A|F0F1-type ATP synthase, beta subunit
TS28Met1778|CDS|CDS	4.5	1.9	10.8	N|C|L|U	COG1372|COG1157|COG1155|COG0055	Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A|F0F1-type ATP synthase, beta subunit
Bryfor1729|CDS|CDS	6.0	2.0	13.6	N|G	COG5492|COG1501	Bacterial surface proteins containing Ig-like domains|Alpha-glucosidases, family 31 of glycosyl hydrolases
TS28Rum05733|CDS|CDS	8.0	1.0	36.3	N|K|T	COG0784|COG2197|COG2114|COG0835	FOG: CheY-like receiver|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Chemotaxis signal transduction protein
TS29Rum17966|CDS|CDS	0.5	24.0	0.1	N|K|T	COG4753|COG2207|COG0784|COG3279|COG4936|COG2197|COG2201	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|FOG: CheY-like receiver|Response regulator of the LytR/AlgR family|Predicted sensor domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain
TS29Rum16752|CDS|CDS	1.0	61.0	0.1	N|K|T	COG0642|COG4753|COG2207|COG2204|COG0784|COG3279|COG4936|COG5001|COG2197|COG2201|COG1776	Signal transduction histidine kinase|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|FOG: CheY-like receiver|Response regulator of the LytR/AlgR family|Predicted sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain|Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain|Chemotaxis protein CheC, inhibitor of MCP methylation
Msmi740101|CDS|CDS	4.1	0.2	93.1	N|L|C|U	COG1372|COG0055|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
Aput2338|CDS|CDS	14.0	2.0	31.8	N|L|C|U	COG1372|COG0055|COG1157|COG1155	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A

Msmi751598|CDS|CDS	4.9	1.0	23.2	N|L|C|U	COG1372|COG0055|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
Msmi751597|CDS|CDS	4.5	0.9	22.9	N|L|C|U	COG1372|COG0055|COG1157|COG1155	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A
Rumhyd1739|CDS|CDS	5.0	1.0	22.7	N|L|C|U	COG1372|COG0055|COG0056|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|F0F1-type ATP synthase, alpha subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
BactD10928|CDS|CDS	2.5	0.5	22.7	N|L|C|U	COG1372|COG0055|COG0056|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|F0F1-type ATP synthase, alpha subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
Rumhyd1738|CDS|CDS	4.0	1.0	18.2	N|L|C|U	COG1372|COG0055|COG1157|COG1155	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A
Dfor1023|CDS|CDS	8.5	3.0	12.9	N|L|C|U	COG1372|COG0056|COG1156|COG1157	Intein/homing endonuclease|F0F1-type ATP synthase, alpha subunit|Archaeal/vacuolar-type H+-ATPase subunit B|Flagellar biosynthesis/type III secretory pathway ATPase
Dfor1022|CDS|CDS	7.8	3.0	11.9	N|L|C|U	COG1372|COG1157|COG1155	Intein/homing endonuclease|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A
Msmi740100|CDS|CDS	4.2	1.9	10.0	N|L|C|U	COG1372|COG0055|COG1157|COG1155	Intein/homing endonuclease|F0F1-type ATP synthase, beta subunit|Flagellar biosynthesis/type III secretory pathway ATPase|Archaeal/vacuolar-type H+-ATPase subunit A
Cbol4151|CDS|CDS	0.3	13.0	0.1	N|U	COG1298|COG4789	Flagellar biosynthesis pathway, component FlhA|Type III secretory pathway, component EscV
TS28Rum00969|CDS|CDS	1.0	63.0	0.1	N|U	COG4962|COG0630	Flp pilus assembly protein, ATPase CpaF|Type IV secretory pathway, VirB11 components, and related ATPases involved in archaeal flagella biosynthesis
Rumhyd1374|CDS|CDS	10.0	2.0	22.7	N|U|W	COG5492|COG5295	Bacterial surface proteins containing Ig-like domains|Autotransporter adhesin
TS28Bac5242|CDS|CDS	77.3	0.3	1,053.2	O	COG0459	Chaperonin GroEL (HSP60 family)
Bova3457|CDS|CDS	108.3	0.5	983.8	O	COG0459	Chaperonin GroEL (HSP60 family)
TS29Bac10141|CDS|CDS	1,471.7	12.5	534.5	O	COG0071	Molecular chaperone (small heat shock protein)
BactD11031|CDS|CDS	164.1	1.5	496.6	O	COG0459	Chaperonin GroEL (HSP60 family)
TS28Bac5566|CDS|CDS	36.0	0.3	490.3	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Buni3363|CDS|CDS	36.0	0.3	490.3	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Aput0213|CDS|CDS	252.8	3.0	382.6	O	COG0443	Molecular chaperone
Buni1622|CDS|CDS	40.2	0.5	365.0	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Bxyl0114|CDS|CDS	44.7	0.6	347.8	O	COG0071	Molecular chaperone (small heat shock protein)
Bfin1972|CDS|CDS	41.2	0.6	320.6	O	COG0071	Molecular chaperone (small heat shock protein)
Buni3583|CDS|CDS	229.2	3.5	297.3	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
BactD13252|CDS|CDS	65.2	1.0	295.9	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS29Bac03134|CDS|CDS	505.2	8.0	286.7	O	COG0459	Chaperonin GroEL (HSP60 family)
Buni0874|CDS|CDS	175.8	3.3	239.5	O	COG0459	Chaperonin GroEL (HSP60 family)
TS28Bac1430|CDS|CDS	69.7	1.3	237.2	O	COG0326	Molecular chaperone, HSP90 family
FpraM2121131|CDS|CDS	24.6	0.5	223.2	O	COG0459	Chaperonin GroEL (HSP60 family)
BactD10743|CDS|CDS	31.9	0.7	217.4	O	COG0443	Molecular chaperone
BactD21332|CDS|CDS	20.7	0.5	188.2	O	COG0459	Chaperonin GroEL (HSP60 family)
TS28Bac6142|CDS|CDS	136.6	3.5	177.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Bac00073|CDS|CDS	286.1	7.5	173.2	O	COG0443	Molecular chaperone
TS29Bac03135|CDS|CDS	389.5	11.3	156.0	O	COG0459	Chaperonin GroEL (HSP60 family)
BactD10134|CDS|CDS	31.5	1.0	142.9	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Bova0387|CDS|CDS	30.5	1.0	138.5	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Bxyl1319|CDS|CDS	14.3	0.5	130.2	O	COG0234	Co-chaperonin GroES (HSP10)
Rtor0277|CDS|CDS	28.5	1.0	129.4	O	COG0459	Chaperonin GroEL (HSP60 family)
Cbol3419|CDS|CDS	28.0	1.0	127.1	O	COG0071	Molecular chaperone (small heat shock protein)
Aput2048|CDS|CDS	250.0	9.0	126.1	O	COG0459	Chaperonin GroEL (HSP60 family)
BactD10815|CDS|CDS	6.5	0.3	118.0	O	COG0071	Molecular chaperone (small heat shock protein)
Buni1264|CDS|CDS	11.5	0.5	104.4	O	COG4826	Serine protease inhibitor
Bfin0905|CDS|CDS	22.9	1.0	103.8	O	COG0071	Molecular chaperone (small heat shock protein)
Buni3570|CDS|CDS	565.3	26.5	96.8	O	COG0443	Molecular chaperone
TS29Bac00097|CDS|CDS	21.2	1.0	96.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Par685|CDS|CDS	39.5	2.0	89.7	O	COG0443	Molecular chaperone
BactD24011|CDS|CDS	28.4	1.5	86.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Bxyl3423|CDS|CDS	68.6	3.7	84.9	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Bova0436|CDS|CDS	8.6	0.5	78.4	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
BactD21825|CDS|CDS	8.6	0.5	78.4	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Bthe3732369|CDS|CDS	22.9	1.3	77.9	O	COG0071	Molecular chaperone (small heat shock protein)
Bthe7331683|CDS|CDS	22.9	1.3	77.9	O	COG0071	Molecular chaperone (small heat shock protein)
BactD12632|CDS|CDS	22.9	1.3	77.9	O	COG0071	Molecular chaperone (small heat shock protein)
Aput2033|CDS|CDS	144.3	8.5	77.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Bac00096|CDS|CDS	469.4	29.0	73.5	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Bxyl1318|CDS|CDS	274.4	17.5	71.2	O	COG0459	Chaperonin GroEL (HSP60 family)
Buni1556|CDS|CDS	150.2	9.8	69.3	O	COG0326	Molecular chaperone, HSP90 family
Acac2680|CDS|CDS	15.1	1.0	68.7	O	COG0459	Chaperonin GroEL (HSP60 family)
Bcap3125|CDS|CDS	15.0	1.0	68.1	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Fae22642|CDS|CDS	80.8	5.5	66.7	O	COG0465	ATP-dependent Zn proteases
BactD13253|CDS|CDS	22.0	1.5	66.7	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS29Bac08977|CDS|CDS	43.4	3.0	65.7	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
BactD10814|CDS|CDS	28.2	2.0	64.1	O	COG0071	Molecular chaperone (small heat shock protein)
TS28RumUnc2062|CDS|CDS	6.9	0.5	62.8	O	COG0443	Molecular chaperone
TS28Bac5202|CDS|CDS	4.0	0.3	54.5	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS28Ali1084|CDS|CDS	12.0	1.0	54.5	O	COG0326	Molecular chaperone, HSP90 family
Cbol3244|CDS|CDS	12.0	1.0	54.5	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Eub5274|CDS|CDS	6.0	0.5	54.5	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
DpigGOR11214|CDS|CDS	11.3	1.0	51.5	O	COG0459	Chaperonin GroEL (HSP60 family)
Acac0820|CDS|CDS	11.0	1.0	49.9	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
FpraM2121935|CDS|CDS	5.4	0.5	49.2	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
Bova4080|CDS|CDS	25.4	2.5	46.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Rum15898|CDS|CDS	25.3	2.5	46.0	O	COG0071	Molecular chaperone (small heat shock protein)
Ehal2235|CDS|CDS	10.1	1.0	45.8	O	COG0459	Chaperonin GroEL (HSP60 family)
Bcap2713|CDS|CDS	10.0	1.0	45.4	O	COG0071	Molecular chaperone (small heat shock protein)

Cbol1826|CDS|CDS	54.9	5.5	45.3	O	COG0443	Molecular chaperone
TS29Bac02290|CDS|CDS	109.0	11.0	45.0	O	COG0576	Molecular chaperone GrpE (heat shock protein)
BactD10727|CDS|CDS	85.6	8.7	44.8	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Robe0689|CDS|CDS	9.7	1.0	43.9	O	COG0071	Molecular chaperone (small heat shock protein)
Aput1682|CDS|CDS	67.0	7.0	43.5	O	COG0326	Molecular chaperone, HSP90 family
Hfil1639|CDS|CDS	9.5	1.0	43.1	O	COG0443	Molecular chaperone
TS28Rum02228|CDS|CDS	9.5	1.0	43.1	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Bac02289|CDS|CDS	109.2	11.5	43.1	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Clo10640|CDS|CDS	145.0	15.5	42.5	O	COG1180	Pyruvate-formate lyase-activating enzyme
TS29Clo0165|CDS|CDS	145.0	15.5	42.5	O	COG1180	Pyruvate-formate lyase-activating enzyme
TS29Bac04323|CDS|CDS	185.2	19.8	42.4	O	COG0326	Molecular chaperone, HSP90 family
Bova0418|CDS|CDS	4.7	0.5	42.2	O	COG2077	Peroxiredoxin
BactD21806|CDS|CDS	4.7	0.5	42.2	O	COG2077	Peroxiredoxin
Bxyl2507|CDS|CDS	6.0	0.7	40.9	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
Bxyl3438|CDS|CDS	69.5	7.8	40.3	O	COG0443	Molecular chaperone
TS29Bac12047|CDS|CDS	48.5	5.6	39.5	O	COG0071	Molecular chaperone (small heat shock protein)
Cbol6209|CDS|CDS	60.8	7.0	39.5	O	COG0459	Chaperonin GroEL (HSP60 family)
TS29Bac08976|CDS|CDS	32.3	4.0	36.6	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
TS28Rum15360|CDS|CDS	52.0	6.5	36.3	O	COG0465	ATP-dependent Zn proteases
TS28BacUnc24|CDS|CDS	8.0	1.0	36.3	O	COG0443	Molecular chaperone
Acac2686|CDS|CDS	8.0	1.0	36.3	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Rumhyd3322|CDS|CDS	8.0	1.0	36.3	O	COG0443	Molecular chaperone
Cbol1825|CDS|CDS	8.0	1.0	36.3	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Fae13136|CDS|CDS	23.8	3.0	36.0	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Rum10465|CDS|CDS	14.2	1.8	35.1	O	COG0443	Molecular chaperone
ShigspD90161|CDS|CDS	3.8	0.5	34.8	O	COG1220	ATP-dependent protease HslVU (ClpYQ), ATPase subunit
Rtor1076|CDS|CDS	33.3	4.5	33.6	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Bac07270|CDS|CDS	116.0	16.3	32.2	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Robe1604|CDS|CDS	2.3	0.3	31.8	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Cbol2325|CDS|CDS	7.0	1.0	31.8	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Fae12055|CDS|CDS	7.0	1.0	31.8	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS29Fae01938|CDS|CDS	7.0	1.0	31.8	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
RintL10144|CDS|CDS	14.0	2.0	31.8	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Rum03617|CDS|CDS	13.0	2.0	29.5	O	COG0326	Molecular chaperone, HSP90 family
TS28Rum13475|CDS|CDS	6.5	1.0	29.5	O	COG4826	Serine protease inhibitor
TS28Clo00136|CDS|CDS	8.3	1.3	28.4	O	COG0443	Molecular chaperone
TS28Rum13617|CDS|CDS	40.5	6.5	28.3	O	COG0326	Molecular chaperone, HSP90 family
TS28Fae19331|CDS|CDS	3.1	0.5	28.0	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS28Fae14370|CDS|CDS	146.4	23.8	27.9	O	COG0071	Molecular chaperone (small heat shock protein)
Buni1869|CDS|CDS	9.2	1.5	27.7	O	COG0826	Collagenase and related proteases
TS29Bac08465|CDS|CDS	80.7	13.3	27.5	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Bste1251|CDS|CDS	42.4	7.0	27.5	O	COG0071	Molecular chaperone (small heat shock protein)
Bova0514|CDS|CDS	6.0	1.0	27.4	O	COG0326	Molecular chaperone, HSP90 family
TS28Fae20436|CDS|CDS	56.1	9.3	27.3	O	COG0071	Molecular chaperone (small heat shock protein)
Bcap0150|CDS|CDS	6.0	1.0	27.2	O	COG0326	Molecular chaperone, HSP90 family
TS28Rum01871|CDS|CDS	3.0	0.5	27.2	O	COG1975|COG2068	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family|Uncharacterized MobA-related protein
Buni2305|CDS|CDS	3.0	0.5	27.2	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
Caer1063|CDS|CDS	3.0	0.5	27.2	O	COG0326	Molecular chaperone, HSP90 family
TS28Rum04455|CDS|CDS	12.0	2.0	27.2	O	COG0071	Molecular chaperone (small heat shock protein)
Msmi741565|CDS|CDS	2.8	0.5	25.7	O	COG0459	Chaperonin GroEL (HSP60 family)
Robe2241|CDS|CDS	5.5	1.0	25.0	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
TS28Rum14890|CDS|CDS	5.5	1.0	25.0	O	COG0826	Collagenase and related proteases
Bcap2192|CDS|CDS	16.5	3.0	25.0	O	COG0443	Molecular chaperone
Bxyl0797|CDS|CDS	24.4	4.5	24.6	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS29Bac03133|CDS|CDS	59.3	11.0	24.5	O	COG0234	Co-chaperonin GroES (HSP10)
TS28Fae21987|CDS|CDS	40.2	7.5	24.3	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Rum02487|CDS|CDS	16.0	3.0	24.2	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Bac11229|CDS|CDS	87.1	16.8	23.5	O	COG0443	Molecular chaperone
TS29Bac03142|CDS|CDS	46.5	9.0	23.5	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
TS28Rum11951|CDS|CDS	5.0	1.0	22.7	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Fae12451|CDS|CDS	10.0	2.0	22.7	O	COG0465	ATP-dependent Zn proteases
Dfor0868|CDS|CDS	5.0	1.0	22.7	O	COG0234	Co-chaperonin GroES (HSP10)
BactD10740|CDS|CDS	1.7	0.3	22.5	O	COG3187	Heat shock protein
FpraM2121832|CDS|CDS	58.0	12.0	21.9	O	COG0443	Molecular chaperone
TS29Rum21189|CDS|CDS	130.3	27.0	21.9	O	COG0071	Molecular chaperone (small heat shock protein)
Bxyl3238|CDS|CDS	3.6	0.8	21.9	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
BactD12826|CDS|CDS	6.0	1.3	21.6	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
TS29Rum21190|CDS|CDS	164.0	34.5	21.6	O	COG0071	Molecular chaperone (small heat shock protein)
TS29Bac08839|CDS|CDS	28.0	6.0	21.2	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Fae16180|CDS|CDS	20.9	4.5	21.1	O	COG0443	Molecular chaperone
TS28Rum15681|CDS|CDS	72.3	16.0	20.5	O	COG0443	Molecular chaperone
TS28Fae00934|CDS|CDS	9.0	2.0	20.4	O	COG0637|COG1214|COG0546	Predicted phosphatase/phosphohexomutase|Inactive homolog of metal-dependent proteases, putative molecular chaperone|Predicted phosphatases
Bhan0480|CDS|CDS	4.5	1.0	20.4	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Clo03064|CDS|CDS	9.0	2.0	20.4	O	COG0443	Molecular chaperone
TS28Fae03680|CDS|CDS	9.0	2.0	20.4	O	COG0459	Chaperonin GroEL (HSP60 family)
Rgna0392|CDS|CDS	9.0	2.0	20.4	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Dor1724|CDS|CDS	4.5	1.0	20.4	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS28Fae03405|CDS|CDS	4.5	1.0	20.4	O	COG0459	Chaperonin GroEL (HSP60 family)
TS29Rum00766|CDS|CDS	35.6	8.0	20.2	O	COG0443	Molecular chaperone
BactD13604|CDS|CDS	13.3	3.0	20.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Fae07607|CDS|CDS	44.0	10.0	20.0	O	COG0443	Molecular chaperone
Msmi750820|CDS|CDS	1.5	0.3	19.7	O	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2
Bxyl3928|CDS|CDS	15.1	3.5	19.6	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Msmi750714|CDS|CDS	5.0	1.2	19.3	O	COG0459	Chaperonin GroEL (HSP60 family)
Buni1555|CDS|CDS	31.5	7.5	19.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
BactD14216|CDS|CDS	4.1	1.0	18.6	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1

TS28Dor2295|CDS|CDS	2.0	0.5	18.2	O	COG0826	Collagenase and related proteases
TS28Rum10110|CDS|CDS	4.0	1.0	18.2	O	COG0309|COG1992	Hydrogenase maturation factor|Uncharacterized conserved protein
Dlon0413|CDS|CDS	2.0	0.5	18.2	O	COG0826	Collagenase and related proteases
Bcap2191|CDS|CDS	4.0	1.0	18.2	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Cmet1180|CDS|CDS	4.0	1.0	18.2	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28BacUnc23|CDS|CDS	4.0	1.0	18.2	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Fae03685|CDS|CDS	4.0	1.0	18.2	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS28Fae00303|CDS|CDS	11.8	3.0	17.9	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Even1759|CDS|CDS	2.0	0.5	17.7	O	COG0465	ATP-dependent Zn proteases
Aput0902|CDS|CDS	27.0	7.0	17.5	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Bova3439|CDS|CDS	6.2	1.6	17.5	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
Acac1769|CDS|CDS	7.7	2.0	17.4	O	COG0443	Molecular chaperone
Buni0216|CDS|CDS	5.0	1.3	17.0	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS29Ali408|CDS|CDS	23.8	6.5	16.6	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
Rtor1695|CDS|CDS	5.5	1.5	16.6	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Rum07454|CDS|CDS	5.5	1.5	16.6	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
TS28Fae21350|CDS|CDS	16.0	4.5	16.1	O	COG0071	Molecular chaperone (small heat shock protein)
BactD23099|CDS|CDS	7.0	2.0	16.0	O	COG0326	Molecular chaperone, HSP90 family
ShigspD91612|CDS|CDS	1.2	0.3	15.9	O	COG0465	ATP-dependent Zn proteases
TS29Bac04280|CDS|CDS	7.0	2.0	15.9	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
TS28Rum13562|CDS|CDS	3.5	1.0	15.9	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Met0356|CDS|CDS	3.5	1.0	15.9	O	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase component
TS28Clo08951|CDS|CDS	3.5	1.0	15.9	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Col1524|CDS|CDS	3.5	1.0	15.9	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Fae18734|CDS|CDS	19.0	5.5	15.7	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Fae10762|CDS|CDS	20.5	6.0	15.5	O	COG0576	Molecular chaperone GrpE (heat shock protein)
BactD12369|CDS|CDS	2.8	0.8	15.4	O	COG3590	Predicted metalloendopeptidase
Bxyl3171|CDS|CDS	7.3	2.2	15.4	O	COG0612|COG1025	Predicted Zn-dependent peptidases|Secreted/periplasmic Zn-dependent peptidases, insulinase-like
TS28Rum13474|CDS|CDS	23.5	7.0	15.2	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
TS28Fae17572|CDS|CDS	40.8	12.3	15.0	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Fae00044|CDS|CDS	34.7	10.5	15.0	O	COG0459	Chaperonin GroEL (HSP60 family)
Rgna0393|CDS|CDS	19.5	6.0	14.8	O	COG0443	Molecular chaperone
Mmul2106|CDS|CDS	6.5	2.0	14.8	O	COG0459	Chaperonin GroEL (HSP60 family)
Csci3942|CDS|CDS	3.3	1.0	14.8	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Rum00574|CDS|CDS	55.3	17.0	14.8	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS28Fae13683|CDS|CDS	14.4	4.5	14.5	O	COG0459	Chaperonin GroEL (HSP60 family)
TS29Bac09072|CDS|CDS	32.0	10.0	14.5	O	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2
TS28Rum07453|CDS|CDS	14.3	4.7	13.9	O	COG0443	Molecular chaperone
Bova3948|CDS|CDS	12.8	4.3	13.7	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
TS28Fae15347|CDS|CDS	3.0	1.0	13.6	O	COG0691	tmRNA-binding protein
TS28Clo05586|CDS|CDS	3.0	1.0	13.6	O	COG0533|COG1214	Metal-dependent proteases with possible chaperone activity|Inactive homolog of metal-dependent proteases, putative molecular chaperone
TS28Bac4190|CDS|CDS	1.5	0.5	13.6	O	COG0465	ATP-dependent Zn proteases
Buni3186|CDS|CDS	3.0	1.0	13.6	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
Svar0626|CDS|CDS	3.0	1.0	13.6	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS29Rum10777|CDS|CDS	1.5	0.5	13.6	O	COG0637|COG1214|COG0546	Predicted phosphatase/phosphohexomutase|Inactive homolog of metal-dependent proteases, putative molecular chaperone|Predicted phosphatases
Rgna2792|CDS|CDS	1.5	0.5	13.6	O	COG0637|COG1214|COG0546	Predicted phosphatase/phosphohexomutase|Inactive homolog of metal-dependent proteases, putative molecular chaperone|Predicted phosphatases
TS28Rum16032|CDS|CDS	6.0	2.0	13.6	O	COG1219	ATP-dependent protease Clp, ATPase subunit
Msmi740680|CDS|CDS	1.5	0.5	13.6	O	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain
Casp1113|CDS|CDS	3.0	1.0	13.6	O	COG0465	ATP-dependent Zn proteases
TS28Rum00999|CDS|CDS	3.0	1.0	13.6	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
ShigspD91293|CDS|CDS	1.5	0.5	13.6	O	COG0330	Membrane protease subunits, stomatin/prohibitin homologs
RintL12108|CDS|CDS	6.0	2.0	13.6	O	COG0459	Chaperonin GroEL (HSP60 family)
Bova1926|CDS|CDS	3.0	1.0	13.6	O	COG0466	ATP-dependent Lon protease, bacterial type
TS29Rum10232|CDS|CDS	18.0	6.0	13.6	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
BactD21345|CDS|CDS	6.2	2.1	13.3	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
Bcap0454|CDS|CDS	20.5	7.0	13.3	O	COG0459	Chaperonin GroEL (HSP60 family)
TS28Rum10464|CDS|CDS	17.5	6.0	13.2	O	COG0576	Molecular chaperone GrpE (heat shock protein)
Bhan0262|CDS|CDS	5.8	2.0	13.1	O	COG0443	Molecular chaperone
TS28Bif0718|CDS|CDS	10.1	3.5	13.0	O	COG0465	ATP-dependent Zn proteases
TS29Rum01497|CDS|CDS	17.0	6.0	12.9	O	COG0071	Molecular chaperone (small heat shock protein)
TS28Rum01574|CDS|CDS	2.8	1.0	12.9	O	COG0234	Co-chaperonin GroES (HSP10)
TS29Bac01271|CDS|CDS	11.3	4.0	12.9	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
Bxyl1074|CDS|CDS	1.4	0.5	12.9	O	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2
Rtor1694|CDS|CDS	14.3	5.2	12.6	O	COG0443	Molecular chaperone
TS29Bac08975|CDS|CDS	24.9	9.0	12.5	O	COG0576	Molecular chaperone GrpE (heat shock protein)
Rgna0856|CDS|CDS	11.0	4.0	12.5	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
TS28Clo06646|CDS|CDS	11.0	4.0	12.5	O	COG1180	Pyruvate-formate lyase-activating enzyme
TS28Met0139|CDS|CDS	5.5	2.0	12.5	O	COG0459	Chaperonin GroEL (HSP60 family)
FpraM2120868|CDS|CDS	26.1	9.5	12.5	O	COG0443	Molecular chaperone
TS29LacUnc038|CDS|CDS	19.0	7.0	12.3	O	COG0465	ATP-dependent Zn proteases
Bxyl0423|CDS|CDS	11.2	4.2	12.2	O	COG0326	Molecular chaperone, HSP90 family
TS28Dor2218|CDS|CDS	5.4	2.0	12.2	O	COG0443	Molecular chaperone
Caer1725|CDS|CDS	25.0	9.5	11.9	O	COG0443	Molecular chaperone
BactD13766|CDS|CDS	7.0	2.7	11.9	O	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component
TS29Rum05274|CDS|CDS	13.0	5.0	11.8	O	COG0443	Molecular chaperone
Bova0386|CDS|CDS	5.2	2.0	11.8	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS28Met1763|CDS|CDS	1.7	0.7	11.6	O	COG0459	Chaperonin GroEL (HSP60 family)
TS28Fae02429|CDS|CDS	5.0	2.0	11.3	O	COG0464|COG0790	ATPases of the AAA+ class|FOG: TPR repeat, SEL1 subfamily
TS29Bac08374|CDS|CDS	2.5	1.0	11.3	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1
Aput2283|CDS|CDS	5.0	2.0	11.3	O	COG0760	Parvulin-like peptidyl-prolyl isomerase
DpigATC1297|CDS|CDS	2.5	1.0	11.3	O	COG0465	ATP-dependent Zn proteases
TS28Rum11937|CDS|CDS	5.0	2.0	11.3	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain

TS29Clo4647|CDS|CDS	2.5	1.0	11.3	O	COG0234	Co-chaperonin GroES (HSP10)
Msmi740790|CDS|CDS	2.5	1.0	11.3	O	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase component
TS29Rum09003|CDS|CDS	5.0	2.0	11.3	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS29Ali162|CDS|CDS	7.5	3.0	11.3	O	COG0466	ATP-dependent Lon protease, bacterial type
TS29Rum04971|CDS|CDS	7.5	3.0	11.3	O	COG0326	Molecular chaperone, HSP90 family
TS29Clo4152|CDS|CDS	1.7	0.7	11.3	O	COG1219	ATP-dependent protease Clp, ATPase subunit
TS28Eub6537|CDS|CDS	2.0	0.8	10.9	O	COG0265	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain
Casp3707|CDS|CDS	1.2	0.5	10.9	O	COG0330	Membrane protease subunits, stomatin/prohibitin homologs
Bxyl2488|CDS|CDS	3.6	1.5	10.7	O	COG0326	Molecular chaperone, HSP90 family
FpraM2121084|CDS|CDS	4.7	2.0	10.7	O	COG0330	Membrane protease subunits, stomatin/prohibitin homologs
BactD13767|CDS|CDS	1.2	0.5	10.6	O	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase component
Rgna1990|CDS|CDS	3.5	1.5	10.6	O	COG0234	Co-chaperonin GroES (HSP10)
TS28Eub0003|CDS|CDS	3.5	1.5	10.6	O	COG0446|COG0492	Uncharacterized NAD(FAD)-dependent dehydrogenases|Thioredoxin reductase
TS29Rum07215|CDS|CDS	3.5	1.5	10.6	O	COG0234	Co-chaperonin GroES (HSP10)
Bxyl0483|CDS|CDS	5.8	2.5	10.6	O	COG0466	ATP-dependent Lon protease, bacterial type
TS28Bac1619|CDS|CDS	5.0	2.2	10.5	O	COG0826	Collagenase and related proteases
Bova0515|CDS|CDS	6.8	3.0	10.3	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Rum12511|CDS|CDS	4.5	2.0	10.2	O	COG0484|COG2214	DnaJ-class molecular chaperone with C-terminal Zn finger domain|DnaJ-class molecular chaperone
TS29Rum10231|CDS|CDS	4.5	2.0	10.2	O	COG0544	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
TS28Clo08817|CDS|CDS	3.3	1.5	10.1	O	COG0326	Molecular chaperone, HSP90 family
TS29Col0010|CDS|CDS	1.0	46.0	0.1	O	COG0826	Collagenase and related proteases
TS29Bif4111|CDS|CDS	1.5	69.8	0.1	O	COG0330	Membrane protease subunits, stomatin/prohibitin homologs
TS28Fae00026|CDS|CDS	0.5	24.5	0.1	O	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase component
TS29Bif0247|CDS|CDS	0.3	17.2	0.1	O	COG3118	Thioredoxin domain-containing protein
TS29Col0525|CDS|CDS	1.0	52.0	0.1	O	COG0826	Collagenase and related proteases
TS28Bif1178|CDS|CDS	0.3	13.1	0.1	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS29Bif0594|CDS|CDS	0.3	13.1	0.1	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS29Col1396|CDS|CDS	0.5	30.0	0.1	O	COG0576	Molecular chaperone GrpE (heat shock protein)
TS29Col1411|CDS|CDS	0.5	31.0	0.1	O	COG0409	Hydrogenase maturation factor
TS29Met0651|CDS|CDS	0.2	13.6	0.1	O	COG1899	Deoxyhypusine synthase
TS29Bac11731|CDS|CDS	0.2	11.3	0.1	O	COG0602|COG3759	Organic radical activating enzymes|Predicted membrane protein
TS28Bif4910|CDS|CDS	0.3	18.0	0.1	O	COG0691	tmRNA-binding protein
TS29Bif3474|CDS|CDS	0.3	18.0	0.1	O	COG0691	tmRNA-binding protein
TS28Bif4312|CDS|CDS	0.1	9.2	0.1	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS28Fae20193|CDS|CDS	0.5	41.0	0.1	O	COG0466	ATP-dependent Lon protease, bacterial type
TS29Bif2556|CDS|CDS	0.5	42.0	0.1	O	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
TS29Bif4028|CDS|CDS	1.1	115.6	0.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Fae00322|CDS|CDS	0.5	57.0	0.0	O	COG0826	Collagenase and related proteases
TS28Bif0650|CDS|CDS	0.5	65.3	0.0	O	COG3590	Predicted metalloendopeptidase
Bpse0350|CDS|CDS	0.1	18.8	0.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Col1409|CDS|CDS	0.5	81.0	0.0	O	COG0068|COG0298	Hydrogenase maturation factor|Hydrogenase maturation factor
TS29Bif3936|CDS|CDS	0.5	102.2	0.0	O	COG3590	Predicted metalloendopeptidase
TS29Bif1659|CDS|CDS	0.1	46.7	0.0	O	COG0542	ATPases with chaperone activity, ATP-binding subunit
TS29Bif3037|CDS|CDS	0.3	104.4	0.0	O	COG0606	Predicted ATPase with chaperone activity
TS29Bac06014|CDS|CDS	33.0	8.0	18.7	O|C	COG0526|COG3118	Thiol-disulfide isomerase and thioredoxins|Thioredoxin domain-containing protein
TS29Rum03180|CDS|CDS	6.0	2.0	13.6	O|C	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
TS29Rum17082|CDS|CDS	0.5	23.5	0.1	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS29Fae06719|CDS|CDS	0.5	29.0	0.1	O|C	COG0526	Thiol-disulfide isomerase and thioredoxins
TS28Fae22864|CDS|CDS	1.0	71.0	0.1	O|C	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
TS29Bif0497|CDS|CDS	1.5	135.9	0.1	O|C	COG0526|COG0492	Thiol-disulfide isomerase and thioredoxins|Thioredoxin reductase
TS29Bac06187|CDS|CDS	3.3	1.5	10.1	O|C|V	COG2274|COG1132|COG5265|COG4987	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
TS29Bif0895|CDS|CDS	3.3	189.8	0.1	O|C|V	COG2274|COG1132|COG5265|COG4988|COG4987	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
TS28Bif0390|CDS|CDS	3.3	189.8	0.1	O|C|V	COG2274|COG1132|COG5265|COG4988|COG4987	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
TS29Rum11430|CDS|CDS	1.0	71.5	0.1	O|C|V	COG1132|COG4987	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components
TS29Col0711|CDS|CDS	1.0	86.0	0.1	O|C|V	COG1132|COG5265|COG4988	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components|ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components
TS29Col1412|CDS|CDS	0.5	31.0	0.1	O|H	COG0611|COG0309|COG1992	Thiamine monophosphate kinase|Hydrogenase maturation factor|Uncharacterized conserved protein
TS29Fae01165|CDS|CDS	0.5	57.0	0.0	O|K	COG0378	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase
TS28Rum01487|CDS|CDS	3.0	0.5	27.2	O|M	COG3914|COG0463|COG1216|COG1887|COG3754	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family|Glycosyltransferases involved in cell wall biogenesis|Predicted glycosyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis protein

TS28Fae18569|CDS|CDS	0.5	57.5	0.0	O|M|I	COG3914|COG0463|COG1216|COG1835|COG1887|COG3754	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family|Glycosyltransferases involved in cell wall biogenesis|Predicted glycosyltransferases|Predicted acyltransferases|Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC|Lipopolysaccharide biosynthesis protein
TS29Rum20133|CDS|CDS	5.0	308.0	0.1	O|M|U|Q	COG4886|COG2931|COG3210|COG1404|COG5632	Leucine-rich repeat (LRR) protein|RTX toxins and related Ca2+-binding proteins|Large exoproteins involved in heme utilization or adhesion|Subtilisin-like serine proteases|N-acetylmuramoyl-L-alanine amidase
TS28Rum14049|CDS|CDS	3.5	0.5	31.8	O|Q	COG0561|COG2050|COG4696|COG0652	Predicted hydrolases of the HAD superfamily|Uncharacterized protein, possibly involved in aromatic compounds catabolism|Uncharacterized protein conserved in bacteria|Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
TS29Bif1891|CDS|CDS	0.7	33.7	0.1	O|T	COG1391	Glutamine synthetase adenylyltransferase
Robe1971|CDS|CDS	2.3	0.3	31.8	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
TS28Rum16034|CDS|CDS	15.9	3.0	24.0	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
TS28Bif0586|CDS|CDS	0.3	11.5	0.1	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
TS29Bif3046|CDS|CDS	0.3	23.5	0.0	O|U	COG0740	Protease subunit of ATP-dependent Clp proteases
b1978|CDS|adhesin	4.0	1.0	18.2	O|U|W	COG1404|COG3210|COG5295	Subtilisin-like serine proteases|Large exoproteins involved in heme utilization or adhesion|Autotransporter adhesin
ShigspD92536|CDS|CDS	3.0	1.0	13.6	O|U|W	COG1404|COG3210|COG5295	Subtilisin-like serine proteases|Large exoproteins involved in heme utilization or adhesion|Autotransporter adhesin
TS29Fae10180|CDS|CDS	1.0	47.5	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS29Fae07435|CDS|CDS	1.0	52.0	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS29Bif2390|CDS|CDS	1.7	87.7	0.1	O|V	COG2274|COG1132|COG5265	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS29Fae08001|CDS|CDS	1.7	96.5	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS28Bif0914|CDS|CDS	1.7	98.2	0.1	O|V	COG2274|COG1132|COG5265	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS28Rum11649|CDS|CDS	0.5	29.5	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS29Col1566|CDS|CDS	1.0	69.0	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS29Fae04222|CDS|CDS	0.5	42.5	0.1	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
TS29Col1883|CDS|CDS	0.5	50.5	0.0	O|V	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
Bste1248|CDS|CDS	56.5	2.0	128.2	P	COG1528	Ferritin-like protein
TS29Bac07333|CDS|CDS	19.0	1.0	86.3	P	COG1528	Ferritin-like protein
Bthe3732372|CDS|CDS	2.6	0.3	47.8	P	COG1528	Ferritin-like protein
Bfin0902|CDS|CDS	2.6	0.3	47.8	P	COG1528	Ferritin-like protein
Bthe7331680|CDS|CDS	2.6	0.3	47.8	P	COG1528	Ferritin-like protein
BactD12629|CDS|CDS	2.6	0.3	47.8	P	COG1528	Ferritin-like protein
TS28Bac1462|CDS|CDS	33.3	3.7	41.3	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Caer0748|CDS|CDS	4.0	0.5	36.3	P	COG0569|COG0475	K+ transport systems, NAD-binding component|Kef-type K+ transport systems, membrane components
TS28Bac3068|CDS|CDS	5.3	0.7	36.3	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
Buni3479|CDS|CDS	5.3	0.7	36.3	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS28Rum15957|CDS|CDS	7.5	1.0	34.0	P	COG1253|COG4536|COG4535	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB|Putative Mg2+ and Co2+ transporter CorC
Aput0641|CDS|CDS	1.5	0.2	33.3	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
TS28Bac1540|CDS|CDS	35.7	5.0	32.4	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Dfor0856|CDS|CDS	7.0	1.0	31.8	P	COG3685|COG3546	Uncharacterized protein conserved in bacteria|Mn-containing catalase
Robe0204|CDS|CDS	3.3	0.5	30.3	P	COG2116	Formate/nitrite family of transporters
Bova3063|CDS|CDS	2.1	0.3	28.4	P	COG2217	Cation transport ATPase
Buni3358|CDS|CDS	9.0	1.5	27.2	P	COG0607|COG2210|COG0446	Rhodanese-related sulfurtransferase|Uncharacterized conserved protein|Uncharacterized NAD(FAD)-dependent dehydrogenases
TS28Rum01418|CDS|CDS	10.5	2.0	23.8	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
TS28Bac1463|CDS|CDS	9.7	2.0	21.9	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Rum05937|CDS|CDS	14.0	3.0	21.2	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
BactD11122|CDS|CDS	2.3	0.5	21.2	P	COG0607|COG2210|COG0446	Rhodanese-related sulfurtransferase|Uncharacterized conserved protein|Uncharacterized NAD(FAD)-dependent dehydrogenases
Buni0931|CDS|CDS	44.5	9.7	20.9	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
BactD11415|CDS|CDS	11.1	2.6	19.5	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Bac1541|CDS|CDS	12.0	2.8	19.2	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Dlon1383|CDS|CDS	2.0	0.5	18.2	P	COG0471|COG1055	Di- and tricarboxylate transporters|Na+/H+ antiporter NhaD and related arsenite permeases
Dfor0125|CDS|CDS	4.0	1.0	18.2	P	COG1918	Fe2+ transport system protein A
TS29Dor0201|CDS|CDS	4.0	1.0	18.2	P	COG1393	Arsenate reductase and related proteins, glutaredoxin family
Bcap0267|CDS|CDS	4.0	1.0	18.2	P	COG0474	Cation transport ATPase
Bxyl2985|CDS|CDS	7.6	1.9	18.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Buni2203|CDS|CDS	1.5	0.4	17.0	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
TS29Par954|CDS|CDS	7.3	2.0	16.6	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
Buni0832|CDS|CDS	3.3	1.0	15.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Rum14589|CDS|CDS	6.5	2.0	14.8	P	COG0569	K+ transport systems, NAD-binding component
Bcoproc1932|CDS|CDS	1.5	0.5	14.4	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
Bsp1162029|CDS|CDS	1.5	0.5	14.4	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
ShigspD92315|CDS|CDS	3.0	1.0	13.6	P	COG0471	Di- and tricarboxylate transporters
TS28Clo02360|CDS|CDS	3.0	1.0	13.6	P	COG0053|COG1433	Predicted Co/Zn/Cd cation transporters|Uncharacterized conserved protein
ShigspD90925|CDS|CDS	1.5	0.5	13.6	P	COG4525|COG1116	ABC-type taurine transport system, ATPase component|ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component
ShigspD90709|CDS|CDS	1.5	0.5	13.6	P	COG1055	Na+/H+ antiporter NhaD and related arsenite permeases

TS28Rum00210|CDS|CDS	4.5	1.5	13.6	P	COG0725	ABC-type molybdate transport system, periplasmic component
BactD11685|CDS|CDS	2.0	0.7	13.4	P	COG2239	Mg/Co/Ni transporter MgtE (contains CBS domain)
ShigspD91055|CDS|CDS	2.8	1.0	12.9	P	COG3696	Putative silver efflux pump
TS29Rum05301|CDS|CDS	2.3	0.8	12.7	P	COG0855	Polyphosphate kinase
TS28Bac7204|CDS|CDS	2.7	1.0	12.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Robe0057|CDS|CDS	84.4	32.0	12.0	P	COG2703	Hemerythrin
Aput0984|CDS|CDS	21.0	8.0	11.9	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac10830|CDS|CDS	62.5	24.3	11.7	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bova3763|CDS|CDS	18.8	7.4	11.5	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Cbol4986|CDS|CDS	5.0	2.0	11.3	P	COG0725	ABC-type molybdate transport system, periplasmic component
Cste0032|CDS|CDS	2.5	1.0	11.3	P	COG0474	Cation transport ATPase
Cbol3683|CDS|CDS	5.0	2.0	11.3	P	COG1253|COG4536	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB
BactD11323|CDS|CDS	1.5	0.6	11.3	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
Bxyl1218|CDS|CDS	1.5	0.6	11.3	P	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component
TS28Clo09514|CDS|CDS	7.0	3.0	10.6	P	COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components
TS28Fae01771|CDS|CDS	1.0	46.0	0.1	P	COG0530	Ca2+/Na+ antiporter
TS29Bac01889|CDS|CDS	0.8	38.3	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Bxyl1533|CDS|CDS	0.5	23.5	0.1	P	COG0474	Cation transport ATPase
TS28Fae16666|CDS|CDS	0.5	23.5	0.1	P	COG1464	ABC-type metal ion transport system, periplasmic component/surface antigen
TS29Rum11503|CDS|CDS	0.5	24.0	0.1	P	COG0619	ABC-type cobalt transport system, permease component CbiQ and related transporters
TS28Fae02401|CDS|CDS	0.5	24.0	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS29Bac00257|CDS|CDS	0.3	16.3	0.1	P	COG3004	Na+/H+ antiporter
TS29Bac00568|CDS|CDS	0.4	19.8	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Bif2077|CDS|CDS	0.5	24.8	0.1	P	COG0855	Polyphosphate kinase
TS29Bac09378|CDS|CDS	0.5	25.0	0.1	P	COG1629	Outer membrane receptor proteins, mostly Fe transport
TS29Bac03557|CDS|CDS	0.5	25.2	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac08851|CDS|CDS	0.3	12.7	0.1	P	COG1629	Outer membrane receptor proteins, mostly Fe transport
TS29Bac01564|CDS|CDS	0.3	17.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
Dlon1344|CDS|CDS	0.2	10.3	0.1	P	COG4172|COG1122	ABC-type uncharacterized transport system, duplicated ATPase component|ABC-type cobalt transport system, ATPase component
TS28Bif0561|CDS|CDS	1.3	65.2	0.1	P	COG0025	NhaP-type Na+/H+ and K+/H+ antiporters
TS28Bif0752|CDS|CDS	0.5	26.3	0.1	P	COG0704	Phosphate uptake regulator
TS29Bif3851|CDS|CDS	0.5	26.3	0.1	P	COG0704	Phosphate uptake regulator
Dfor0464|CDS|CDS	0.3	17.5	0.1	P	COG2217	Cation transport ATPase
TS28Fae17862|CDS|CDS	1.5	79.0	0.1	P	COG0025	NhaP-type Na+/H+ and K+/H+ antiporters
TS29Bac07894|CDS|CDS	0.5	27.0	0.1	P	COG1629	Outer membrane receptor proteins, mostly Fe transport
Dfor0169|CDS|CDS	1.3	69.8	0.1	P	COG0607|COG2210|COG0446	Rhodanese-related sulfurtransferase|Uncharacterized conserved protein|Uncharacterized NAD(FAD)-dependent dehydrogenases
TS29Bac02235|CDS|CDS	0.8	42.3	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac05029|CDS|CDS	0.3	19.0	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Fae06759|CDS|CDS	1.0	57.5	0.1	P	COG1253|COG4536	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB
TS29Bac05005|CDS|CDS	0.5	29.5	0.1	P	COG0474	Cation transport ATPase
TS29Bif0690|CDS|CDS	2.6	152.5	0.1	P	COG2217	Cation transport ATPase
CspSS21658|CDS|CDS	0.3	20.0	0.1	P	COG2217	Cation transport ATPase
TS29Fae00780|CDS|CDS	1.5	90.5	0.1	P	COG0053|COG1433	Predicted Co/Zn/Cd cation transporters|Uncharacterized conserved protein
TS29Bac10197|CDS|CDS	0.5	30.3	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac04473|CDS|CDS	0.3	20.3	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Rum20623|CDS|CDS	1.0	62.0	0.1	P	COG0855	Polyphosphate kinase
TS28Fae21563|CDS|CDS	0.3	21.0	0.1	P	COG0569	K+ transport systems, NAD-binding component
Bxyl4192|CDS|CDS	0.4	25.8	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS28Fae10075|CDS|CDS	0.3	21.5	0.1	P	COG2217	Cation transport ATPase
TS29Col0235|CDS|CDS	1.0	65.0	0.1	P	COG2217	Cation transport ATPase
TS29Rum17043|CDS|CDS	1.0	65.0	0.1	P	COG1613|COG4150	ABC-type sulfate transport system, periplasmic component|ABC-type sulfate transport system, periplasmic component
TS29Rum15278|CDS|CDS	1.0	65.5	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
FpraM2120536|CDS|CDS	1.0	70.0	0.1	P	COG0530	Ca2+/Na+ antiporter
TS29Bac10034|CDS|CDS	0.7	47.8	0.1	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Bac10803|CDS|CDS	0.5	36.5	0.1	P	COG2217|COG2216	Cation transport ATPase|High-affinity K+ transport system, ATPase chain B
TS28Fae11140|CDS|CDS	0.1	7.0	0.1	P	COG1117	ABC-type phosphate transport system, ATPase component
TS28Fae21503|CDS|CDS	0.5	40.5	0.1	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS29Col0741|CDS|CDS	0.5	43.0	0.1	P	COG3004	Na+/H+ antiporter
TS29Bif3201|CDS|CDS	0.6	53.5	0.1	P	COG0861	Membrane protein TerC, possibly involved in tellurium resistance
TS28Bif4600|CDS|CDS	0.6	53.5	0.1	P	COG0861	Membrane protein TerC, possibly involved in tellurium resistance
BL1038|CDS|PacL2	0.3	22.7	0.1	P	COG0474	Cation transport ATPase
TS29Col0056|CDS|CDS	1.0	91.0	0.0	P	COG0370|COG1918	Fe2+ transport system protein B|Fe2+ transport system protein A
TS29Bif3321|CDS|CDS	0.5	48.0	0.0	P	COG0168	Trk-type K+ transport systems, membrane components
TS28Bif4727|CDS|CDS	0.5	48.0	0.0	P	COG0168	Trk-type K+ transport systems, membrane components
TS29Fae08645|CDS|CDS	1.5	145.0	0.0	P	COG2217	Cation transport ATPase
TS29Fae00225|CDS|CDS	1.5	145.5	0.0	P	COG2217	Cation transport ATPase
TS28Fae12478|CDS|CDS	0.1	9.0	0.0	P	COG1117	ABC-type phosphate transport system, ATPase component
TS28Bif1089|CDS|CDS	0.8	78.7	0.0	P	COG0004	Ammonia permease
TS29Bif0665|CDS|CDS	0.8	78.7	0.0	P	COG0004	Ammonia permease
TS29Col1439|CDS|CDS	0.5	53.0	0.0	P	COG2239	Mg/Co/Ni transporter MgtE (contains CBS domain)
TS29Bif0431|CDS|CDS	1.3	139.0	0.0	P	COG0025	NhaP-type Na+/H+ and K+/H+ antiporters
TS28Bif4447|CDS|CDS	0.2	25.9	0.0	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
TS29Bif0493|CDS|CDS	0.2	25.9	0.0	P	COG0783	DNA-binding ferritin-like protein (oxidative damage protectant)
TS29Fae04753|CDS|CDS	0.5	72.0	0.0	P	COG0569	K+ transport systems, NAD-binding component
TS29Bif3206|CDS|CDS	0.3	37.9	0.0	P	COG0803	ABC-type metal ion transport system, periplasmic component/surface adhesin
TS28Bif3287|CDS|CDS	0.3	42.6	0.0	P	COG3004	Na+/H+ antiporter
TS29Bac02117|CDS|CDS	0.3	57.5	0.0	P	COG4771	Outer membrane receptor for ferrienterochelin and colicins
TS29Rum13846|CDS|CDS	0.5	93.0	0.0	P	COG1055	Na+/H+ antiporter NhaD and related arsenite permeases
TS29Bif1132|CDS|CDS	0.3	62.0	0.0	P	COG0855	Polyphosphate kinase
TS29Bif3625|CDS|CDS	0.8	162.1	0.0	P	COG0855	Polyphosphate kinase
TS29Bif0494|CDS|CDS	1.0	196.5	0.0	P	COG1253|COG4536	Hemolysins and related proteins containing CBS domains|Putative Mg2+ and Co2+ transporter CorB
TS28Bif4606|CDS|CDS	0.3	65.9	0.0	P	COG0803	ABC-type metal ion transport system, periplasmic component/surface adhesin
TS29Bif3043|CDS|CDS	0.3	81.6	0.0	P	COG3004	Na+/H+ antiporter
TS29Bif0560|CDS|CDS	0.5	194.8	0.0	P	COG2217	Cation transport ATPase
TS29Rum19591|CDS|CDS	0.2	78.3	0.0	P	COG1123|COG1122|COG4172	ATPase components of various ABC-type transport systems, contain duplicated ATPase|ABC-type cobalt transport system, ATPase component|ABC-type uncharacterized transport system, duplicated ATPase component

TS29Bif3314|CDS|CDS	0.3	102.7	0.0	P	COG0474	Cation transport ATPase
TS28Bif4716|CDS|CDS	0.3	126.7	0.0	P	COG0474	Cation transport ATPase
Dlon1716|CDS|CDS	4.0	1.0	18.2	P|C	COG2710|COG1348	Nitrogenase molybdenum-iron protein, alpha and beta chains|Nitrogenase subunit NifH (ATPase)
TS28Fae09778|CDS|CDS	8.0	1.0	36.3	P|D	COG2884|COG2177|COG1135	Predicted ATPase involved in cell division|Cell division protein|ABC-type metal ion transport system, ATPase component
Dfor2414|CDS|CDS	3.0	1.0	13.6	P|D	COG1135|COG2884|COG2177	ABC-type metal ion transport system, ATPase component|Predicted ATPase involved in cell division|Cell division protein
Rtor1523|CDS|CDS	3.0	0.5	27.2	P|E	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
Cste1321|CDS|CDS	5.0	1.0	22.7	P|E	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
Aput1512|CDS|CDS	4.0	1.0	18.2	P|E|G	COG0477	Permeases of the major facilitator superfamily
BactD11807|CDS|CDS	3.0	0.8	16.3	P|E|G	COG0477	Permeases of the major facilitator superfamily
Bova3703|CDS|CDS	3.5	1.0	15.9	P|E|G	COG0477	Permeases of the major facilitator superfamily
BactD12837|CDS|CDS	3.0	1.0	13.6	P|E|G	COG0477	Permeases of the major facilitator superfamily
Aput0386|CDS|CDS	6.0	2.0	13.6	P|E|G	COG0477	Permeases of the major facilitator superfamily
BactD11455|CDS|CDS	3.3	1.5	10.1	P|E|G	COG0477	Permeases of the major facilitator superfamily
Bbre0851|CDS|CDS	0.1	5.3	0.1	P|E|G	COG0477	Permeases of the major facilitator superfamily
BactD10045|CDS|CDS	6.5	2.5	11.8	P|E|Q	COG1126|COG1135|COG4175|COG1127|COG4598	ABC-type polar amino acid transport system, ATPase component|ABC-type metal ion transport system, ATPase component|ABC-type proline/glycine betaine transport system, ATPase component|ABC-type transport system involved in resistance to organic solvents, ATPase component|ABC-type histidine transport system, ATPase component
Casp1491|CDS|CDS	179.0	3.0	270.9	P|H	COG0607|COG0301	Rhodanese-related sulfurtransferase|Thiamine biosynthesis ATP pyrophosphatase
Cbol5280|CDS|CDS	5.0	1.0	22.7	P|H	COG0607|COG0301	Rhodanese-related sulfurtransferase|Thiamine biosynthesis ATP pyrophosphatase
Buni2204|CDS|CDS	5.1	2.0	11.7	P|H	COG4771|COG4206	Outer membrane receptor for ferrienterochelin and colicins|Outer membrane cobalamin receptor protein
TS29Col0997|CDS|CDS	0.5	34.0	0.1	P|H	COG0303|COG1763|COG1910	Molybdopterin biosynthesis enzyme|Molybdopterin-guanine dinucleotide biosynthesis protein|Periplasmic molybdate-binding protein/domain
TS28Bif4607|CDS|CDS	0.3	17.6	0.1	P|H|V	COG1136|COG1121|COG1120|COG1865|COG1118|COG1116|COG3638	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type Mn/Zn transport systems, ATPase component|ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components|Uncharacterized conserved protein|ABC-type sulfate/molybdate transport systems, ATPase component|ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component|ABC-type phosphate/phosphonate transport system, ATPase component
TS29Bif3207|CDS|CDS	0.3	17.6	0.1	P|H|V	COG1136|COG1121|COG1120|COG1865|COG1118|COG1116|COG3638	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type Mn/Zn transport systems, ATPase component|ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components|Uncharacterized conserved protein|ABC-type sulfate/molybdate transport systems, ATPase component|ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component|ABC-type phosphate/phosphonate transport system, ATPase component
TS28Fae00228|CDS|CDS	4.5	0.5	40.9	P|I	COG0657|COG2072	Esterase/lipase|Predicted flavoprotein involved in K+ transport
TS29Bif3388|CDS|CDS	0.3	35.5	0.0	P|I	COG0657|COG2072	Esterase/lipase|Predicted flavoprotein involved in K+ transport
TS28Clo07100|CDS|CDS	8.0	1.0	36.3	P|J	COG0566|COG0474	rRNA methylases|Cation transport ATPase
TS29Fae08579|CDS|CDS	2.0	163.5	0.1	P|J	COG0566|COG0474	rRNA methylases|Cation transport ATPase
TS29Bif2507|CDS|CDS	0.3	33.1	0.0	P|J	COG0566|COG0474|COG2217	rRNA methylases|Cation transport ATPase|Cation transport ATPase
Aput1589|CDS|CDS	5.0	2.0	11.3	P|K|H|C	COG0543|COG2871|COG2186|COG1018|COG0369	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases|Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrF|Transcriptional regulators|Flavodoxin reductases (ferredoxin-NADPH reductases) family 1|Sulfite reductase, alpha subunit (flavoprotein)
Bxyl0400|CDS|CDS	1.6	0.5	14.5	P|L|C|V	COG3666|COG1131|COG4555|COG4152	Transposase and inactivated derivatives|ABC-type multidrug transport system, ATPase component|ABC-type Na+ transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component
TS28Fae14027|CDS|CDS	2.5	0.5	22.7	P|M	COG0226|COG2885	ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS28Fae03517|CDS|CDS	9.0	2.0	20.4	P|M	COG0226|COG2885	ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins
Bxyl1504|CDS|CDS	0.1	6.0	0.1	P|M	COG0226|COG2885	ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins
BactD11203|CDS|CDS	0.1	8.0	0.1	P|M	COG0226|COG2885	ABC-type phosphate transport system, periplasmic component|Outer membrane protein and related peptidoglycan-associated (lipo)proteins
TS29Rum21222|CDS|CDS	0.3	17.0	0.1	P|Q|V	COG1136|COG1135|COG4181	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type metal ion transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component
TS28Rum13513|CDS|CDS	0.3	20.0	0.1	P|Q|V	COG1136|COG1135|COG4181	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type metal ion transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component
Buni2419|CDS|CDS	2.0	0.5	18.2	P|T	COG3712	Fe2+-dicitrate sensor, membrane component
TS28Rum06092|CDS|CDS	2.0	0.5	18.2	P|T	COG0038|COG0517|COG0589	Chloride channel protein EriC|FOG: CBS domain|Universal stress protein UspA and related nucleotide-binding proteins
Buni0180|CDS|CDS	3.0	0.8	16.3	P|T	COG0589|COG0475	Universal stress protein UspA and related nucleotide-binding proteins|Kef-type K+ transport systems, membrane components
TS28Eub6565|CDS|CDS	1.7	0.5	15.1	P|T	COG3887|COG1226	Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain|Kef-type K+ transport systems, predicted NAD-binding component
TS28Fae07803|CDS|CDS	10.5	3.5	13.6	P|T	COG3887|COG1226	Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain|Kef-type K+ transport systems, predicted NAD-binding component
TS29Bac11361|CDS|CDS	0.5	29.4	0.1	P|T	COG0569|COG0589|COG0475	K+ transport systems, NAD-binding component|Universal stress protein UspA and related nucleotide-binding proteins|Kef-type K+ transport systems, membrane components
TS29Bac09700|CDS|CDS	0.3	20.0	0.1	P|T	COG0569|COG0589|COG0475	K+ transport systems, NAD-binding component|Universal stress protein UspA and related nucleotide-binding proteins|Kef-type K+ transport systems, membrane components
Buni2748|CDS|CDS	2.3	1.0	10.6	P|V	COG0841|COG3696	Cation/multidrug efflux pump|Putative silver efflux pump
TS29Fae01231|CDS|CDS	3.0	142.0	0.1	P|V	COG0841|COG3696	Cation/multidrug efflux pump|Putative silver efflux pump

Edol0091|CDS|CDS	1.0	47.5	0.1	P|V	COG1132|COG2375	ABC-type multidrug transport system, ATPase and permease components|Siderophore-interacting protein
Ceut1709|CDS|CDS	0.3	15.0	0.1	P|V|Q	COG1136|COG4181|COG1135	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component|ABC-type metal ion transport system, ATPase component
TS28Fae00474|CDS|CDS	8.3	0.5	75.7	Q	COG3882	Predicted enzyme involved in methoxymalonyl-ACP biosynthesis
TS29RumUnc0371|CDS|CDS	41.3	3.5	53.6	Q	COG4909	Propanediol dehydratase, large subunit
TS28Eub0622|CDS|CDS	4.5	0.5	40.9	Q	COG4909	Propanediol dehydratase, large subunit
Robe3274|CDS|CDS	4.5	0.5	40.9	Q	COG4869	Propanediol utilization protein
Cbol2174|CDS|CDS	7.0	1.0	31.8	Q	COG1020	Non-ribosomal peptide synthetase modules and related proteins
TS29RumUnc0370|CDS|CDS	26.3	4.0	29.9	Q	COG4910	Propanediol dehydratase, small subunit
TS29RumUnc0372|CDS|CDS	36.0	7.5	21.8	Q	COG4909	Propanediol dehydratase, large subunit
Ehal0411|CDS|CDS	6.0	1.5	18.2	Q	COG4909	Propanediol dehydratase, large subunit
Bcap0189|CDS|CDS	17.0	5.0	15.4	Q	COG2313	Uncharacterized enzyme involved in pigment biosynthesis
TS28Fae07700|CDS|CDS	1.7	0.5	15.1	Q	COG0500	SAM-dependent methyltransferases
Rgna1124|CDS|CDS	1.5	0.5	13.6	Q	COG4909	Propanediol dehydratase, large subunit
Rgna1123|CDS|CDS	3.0	1.0	13.6	Q	COG4909	Propanediol dehydratase, large subunit
Cbol3567|CDS|CDS	3.0	1.0	13.6	Q	COG0500	SAM-dependent methyltransferases
TS28Rum15590|CDS|CDS	5.5	2.0	12.5	Q	COG0500	SAM-dependent methyltransferases
TS28Rum15625|CDS|CDS	23.0	9.5	11.0	Q	COG4869	Propanediol utilization protein
TS29Rum07213|CDS|CDS	9.0	4.0	10.2	Q	COG1020|COG3321|COG3319|COG3320	Non-ribosomal peptide synthetase modules and related proteins|Polyketide synthase modules and related proteins|Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases|Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes
TS29Bif0384|CDS|CDS	3.0	147.0	0.1	Q	COG2931	RTX toxins and related Ca2+-binding proteins
TS29Bac03301|CDS|CDS	1.0	51.0	0.1	Q	COG3882	Predicted enzyme involved in methoxymalonyl-ACP biosynthesis
TS29Rum19598|CDS|CDS	2.0	123.0	0.1	Q	COG1020|COG3321|COG3319|COG3208|COG3433	Non-ribosomal peptide synthetase modules and related proteins|Polyketide synthase modules and related proteins|Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases|Predicted thioesterase involved in non-ribosomal peptide biosynthesis|Aryl carrier domain
TS29Bif1003|CDS|CDS	0.7	44.3	0.1	Q	COG0500	SAM-dependent methyltransferases
TS29Rum01250|CDS|CDS	0.7	45.8	0.1	Q	COG1020|COG3321|COG3319|COG3320	Non-ribosomal peptide synthetase modules and related proteins|Polyketide synthase modules and related proteins|Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases|Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes
TS29Bif2614|CDS|CDS	0.5	54.8	0.0	Q	COG1228	Imidazolonepropionase and related amidohydrolases
TS29Bif3551|CDS|CDS	0.3	96.5	0.0	Q|V	COG1136|COG4181	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component
CspSS21278|CDS|CDS	36.3	0.5	329.9	T	COG0642|COG2202|COG5002	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase
TS28Bac2716|CDS|CDS	15.3	0.3	208.8	T	COG1875	Predicted ATPase related to phosphate starvation-inducible protein PhoH
Buni3403|CDS|CDS	33.3	1.8	82.5	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase
ShigspD90633|CDS|CDS	6.0	0.3	81.7	T	COG0642	Signal transduction histidine kinase
Ceut1707|CDS|CDS	6.3	0.5	56.7	T	COG0642|COG2202|COG5002|COG2770	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: HAMP domain
RintL10992|CDS|CDS	10.0	1.0	45.4	T	COG2310|COG4110	Uncharacterized proteins involved in stress response, homologs of TerZ and putative cAMP-binding protein CABP1|Uncharacterized protein involved in stress response
Caer2190|CDS|CDS	4.5	0.5	40.9	T	COG1966	Carbon starvation protein, predicted membrane protein
Cbol2858|CDS|CDS	8.0	1.0	36.3	T	COG0784	FOG: CheY-like receiver
TS29Clo3308|CDS|CDS	29.0	4.0	32.9	T	COG0642|COG5002|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
TS28Bac3380|CDS|CDS	2.0	0.3	27.2	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins
TS28Rum13607|CDS|CDS	6.0	1.0	27.2	T	COG1702	Phosphate starvation-inducible protein PhoH, predicted ATPase
TS29Clo0517|CDS|CDS	6.0	1.0	27.2	T	COG2172	Anti-sigma regulatory factor (Ser/Thr protein kinase)
TS28Dor2864|CDS|CDS	6.0	1.0	27.2	T	COG0642|COG5002|COG2202|COG2203|COG3292	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain
TS29Par396|CDS|CDS	5.0	1.0	22.7	T	COG4753	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain
TS28Dor0301|CDS|CDS	2.5	0.5	22.7	T	COG0642|COG5002|COG2202|COG2770|COG0784|COG3322|COG4251|COG2205|COG3447	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase|Predicted integral membrane sensor domain
TS29Bac07312|CDS|CDS	50.3	10.8	21.1	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase
BactD22463|CDS|CDS	1.2	0.3	20.9	T	COG2972|COG3275|COG5012	Predicted signal transduction protein with a C-terminal ATPase domain|Putative regulator of cell autolysis|Predicted cobalamin binding protein
TS28Dor2028|CDS|CDS	2.0	0.5	18.2	T	COG0642|COG5002|COG2202|COG2770|COG0784|COG3292	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain|FOG: CheY-like receiver|Predicted periplasmic ligand-binding sensor domain
TS28Rum16392|CDS|CDS	2.0	0.5	18.2	T	COG2172	Anti-sigma regulatory factor (Ser/Thr protein kinase)
Dlon0350|CDS|CDS	4.0	1.0	18.2	T	COG0618|COG3887	Exopolyphosphatase-related proteins|Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain
TS28Rum14387|CDS|CDS	3.5	1.0	15.9	T	COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism
TS28Rum01816|CDS|CDS	3.5	1.0	15.9	T	COG0642|COG5002|COG2202|COG2770	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain
Dlon0876|CDS|CDS	1.7	0.5	15.1	T	COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism
TS28Dor0558|CDS|CDS	1.7	0.5	15.1	T	COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism
Begg0972|CDS|CDS	10.0	3.0	15.1	T	COG3275	Putative regulator of cell autolysis
BactD10114|CDS|CDS	5.7	1.8	14.1	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase
TS29Par236|CDS|CDS	23.0	7.5	13.9	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase

TS28Bac4603|CDS|CDS	1.0	0.3	13.6	T	COG5002|COG4753|COG3292|COG3706	Signal transduction histidine kinase|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Predicted periplasmic ligand-binding sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain
TS28Bac3538|CDS|CDS	1.0	0.3	13.6	T	COG0642|COG5002	Signal transduction histidine kinase|Signal transduction histidine kinase
Acac2081|CDS|CDS	6.0	2.0	13.6	T	COG2202|COG5278|COG3300|COG3706|COG5001|COG2199|COG4251|COG2200	FOG: PAS/PAC domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: EAL domain
Cbol4133|CDS|CDS	3.0	1.0	13.6	T	COG1551	Carbon storage regulator (could also regulate swarming and quorum sensing)
TS28Eub2068|CDS|CDS	3.0	1.0	13.6	T	COG1493	Serine kinase of the HPr protein, regulates carbohydrate metabolism
TS28Col1553|CDS|CDS	6.0	2.0	13.6	T	COG1217	Predicted membrane GTPase involved in stress response
Dfor2384|CDS|CDS	3.0	1.0	13.6	T	COG0642|COG2202|COG5002|COG2770	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: HAMP domain
TS28Rum01417|CDS|CDS	3.0	1.0	13.6	T	COG0631	Serine/threonine protein phosphatase
TS29Bac07370|CDS|CDS	5.9	2.0	13.3	T	COG2337	Growth inhibitor
Aput0435|CDS|CDS	8.0	3.0	12.1	T	COG0618|COG3887	Exopolyphosphatase-related proteins|Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain
ShigspD93102|CDS|CDS	2.5	1.0	11.3	T	COG0642|COG2205	Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase
Bxyl3946|CDS|CDS	6.9	2.8	11.0	T	COG1875|COG1702	Predicted ATPase related to phosphate starvation-inducible protein PhoH|Phosphate starvation-inducible protein PhoH, predicted ATPase
TS28Rum15985|CDS|CDS	0.5	23.0	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Col1870|CDS|CDS	1.0	46.5	0.1	T	COG3275|COG2972|COG5012	Putative regulator of cell autolysis|Predicted signal transduction protein with a C-terminal ATPase domain|Predicted cobalamin binding protein
Even0457|CDS|CDS	0.3	11.8	0.1	T	COG0642|COG2202|COG5002|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS29Fae08949|CDS|CDS	2.0	95.0	0.1	T	COG0642|COG5002|COG2202|COG0784|COG2203|COG3322	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain
TS29Rum20147|CDS|CDS	1.5	72.5	0.1	T	COG0642|COG5002|COG4251|COG2205|COG3447	Signal transduction histidine kinase|Signal transduction histidine kinase|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase|Predicted integral membrane sensor domain
Bpse1848|CDS|CDS	0.5	24.5	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Bac01917|CDS|CDS	1.0	52.0	0.1	T	COG0642|COG4191	Signal transduction histidine kinase|Signal transduction histidine kinase regulating C4-dicarboxylate transport system
TS28Fae12844|CDS|CDS	0.3	17.5	0.1	T	COG0642|COG5002|COG2202|COG4251|COG2205|COG3447	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase|Predicted integral membrane sensor domain
TS29Rum11420|CDS|CDS	1.0	53.0	0.1	T	COG0642|COG5002|COG0784|COG5001	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: CheY-like receiver|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain
Ehal1053|CDS|CDS	0.4	19.8	0.1	T	COG0642|COG2202|COG5002|COG2203|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: GAF domain|Osmosensitive K+ channel histidine kinase
TS29Rum00173|CDS|CDS	1.0	57.0	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Rum20465|CDS|CDS	1.3	77.5	0.1	T	COG0642|COG5002|COG2202|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Osmosensitive K+ channel histidine kinase
TS29Bac11581|CDS|CDS	0.3	19.5	0.1	T	COG2204	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains
FpraM2122506|CDS|CDS	1.3	74.3	0.1	T	COG0642|COG2202|COG5002|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS29Fae04768|CDS|CDS	1.0	59.0	0.1	T	COG0642|COG5002|COG2202	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain
Dfor2928|CDS|CDS	0.5	30.8	0.1	T	COG0642|COG2198|COG2202|COG0784|COG2203|COG5278|COG3300|COG3322|COG5001|COG3452|COG3614	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain
TS29Rum11911|CDS|CDS	1.0	63.0	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Fae09332|CDS|CDS	0.3	22.2	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Rum13807|CDS|CDS	1.0	68.0	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Rum20524|CDS|CDS	1.2	84.4	0.1	T	COG0642|COG5002|COG2202|COG3292|COG2205|COG4250	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS28Bif4500|CDS|CDS	0.5	37.3	0.1	T	COG1716	FOG: FHA domain
TS29Bif0531|CDS|CDS	0.5	37.3	0.1	T	COG1716	FOG: FHA domain
TS28Bif4614|CDS|CDS	0.3	18.8	0.1	T	COG0642|COG5002|COG2770	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: HAMP domain
TS29Bif0029|CDS|CDS	0.5	39.5	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Fae05518|CDS|CDS	1.0	90.0	0.1	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Rum19569|CDS|CDS	0.2	19.0	0.0	T	COG2337	Growth inhibitor
TS29Fae07232|CDS|CDS	1.0	96.0	0.0	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Fae03339|CDS|CDS	1.0	99.0	0.0	T	COG2972|COG3290	Predicted signal transduction protein with a C-terminal ATPase domain|Signal transduction histidine kinase regulating citrate/malate metabolism
TS29Bac01323|CDS|CDS	0.3	33.0	0.0	T	COG0642|COG5002|COG2202|COG2770|COG2203|COG2205	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: HAMP domain|FOG: GAF domain|Osmosensitive K+ channel histidine kinase
TS28Bif4630|CDS|CDS	0.5	52.0	0.0	T	COG5278|COG4251|COG3920	Predicted periplasmic ligand-binding sensor domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Signal transduction histidine kinase
TS29Fae07303|CDS|CDS	1.0	109.0	0.0	T	COG2972|COG3290	Predicted signal transduction protein with a C-terminal ATPase domain|Signal transduction histidine kinase regulating citrate/malate metabolism
TS29Bif3213|CDS|CDS	0.3	27.3	0.0	T	COG0642|COG5002|COG2770	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: HAMP domain

TS29Bif1702|CDS|CDS	0.5	55.0	0.0	T	COG4564|COG3850|COG4585|COG3851	Signal transduction histidine kinase|Signal transduction histidine kinase, nitrate/nitrite-specific|Signal transduction histidine kinase|Signal transduction histidine kinase, glucose-6-phosphate specific
TS29Col1611|CDS|CDS	0.5	58.5	0.0	T	COG0642|COG5002|COG2202	Signal transduction histidine kinase|Signal transduction histidine kinase|FOG: PAS/PAC domain
TS29Bif3028|CDS|CDS	1.5	203.5	0.0	T	COG4564|COG3850|COG4585|COG3851	Signal transduction histidine kinase|Signal transduction histidine kinase, nitrate/nitrite-specific|Signal transduction histidine kinase|Signal transduction histidine kinase, glucose-6-phosphate specific
FpraM2122299|CDS|CDS	0.3	45.5	0.0	T	COG0642|COG2202|COG5002|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
FpraM2121357|CDS|CDS	0.5	68.5	0.0	T	COG2972	Predicted signal transduction protein with a C-terminal ATPase domain
TS29Bif3224|CDS|CDS	0.5	89.0	0.0	T	COG5278|COG4251|COG3920	Predicted periplasmic ligand-binding sensor domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Signal transduction histidine kinase
Ccom0780|CDS|CDS	0.2	34.7	0.0	T	COG0642|COG2202|COG5002|COG2203|COG3322|COG2205|COG4250	Signal transduction histidine kinase|FOG: PAS/PAC domain|Signal transduction histidine kinase|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|Osmosensitive K+ channel histidine kinase|Predicted sensor protein/domain
TS29Bif2997|CDS|CDS	0.3	58.3	0.0	T	COG1966	Carbon starvation protein, predicted membrane protein
TS29Col1577|CDS|CDS	0.3	79.0	0.0	T	COG1217	Predicted membrane GTPase involved in stress response
TS28Bif0284|CDS|CDS	0.3	85.3	0.0	T	COG1966	Carbon starvation protein, predicted membrane protein
Msmi751535|CDS|CDS	0.8	0.3	13.6	T|C	COG5635|COG1413	Predicted NTPase (NACHT family)|FOG: HEAT repeat
Dlon0584|CDS|CDS	1.5	0.5	13.6	T|E	COG0589|COG0531	Universal stress protein UspA and related nucleotide-binding proteins|Amino acid transporters
Buni0990|CDS|CDS	1.5	0.5	13.6	T|E	COG0642|COG2202|COG0784|COG5002|COG0834|COG2203|COG5278|COG3300|COG2770|COG3614	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|FOG: HAMP domain|Predicted periplasmic ligand-binding sensor domain
Aput0287|CDS|CDS	6.0	2.0	13.6	T|E	COG0560|COG3830	Phosphoserine phosphatase|ACT domain-containing protein
Robe2500|CDS|CDS	1.5	0.5	13.6	T|E	COG0642|COG2202|COG3447|COG0784|COG5002|COG0834|COG3322|COG3706|COG4251|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|Predicted integral membrane sensor domain|FOG: CheY-like receiver|Signal transduction histidine kinase|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|Osmosensitive K+ channel histidine kinase
Csym0488|CDS|CDS	5.5	1.0	25.0	T|E|K	COG0642|COG2198|COG2202|COG0784|COG0834|COG2203|COG3437|COG5278|COG3300|COG4252|COG3452|COG3614	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Predicted periplasmic ligand-binding sensor domain|MHYT domain (predicted integral membrane sensor domain)|Predicted transmembrane sensor domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain
Ehal0754|CDS|CDS	0.5	23.8	0.1	T|E|K	COG0642|COG2198|COG2202|COG0834|COG2203|COG3437|COG3300|COG3452	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|MHYT domain (predicted integral membrane sensor domain)|Predicted periplasmic ligand-binding sensor domain
BactD14130|CDS|CDS	9.2	1.3	31.2	T|E|K|G	COG0642|COG2202|COG0784|COG5002|COG3292|COG0834|COG4753|COG3706|COG0745|COG2972|COG1879|COG2114|COG4251|COG2770|COG2172	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain|Anti-sigma regulatory factor (Ser/Thr protein kinase)
Bova2060|CDS|CDS	10.7	3.5	13.8	T|E|K|G	COG0642|COG2202|COG0784|COG5002|COG3292|COG0834|COG4753|COG3706|COG5001|COG0745|COG2972|COG1879|COG2114|COG4251|COG2770|COG2172	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain|Anti-sigma regulatory factor (Ser/Thr protein kinase)
Buni3603|CDS|CDS	1.5	0.5	13.6	T|E|M	COG0834|COG4623	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein
Caer0098|CDS|CDS	5.0	0.5	45.4	T|G	COG1762|COG1445|COG3925	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)|Phosphotransferase system fructose-specific component IIB|N-terminal domain of the phosphotransferase system fructose-specific component IIB
Cbol4935|CDS|CDS	8.0	1.0	36.3	T|G	COG2202|COG1879|COG1172|COG4158|COG4211|COG4214	FOG: PAS/PAC domain|ABC-type sugar transport system, periplasmic component|Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components|Predicted ABC-type sugar transport system, permease component|ABC-type glucose/galactose transport system, permease component|ABC-type xylose transport system, permease component

Rtor1814|CDS|CDS	5.3	0.7	36.3	T|G	COG1080|COG4668|COG3412|COG2190|COG3605|COG1762|COG1925	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components|Signal transduction protein containing GAF and PtsI domains|Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)|Phosphotransferase system, HPr-related proteins
Cbol4938|CDS|CDS	14.0	3.0	21.2	T|G	COG5002|COG1879	Signal transduction histidine kinase|ABC-type sugar transport system, periplasmic component
Robe1265|CDS|CDS	20.5	5.0	18.6	T|G	COG5002|COG1879	Signal transduction histidine kinase|ABC-type sugar transport system, periplasmic component
Ccom0083|CDS|CDS	4.0	1.0	18.2	T|G	COG1080|COG4668|COG3412|COG3605	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria|Signal transduction protein containing GAF and PtsI domains
Csym3615|CDS|CDS	3.0	1.0	13.6	T|G	COG5002|COG1879	Signal transduction histidine kinase|ABC-type sugar transport system, periplasmic component
Rtor1612|CDS|CDS	6.0	0.5	54.5	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Buni1321|CDS|CDS	3.0	0.5	27.2	T|K	COG3708|COG0789|COG4978	Uncharacterized protein conserved in bacteria|Predicted transcriptional regulators|Transcriptional regulator, effector-binding domain/component
Cbol6625|CDS|CDS	5.0	1.0	22.7	T|K	COG5002|COG2972|COG3275|COG5012|COG4936	Signal transduction histidine kinase|Predicted signal transduction protein with a C-terminal ATPase domain|Putative regulator of cell autolysis|Predicted cobalamin binding protein|Predicted sensor domain
Casp2521|CDS|CDS	5.0	1.0	22.7	T|K	COG2972|COG3275|COG5012|COG4936	Predicted signal transduction protein with a C-terminal ATPase domain|Putative regulator of cell autolysis|Predicted cobalamin binding protein|Predicted sensor domain
Cbol5796|CDS|CDS	4.0	1.0	18.2	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
BactD14035|CDS|CDS	1.3	0.3	18.2	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
ShigspD92392|CDS|CDS	3.5	1.0	15.9	T|K	COG2202|COG5001|COG2200|COG3614|COG2771|COG4943	FOG: PAS/PAC domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|FOG: EAL domain|Predicted periplasmic ligand-binding sensor domain|DNA-binding HTH domain-containing proteins|Predicted signal transduction protein containing sensor and EAL domains
BactD24148|CDS|CDS	3.3	1.0	15.1	T|K	COG2204|COG1221|COG3604|COG3829	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain|Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains|Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains
BactD11673|CDS|CDS	1.0	0.3	13.6	T|K	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases
BactD23419|CDS|CDS	1.5	0.5	13.6	T|K	COG2972|COG3275|COG4936	Predicted signal transduction protein with a C-terminal ATPase domain|Putative regulator of cell autolysis|Predicted sensor domain
Rtor0116|CDS|CDS	3.0	1.0	13.6	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Bova2994|CDS|CDS	1.5	0.5	13.6	T|K	COG2972|COG3275|COG4936	Predicted signal transduction protein with a C-terminal ATPase domain|Putative regulator of cell autolysis|Predicted sensor domain
Rtor0202|CDS|CDS	17.3	6.0	13.1	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
Buni2583|CDS|CDS	8.6	3.0	13.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Aput1211|CDS|CDS	8.0	3.0	12.1	T|K	COG2198|COG0784|COG3437|COG2204|COG4753|COG3706|COG0745|COG3920	FOG: HPt domain|FOG: CheY-like receiver|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Signal transduction histidine kinase
Buni2582|CDS|CDS	36.6	14.0	11.9	T|K	COG0642|COG2202|COG0784|COG5002|COG2203|COG3437|COG2770|COG2205	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|FOG: GAF domain|Response regulator containing a CheY-like receiver domain and an HD-GYP domain|FOG: HAMP domain|Osmosensitive K+ channel histidine kinase
BactD11047|CDS|CDS	5.8	2.5	10.4	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
Bxyl1337|CDS|CDS	5.8	2.5	10.4	T|K	COG4753|COG2207	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins
Dlon2015|CDS|CDS	0.9	45.5	0.1	T|K	COG0317|COG2357	Guanosine polyphosphate pyrophosphohydrolases/synthetases|Uncharacterized protein conserved in bacteria
Ccom0781|CDS|CDS	0.3	21.5	0.1	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
CspM6210567|CDS|CDS	0.9	64.2	0.1	T|K	COG0317|COG2357	Guanosine polyphosphate pyrophosphohydrolases/synthetases|Uncharacterized protein conserved in bacteria
Ehal1052|CDS|CDS	0.3	27.1	0.1	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Bryfor3294|CDS|CDS	0.2	36.9	0.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Rumhyd1507|CDS|CDS	0.2	65.4	0.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Even0023|CDS|CDS	0.2	68.8	0.0	T|K	COG0745	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain

Bxyl3038|CDS|CDS	1.0	46.8	0.1	T|K|G	COG0642|COG2198|COG2202|COG0784|COG5002|COG3292|COG4753|COG3706|COG5001|COG0745|COG2972|COG1879|COG2114|COG4251	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)
RintL12266|CDS|CDS	19.0	5.0	17.3	T|K|L	COG0515	Serine/threonine protein kinase
Dlon0840|CDS|CDS	0.3	14.8	0.1	T|K|L|G	COG4753|COG2207|COG3449|COG3664	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|AraC-type DNA-binding domain-containing proteins|DNA gyrase inhibitor|Beta-xylosidase
Buni1598|CDS|CDS	11.5	3.5	14.9	T|K|L|O	COG0457|COG0515|COG4995|COG4249|COG5549|COG1912|COG3914|COG4248	FOG: TPR repeat|Serine/threonine protein kinase|Uncharacterized protein conserved in bacteria|Uncharacterized protein containing caspase domain|Predicted Zn-dependent protease|Uncharacterized conserved protein|Predicted O-linked N-acetylglucosamine transferase, SPINDLY family|Uncharacterized protein with protein kinase and helix-hairpin-helix DNA-binding domains
Casp2508|CDS|CDS	3.3	1.0	15.1	T|K|Q	COG2508|COG3835	Regulator of polyketide synthase expression|Sugar diacid utilization regulator
Rumhyd2532|CDS|CDS	13.7	2.0	31.0	T|L|G	COG1372|COG0574|COG1080|COG4668|COG3412|COG2190|COG3605	Intein/homing endonuclease|Phosphoenolpyruvate synthase/pyruvate phosphate dikinase|Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)|Mannitol/fructose-specific phosphotransferase system, IIA domain|Uncharacterized protein conserved in bacteria|Phosphotransferase system IIA components|Signal transduction protein containing GAF and PtsI domains
Rumhyd0677|CDS|CDS	3.0	1.0	13.6	T|M	COG1388|COG3409|COG3103|COG0791|COG3883|COG3209	FOG: LysM repeat|Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria|Rhs family protein
Ccom1842|CDS|CDS	3.0	1.0	13.6	T|M	COG1388|COG3409|COG3103|COG0791|COG3883|COG3209|COG3584	FOG: LysM repeat|Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria|Rhs family protein|Uncharacterized protein conserved in bacteria
Rgna1535|CDS|CDS	8.0	3.0	12.1	T|M	COG3409|COG3103|COG0860|COG2247|COG2861	Putative peptidoglycan-binding domain-containing protein|SH3 domain protein|N-acetylmuramoyl-L-alanine amidase|Putative cell wall-binding domain|Uncharacterized protein conserved in bacteria
FpraM2121016|CDS|CDS	3.7	1.5	11.1	T|M	COG3103|COG0791|COG3883|COG0739	SH3 domain protein|Cell wall-associated hydrolases (invasion-associated proteins)|Uncharacterized protein conserved in bacteria|Membrane proteins related to metalloendopeptidases
ShigspD92591|CDS|CDS	4.0	1.0	18.2	T|N	COG2202|COG0840	FOG: PAS/PAC domain|Methyl-accepting chemotaxis protein
RintL13689|CDS|CDS	3.0	1.0	13.6	T|N	COG2202|COG5278|COG0840	FOG: PAS/PAC domain|Predicted periplasmic ligand-binding sensor domain|Methyl-accepting chemotaxis protein
Bthe3732589|CDS|CDS	0.4	24.7	0.1	T|N|E	COG0642|COG2198|COG2202|COG3447|COG1352|COG0784|COG5002|COG0834|COG5278|COG4252|COG2770	Signal transduction histidine kinase|FOG: HPt domain|FOG: PAS/PAC domain|Predicted integral membrane sensor domain|Methylase of chemotaxis methyl-accepting proteins|FOG: CheY-like receiver|Signal transduction histidine kinase|ABC-type amino acid transport/signal transduction systems, periplasmic component/domain|Predicted periplasmic ligand-binding sensor domain|Predicted transmembrane sensor domain|FOG: HAMP domain
Bova3378|CDS|CDS	0.3	14.7	0.1	T|N|K|G	COG0642|COG2202|COG0784|COG5002|COG3292|COG5278|COG3322|COG4753|COG3706|COG5001|COG2972|COG1879|COG2114|COG4251|COG2770|COG2207|COG2201	Signal transduction histidine kinase|FOG: PAS/PAC domain|FOG: CheY-like receiver|Signal transduction histidine kinase|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Predicted periplasmic ligand-binding sensor domain|Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain|Response regulator containing a CheY-like receiver domain and a GGDEF domain|Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain|Predicted signal transduction protein with a C-terminal ATPase domain|ABC-type sugar transport system, periplasmic component|Adenylate cyclase, family 3 (some proteins contain HAMP domain)|Bacteriophytochrome (light-regulated signal transduction histidine kinase)|FOG: HAMP domain|AraC-type DNA-binding domain-containing proteins|Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain
Cbol4366|CDS|CDS	3.0	1.0	13.6	T|Q	COG2508	Regulator of polyketide synthase expression
Buni1536|CDS|CDS	12.3	0.5	112.0	U	COG0552	Signal recognition particle GTPase
TS29Bac09292|CDS|CDS	9.1	0.5	83.0	U	COG0811	Biopolymer transport proteins
Bthe7335617|CDS|CDS	8.5	0.7	57.6	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
Bxyl2358|CDS|CDS	3.8	0.3	52.2	U	COG0681	Signal peptidase I
Svar0325|CDS|CDS	8.0	1.0	36.3	U	COG0541	Signal recognition particle GTPase
BactD20441|CDS|CDS	3.8	0.5	34.8	U	COG0706	Preprotein translocase subunit YidC
Acol3157|CDS|CDS	7.0	1.0	31.8	U	COG3451	Type IV secretory pathway, VirB4 components
Bova0458|CDS|CDS	3.2	0.5	29.4	U	COG0811	Biopolymer transport proteins
TS28Rum11474|CDS|CDS	35.5	5.5	29.3	U	COG0201	Preprotein translocase subunit SecY
TS28Clo09614|CDS|CDS	2.5	0.5	22.7	U	COG0201	Preprotein translocase subunit SecY
Bste1743|CDS|CDS	4.6	1.0	20.8	U	COG0342	Preprotein translocase subunit SecD
BactD24164|CDS|CDS	8.3	2.0	18.8	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
Rlac1919|CDS|CDS	4.0	1.0	18.2	U	COG0342|COG0341	Preprotein translocase subunit SecD|Preprotein translocase subunit SecF
ShigspD90951|CDS|CDS	4.0	1.0	18.2	U	COG0342	Preprotein translocase subunit SecD
Bxyl1098|CDS|CDS	5.3	1.3	18.1	U	COG0811	Biopolymer transport proteins
TS29Met0454|CDS|CDS	30.5	8.0	17.3	U	COG3210	Large exoproteins involved in heme utilization or adhesion
Csci0116|CDS|CDS	7.0	2.0	15.9	U	COG3505	Type IV secretory pathway, VirD4 components
TS28Rum12577|CDS|CDS	10.0	3.0	15.1	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
BactD12818|CDS|CDS	17.5	5.5	14.4	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
TS29Bac09291|CDS|CDS	3.1	1.0	14.1	U	COG0811	Biopolymer transport proteins
Bxyl3230|CDS|CDS	20.2	6.5	14.1	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
Bova0531|CDS|CDS	1.0	0.3	13.6	U	COG0552	Signal recognition particle GTPase
Dlon0062|CDS|CDS	1.5	0.5	13.6	U	COG0681	Signal peptidase I
TS28Dor2597|CDS|CDS	1.5	0.5	13.6	U	COG0681	Signal peptidase I
TS28Rum08891|CDS|CDS	3.0	1.0	13.6	U	COG0552	Signal recognition particle GTPase
FpraM2121290|CDS|CDS	17.0	6.0	12.9	U	COG0706	Preprotein translocase subunit YidC
Msmi750624|CDS|CDS	0.7	0.3	12.7	U	COG0201	Preprotein translocase subunit SecY

Msmi741055|CDS|CDS	0.7	0.3	12.7	U	COG0201	Preprotein translocase subunit SecY
TS28Met0775|CDS|CDS	0.7	0.3	12.7	U	COG0201	Preprotein translocase subunit SecY
Buni1275|CDS|CDS	23.2	9.0	11.7	U	COG0811	Biopolymer transport proteins
Bxyl1665|CDS|CDS	7.5	3.2	10.7	U	COG0201	Preprotein translocase subunit SecY
Buni0653|CDS|CDS	1.2	0.5	10.6	U	COG2095	Multiple antibiotic transporter
TS28Rum14251|CDS|CDS	12.5	5.5	10.3	U	COG0541	Signal recognition particle GTPase
TS29Par585|CDS|CDS	26.5	12.0	10.0	U	COG0811	Biopolymer transport proteins
TS29Fae01397|CDS|CDS	2.0	92.0	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Fae01289|CDS|CDS	1.3	63.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Rum11722|CDS|CDS	2.0	103.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Fae10381|CDS|CDS	0.8	43.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Bif1382|CDS|CDS	0.5	26.0	0.1	U	COG0201	Preprotein translocase subunit SecY
TS29Fae00098|CDS|CDS	2.5	130.5	0.1	U	COG0342|COG0341	Preprotein translocase subunit SecD|Preprotein translocase subunit SecF
TS29Bac10726|CDS|CDS	1.2	61.0	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
TS29Fae04674|CDS|CDS	2.0	105.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Bac00458|CDS|CDS	1.0	53.5	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Fae13923|CDS|CDS	1.0	53.7	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Ceut2212|CDS|CDS	0.1	6.1	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
CspL20085|CDS|CDS	0.7	39.5	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
FpraM2122499|CDS|CDS	0.7	39.5	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Fae09127|CDS|CDS	2.0	115.0	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
TS29Col1918|CDS|CDS	1.6	93.0	0.1	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
TS29Rum20437|CDS|CDS	1.0	58.7	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Dor2297|CDS|CDS	0.1	6.6	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Bac05888|CDS|CDS	0.3	15.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS28Bif3841|CDS|CDS	0.3	15.8	0.1	U	COG0541	Signal recognition particle GTPase
TS29Rum21254|CDS|CDS	1.5	101.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Fae06656|CDS|CDS	1.0	69.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Bif0851|CDS|CDS	1.3	87.2	0.1	U	COG0541	Signal recognition particle GTPase
TS29Rum18707|CDS|CDS	1.0	72.0	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Eub2193|CDS|CDS	0.5	36.3	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS28Fae13937|CDS|CDS	0.3	18.5	0.1	U	COG3505	Type IV secretory pathway, VirD4 components
TS29Fae09693|CDS|CDS	0.4	29.9	0.1	U	COG3451	Type IV secretory pathway, VirB4 components
Ccom2214|CDS|CDS	0.1	12.5	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
CspM6211931|CDS|CDS	0.1	12.5	0.1	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Fae08481|CDS|CDS	0.3	31.0	0.0	U	COG0541	Signal recognition particle GTPase
TS29Fae10403|CDS|CDS	0.5	47.0	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Fae07278|CDS|CDS	2.0	194.0	0.0	U	COG3505	Type IV secretory pathway, VirD4 components
Bcap2364|CDS|CDS	0.3	33.5	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS29Rum11716|CDS|CDS	0.5	51.5	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS29Bif1234|CDS|CDS	0.3	28.8	0.0	U	COG0541	Signal recognition particle GTPase
Rbro1725|CDS|CDS	0.1	13.9	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Dfor2029|CDS|CDS	0.1	13.9	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Cnex2284|CDS|CDS	0.1	13.9	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
CspM6211851|CDS|CDS	0.1	13.9	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Rum11726|CDS|CDS	1.0	127.0	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Acol2785|CDS|CDS	0.1	14.4	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
FpraM2122489|CDS|CDS	0.4	53.2	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Eub6909|CDS|CDS	0.5	69.0	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Bif3026|CDS|CDS	0.1	10.7	0.0	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
Acac2256|CDS|CDS	0.1	15.4	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
CspL20091|CDS|CDS	0.4	57.2	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
TS28Bif0433|CDS|CDS	0.3	37.7	0.0	U	COG0541	Signal recognition particle GTPase
TS29Fae04668|CDS|CDS	0.1	22.2	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Cmet2529|CDS|CDS	0.1	23.5	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Bif0664|CDS|CDS	0.3	43.9	0.0	U	COG0552	Signal recognition particle GTPase
TS28Bif1091|CDS|CDS	0.3	43.9	0.0	U	COG0552	Signal recognition particle GTPase
TS29Fae03326|CDS|CDS	1.0	183.0	0.0	U	COG3451	Type IV secretory pathway, VirB4 components
Bpse1555|CDS|CDS	0.1	16.2	0.0	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
FpraM2120047|CDS|CDS	0.1	30.9	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS29Bif2193|CDS|CDS	0.1	27.2	0.0	U	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)
Cnex1094|CDS|CDS	0.1	47.7	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
FpraM2122523|CDS|CDS	0.1	59.2	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
Bhan2474|CDS|CDS	0.1	69.8	0.0	U	COG3843	Type IV secretory pathway, VirD2 components (relaxase)
TS28Clo00181|CDS|CDS	0.1	6.0	0.1	U|V	COG1131|COG3843	ABC-type multidrug transport system, ATPase component|Type IV secretory pathway, VirD2 components (relaxase)
Robe0610|CDS|CDS	33.5	1.5	101.4	V	COG1131	ABC-type multidrug transport system, ATPase component
Cbol3940|CDS|CDS	25.0	2.0	56.7	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
Buni0096|CDS|CDS	5.0	0.5	45.4	V	COG1566	Multidrug resistance efflux pump
TS28Bac7264|CDS|CDS	3.2	0.3	43.1	V	COG1680	Beta-lactamase class C and other penicillin binding proteins
TS29Rum04363|CDS|CDS	34.5	4.5	34.8	V	COG1131	ABC-type multidrug transport system, ATPase component
TS28Eub4107|CDS|CDS	22.3	3.0	33.8	V	COG0534	Na+-driven multidrug efflux pump
TS28Rum00257|CDS|CDS	14.5	2.0	32.9	V	COG1511|COG0577	Predicted membrane protein|ABC-type antimicrobial peptide transport system, permease component
TS28Fae03234|CDS|CDS	7.0	1.0	31.8	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
BactD14371|CDS|CDS	1.7	0.3	30.3	V	COG1566	Multidrug resistance efflux pump
TS28Col0035|CDS|CDS	6.0	1.0	27.2	V	COG2720	Uncharacterized vancomycin resistance protein
Acac2646|CDS|CDS	6.0	1.0	27.2	V	COG0534	Na+-driven multidrug efflux pump
TS28Clo02834|CDS|CDS	10.0	2.0	22.7	V	COG0534	Na+-driven multidrug efflux pump
TS28Fae15041|CDS|CDS	5.0	1.0	22.7	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
Bfin1971|CDS|CDS	2.3	0.5	20.4	V	COG1131|COG0842	ABC-type multidrug transport system, ATPase component|ABC-type multidrug transport system, permease component
Ccom1393|CDS|CDS	4.0	1.0	18.2	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
ShigspD91560|CDS|CDS	2.0	0.5	18.2	V	COG0841	Cation/multidrug efflux pump
TS28Fae16886|CDS|CDS	7.3	2.0	16.6	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Met1299|CDS|CDS	20.0	6.0	15.1	V	COG3587	Restriction endonuclease
Bfin1970|CDS|CDS	0.8	0.3	15.1	V	COG1131|COG0842	ABC-type multidrug transport system, ATPase component|ABC-type multidrug transport system, permease component
Casp3525|CDS|CDS	3.0	1.0	13.6	V	COG0841	Cation/multidrug efflux pump
TS29Eub1048|CDS|CDS	1.5	0.5	13.6	V	COG2367	Beta-lactamase class A
TS28Fae09515|CDS|CDS	1.5	0.5	13.6	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Rumhyd1358|CDS|CDS	3.0	1.0	13.6	V	COG0534	Na+-driven multidrug efflux pump
Dlon2263|CDS|CDS	3.0	1.0	13.6	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
Buni1907|CDS|CDS	1.5	0.5	13.6	V	COG0534	Na+-driven multidrug efflux pump
Rgna1186|CDS|CDS	6.0	2.0	13.6	V	COG1131	ABC-type multidrug transport system, ATPase component

TS28Rum01498|CDS|CDS	8.0	3.0	12.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS29Clo1723|CDS|CDS	5.0	2.0	11.3	V	COG0534	Na+-driven multidrug efflux pump
Svar1818|CDS|CDS	3.5	1.5	10.6	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS28Bac0828|CDS|CDS	2.3	1.0	10.6	V	COG0842	ABC-type multidrug transport system, permease component
Buni2397|CDS|CDS	2.3	1.0	10.6	V	COG0842	ABC-type multidrug transport system, permease component
TS29Fae04986|CDS|CDS	0.5	23.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS29RumUnc0805|CDS|CDS	1.2	56.0	0.1	V	COG2274|COG1132	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain|ABC-type multidrug transport system, ATPase and permease components
TS29Rum00887|CDS|CDS	1.0	47.0	0.1	V	COG1131|COG4586	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component
TS28Bif2147|CDS|CDS	1.8	83.8	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Bif3576|CDS|CDS	1.8	83.8	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS28Fae16686|CDS|CDS	1.0	49.0	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Col0612|CDS|CDS	0.5	25.0	0.1	V	COG1136|COG0577	ABC-type antimicrobial peptide transport system, ATPase component|ABC-type antimicrobial peptide transport system, permease component
TS29Col0160|CDS|CDS	2.0	100.0	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Met1109|CDS|CDS	0.2	10.0	0.1	V	COG1968	Uncharacterized bacitracin resistance protein
TS28Fae10051|CDS|CDS	0.3	12.5	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS29Fae00033|CDS|CDS	1.0	50.5	0.1	V	COG1131|COG4152	ABC-type multidrug transport system, ATPase component|ABC-type uncharacterized transport system, ATPase component
TS29Eub2241|CDS|CDS	0.7	34.8	0.1	V	COG1131	ABC-type multidrug transport system, ATPase component
TS29Rum00591|CDS|CDS	2.0	105.0	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae03185|CDS|CDS	1.5	81.5	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Bif2178|CDS|CDS	3.0	170.5	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae05986|CDS|CDS	4.5	265.5	0.1	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS29Col0183|CDS|CDS	1.0	61.0	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Dfor3033|CDS|CDS	0.8	51.0	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Rum17015|CDS|CDS	1.0	62.0	0.1	V	COG2367	Beta-lactamase class A
TS28Bif0394|CDS|CDS	0.7	46.7	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Rum17812|CDS|CDS	1.0	64.3	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae09999|CDS|CDS	1.5	97.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Fae20830|CDS|CDS	1.0	65.0	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS29Met0430|CDS|CDS	0.2	13.0	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Bac03034|CDS|CDS	0.3	22.3	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Bif3386|CDS|CDS	1.1	74.5	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
TS29Bif2482|CDS|CDS	1.1	74.5	0.1	V	COG1136	ABC-type antimicrobial peptide transport system, ATPase component
Cnex0563|CDS|CDS	0.5	34.5	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Caer1097|CDS|CDS	1.0	69.0	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Col0414|CDS|CDS	1.0	69.0	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS28Fae19470|CDS|CDS	0.5	35.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Fae21401|CDS|CDS	0.5	35.5	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Bhan2441|CDS|CDS	0.5	35.5	0.1	V	COG1131	ABC-type multidrug transport system, ATPase component
CspM6212143|CDS|CDS	0.4	28.6	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
RintL10498|CDS|CDS	0.4	28.6	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Ehal1055|CDS|CDS	0.3	23.9	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Col0734|CDS|CDS	0.5	36.0	0.1	V	COG1968	Uncharacterized bacitracin resistance protein
TS28Bif0409|CDS|CDS	1.0	73.9	0.1	V	COG2348	Uncharacterized protein involved in methicillin resistance
TS29Bif0875|CDS|CDS	1.0	73.9	0.1	V	COG2348	Uncharacterized protein involved in methicillin resistance
TS29Rum17241|CDS|CDS	1.0	75.5	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS29Bac10525|CDS|CDS	1.0	76.0	0.1	V	COG1401	GTPase subunit of restriction endonuclease
TS29Rum17801|CDS|CDS	0.4	30.8	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Bif2905|CDS|CDS	1.5	116.5	0.1	V	COG0732|COG0286	Restriction endonuclease S subunits|Type I restriction-modification system methyltransferase subunit
TS29Rum16961|CDS|CDS	1.0	79.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS29Bif0890|CDS|CDS	0.7	58.7	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
CspSS20181|CDS|CDS	0.4	32.1	0.1	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Fae00274|CDS|CDS	1.0	84.0	0.1	V	COG2367	Beta-lactamase class A
TS29Fae03651|CDS|CDS	0.3	21.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Bif0499|CDS|CDS	1.0	87.5	0.1	V	COG1401	GTPase subunit of restriction endonuclease
TS29Bif0791|CDS|CDS	1.0	87.5	0.1	V	COG1401	GTPase subunit of restriction endonuclease
TS29Fae08598|CDS|CDS	1.0	87.5	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Bif2146|CDS|CDS	0.5	44.4	0.1	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Fae08216|CDS|CDS	1.0	89.0	0.1	V	COG0534	Na+-driven multidrug efflux pump
TS28Fae02079|CDS|CDS	0.5	46.5	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS28Fae21416|CDS|CDS	0.5	47.5	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Robe3151|CDS|CDS	0.3	32.9	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae07758|CDS|CDS	1.0	101.0	0.0	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS28Fae00028|CDS|CDS	1.0	101.0	0.0	V	COG0534	Na+-driven multidrug efflux pump
TS29Bif2733|CDS|CDS	1.0	106.0	0.0	V	COG0534	Na+-driven multidrug efflux pump
TS29Fae05673|CDS|CDS	0.5	54.5	0.0	V	COG1131	ABC-type multidrug transport system, ATPase component
TS28Bif2167|CDS|CDS	0.8	83.0	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Bif3559|CDS|CDS	0.8	83.0	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Fae03471|CDS|CDS	1.0	113.0	0.0	V	COG0732|COG0286	Restriction endonuclease S subunits|Type I restriction-modification system methyltransferase subunit
Ccom2195|CDS|CDS	0.3	30.2	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Rum01134|CDS|CDS	0.3	30.4	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Dor2331|CDS|CDS	1.7	214.5	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS28Bif0393|CDS|CDS	0.4	52.5	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Rum20467|CDS|CDS	0.8	111.0	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Bif3989|CDS|CDS	1.0	136.4	0.0	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
Cbol3892|CDS|CDS	1.0	142.5	0.0	V	COG1131	ABC-type multidrug transport system, ATPase component
TS29Fae06705|CDS|CDS	0.5	71.5	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Bif1724|CDS|CDS	0.5	81.0	0.0	V	COG4096|COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases|Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS29Fae09855|CDS|CDS	0.5	83.0	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae00901|CDS|CDS	0.8	146.5	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Bif1718|CDS|CDS	0.3	59.0	0.0	V	COG0286	Type I restriction-modification system methyltransferase subunit
TS28Dor2457|CDS|CDS	0.3	45.8	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
Dfor1879|CDS|CDS	0.3	45.8	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Bif0891|CDS|CDS	0.4	75.5	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component

TS29Fae05251|CDS|CDS	1.0	210.0	0.0	V	COG0610	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases
TS29Fae00939|CDS|CDS	1.0	217.0	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae05248|CDS|CDS	1.0	241.0	0.0	V	COG0286	Type I restriction-modification system methyltransferase subunit
TS29Bif3577|CDS|CDS	0.5	127.1	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Fae00937|CDS|CDS	0.5	146.5	0.0	V	COG0577	ABC-type antimicrobial peptide transport system, permease component
TS29Fae00900|CDS|CDS	0.5	159.5	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS29Bif3560|CDS|CDS	0.3	88.1	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
TS28Bif2166|CDS|CDS	0.3	88.1	0.0	V	COG1132	ABC-type multidrug transport system, ATPase and permease components
Caer1663|CDS|CDS	9.5	2.0	21.6	V|O	COG1132|COG5265	ABC-type multidrug transport system, ATPase and permease components|ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components
Cnex0562|CDS|CDS	0.2	67.0	0.0	V|Q	COG1136|COG4181	ABC-type antimicrobial peptide transport system, ATPase component|Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component
TS28Col0184|CDS|CDS	3.0	1.0	13.6	Z	COG5022|COG4603	Myosin heavy chain|ABC-type uncharacterized transport system, permease component
Buni1778|CDS|CDS	8.8	1.5	26.5	R	COG0073	EMAP domain
Cbol1818|CDS|CDS	8.0	3.0	12.1	R	COG0073	EMAP domain
TS29Fae08154|CDS|CDS	1.0	133.5	0.0	R	COG0073	EMAP domain
TS28Rum00691|CDS|CDS	4.0	1.0	18.2	R	COG0217	Uncharacterized conserved protein
Buni2387|CDS|CDS	2.8	0.3	38.6	R	COG0220	Predicted S-adenosylmethionine-dependent methyltransferase
Buni0170|CDS|CDS	9.0	1.5	27.2	R	COG0312	Predicted Zn-dependent proteases and their inactivated homologs
BFych460661|CDS|methyltransferase	4.0	0.5	36.3	R	COG0313	Predicted methyltransferases
Cbol3709|CDS|CDS	4.0	1.0	18.2	R	COG0319	Predicted metal-dependent hydrolase
TS29Rum10537|CDS|CDS	10.0	4.0	11.3	R	COG0319	Predicted metal-dependent hydrolase
TS28Bif5350|CDS|CDS	1.5	0.7	10.2	R	COG0327|COG3323	Uncharacterized conserved protein|Uncharacterized protein conserved in bacteria
TS28Rum01430|CDS|CDS	2.5	0.5	22.7	R	COG0327|COG3323|COG1579	Uncharacterized conserved protein|Uncharacterized protein conserved in bacteria|Zn-ribbon protein, possibly nucleic acid-binding
TS28Rum01029|CDS|CDS	3.0	1.0	13.6	R	COG0385	Predicted Na+-dependent transporter
Buni1333|CDS|CDS	2.5	1.0	11.3	R	COG0385	Predicted Na+-dependent transporter
TS29Bif3380|CDS|CDS	0.5	48.8	0.0	R	COG0385	Predicted Na+-dependent transporter
TS28Rum14875|CDS|CDS	2.5	0.5	22.7	R	COG0388	Predicted amidohydrolase
ShigspD91095|CDS|CDS	6.0	2.0	13.6	R	COG0388	Predicted amidohydrolase
TS28Fae22062|CDS|CDS	0.5	24.5	0.1	R	COG0388	Predicted amidohydrolase
TS29Bac05743|CDS|CDS	0.2	16.3	0.1	R	COG0388	Predicted amidohydrolase
BactD23506|CDS|CDS	3.0	1.0	13.6	R	COG0393	Uncharacterized conserved protein
TS29Bif4100|CDS|CDS	0.3	37.5	0.0	R	COG0400	Predicted esterase
TS28Rum05327|CDS|CDS	3.0	1.0	13.6	R	COG0432	Uncharacterized conserved protein
ShigspD91354|CDS|CDS	12.0	1.0	54.5	R	COG0433	Predicted ATPase
BactD21452|CDS|CDS	3.0	0.5	26.8	R	COG0457	FOG: TPR repeat
Buni2992|CDS|CDS	7.5	1.3	25.5	R	COG0457	FOG: TPR repeat
Bxyl3971|CDS|CDS	2.5	0.5	22.7	R	COG0457	FOG: TPR repeat
Bova3352|CDS|CDS	7.3	1.5	22.0	R	COG0457	FOG: TPR repeat
Bxyl4287|CDS|CDS	13.9	3.3	18.9	R	COG0457	FOG: TPR repeat
TS28Bac1584|CDS|CDS	4.0	1.3	13.6	R	COG0457	FOG: TPR repeat
BactD13074|CDS|CDS	2.7	1.0	12.1	R	COG0457	FOG: TPR repeat
TS28Bif4059|CDS|CDS	2.5	1.0	11.3	R	COG0457	FOG: TPR repeat
Bxyl3879|CDS|CDS	4.7	2.0	10.6	R	COG0457	FOG: TPR repeat
BactD10941|CDS|CDS	13.3	5.8	10.3	R	COG0457	FOG: TPR repeat
Bxyl2812|CDS|CDS	2.0	0.5	18.2	R	COG0457|COG1912	FOG: TPR repeat|Uncharacterized conserved protein
TS28Fae14951|CDS|CDS	2.0	0.5	18.2	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains
Buni1258|CDS|CDS	2.0	0.5	18.2	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains
Bcap1022|CDS|CDS	12.0	3.0	18.2	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains
Bova2773|CDS|CDS	1.2	0.5	10.9	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains
TS28Bif0429|CDS|CDS	0.5	63.5	0.0	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains
TS29Bif0855|CDS|CDS	0.5	63.5	0.0	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains
TS28Rum13360|CDS|CDS	2.0	0.5	18.2	R	COG0491	Zn-dependent hydrolases, including glyoxylases
Cbol0207|CDS|CDS	15.0	2.0	34.0	R	COG0517	FOG: CBS domain
TS28Rum09595|CDS|CDS	5.2	1.0	23.5	R	COG0517	FOG: CBS domain
TS28Met0799|CDS|CDS	2.3	1.0	10.2	R	COG0517	FOG: CBS domain
TS28Bif0660|CDS|CDS	0.5	31.5	0.1	R	COG0517	FOG: CBS domain
TS29Bif3927|CDS|CDS	0.5	31.5	0.1	R	COG0517	FOG: CBS domain
TS28Fae16383|CDS|CDS	9.5	0.5	86.3	R	COG0523	Putative GTPases (G3E family)
FpraM2120183|CDS|CDS	7.0	1.0	31.8	R	COG0523	Putative GTPases (G3E family)
TS28Rum00814|CDS|CDS	3.0	1.0	13.6	R	COG0523	Putative GTPases (G3E family)
Buni1210|CDS|CDS	2.5	1.0	11.3	R	COG0523	Putative GTPases (G3E family)
TS28Fae15327|CDS|CDS	1.0	0.3	13.6	R	COG0535|COG0641	Predicted Fe-S oxidoreductases|Arylsulfatase regulator (Fe-S oxidoreductase)
TS29Rum20306|CDS|CDS	1.0	49.0	0.1	R	COG0535|COG4001	Predicted Fe-S oxidoreductases|Predicted metal-binding protein
TS28Bac3716|CDS|CDS	5.7	1.0	25.7	R	COG0536	Predicted GTPase
Buni2659|CDS|CDS	5.7	1.0	25.7	R	COG0536	Predicted GTPase
Bcap0610|CDS|CDS	9.0	2.0	20.4	R	COG0536	Predicted GTPase
BactD24141|CDS|CDS	8.0	2.0	18.2	R	COG0536	Predicted GTPase
TS28Fae13876|CDS|CDS	0.3	20.5	0.1	R	COG0536	Predicted GTPase
ShigspD90619|CDS|CDS	2.0	0.5	18.2	R	COG0546	Predicted phosphatases
Aput0764|CDS|CDS	6.0	1.5	18.2	R	COG0546	Predicted phosphatases
TS29Rum07641|CDS|CDS	1.7	0.7	11.3	R	COG0546	Predicted phosphatases
TS29Ali387|CDS|CDS	6.0	2.5	10.9	R	COG0546	Predicted phosphatases
TS29Eub1228|CDS|CDS	18.0	6.0	13.6	R	COG0561	Predicted hydrolases of the HAD superfamily
Bpse0301|CDS|CDS	0.3	16.7	0.1	R	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
TS29Bif1703|CDS|CDS	0.3	34.7	0.0	R	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
Aput0061|CDS|CDS	10.0	2.0	22.7	R	COG0612	Predicted Zn-dependent peptidases
Buni1909|CDS|CDS	2.0	0.5	18.2	R	COG0612	Predicted Zn-dependent peptidases
TS29Clo4230|CDS|CDS	0.3	15.5	0.1	R	COG0612	Predicted Zn-dependent peptidases
TS28Rum14512|CDS|CDS	6.0	0.5	54.5	R	COG0618	Exopolyphosphatase-related proteins
TS28Met0650|CDS|CDS	0.8	0.3	11.3	R	COG0622	Predicted phosphoesterase
TS29Rum20812|CDS|CDS	1.0	51.0	0.1	R	COG0627|COG2845	Predicted esterase|Uncharacterized protein conserved in bacteria
Buni2732|CDS|CDS	3.5	0.5	31.8	R	COG0628	Predicted permease
TS29Fae08388|CDS|CDS	1.0	88.5	0.1	R	COG0628	Predicted permease
TS29Bif3870|CDS|CDS	0.3	126.6	0.0	R	COG0628	Predicted permease
TS29Bac07753|CDS|CDS	10.0	1.5	30.3	R	COG0641	Arylsulfatase regulator (Fe-S oxidoreductase)
TS28Rum01976|CDS|CDS	3.0	0.5	27.2	R	COG0641	Arylsulfatase regulator (Fe-S oxidoreductase)
TS29Bac12283|CDS|CDS	0.5	30.0	0.1	R	COG0641	Arylsulfatase regulator (Fe-S oxidoreductase)
TS29Bif2391|CDS|CDS	1.0	63.0	0.1	R	COG0656	Aldo/keto reductases, related to diketogulonate reductase
TS29Bif0905|CDS|CDS	1.0	98.5	0.0	R	COG0656	Aldo/keto reductases, related to diketogulonate reductase

Buni2529|CDS|CDS	2.3	0.5	21.2	R	COG0658|COG2333	Predicted membrane metal-binding protein|Predicted hydrolase (metallo-beta-lactamase superfamily)
TS28Bif0324|CDS|CDS	0.3	27.3	0.1	R	COG0658|COG2333	Predicted membrane metal-binding protein|Predicted hydrolase (metallo-beta-lactamase superfamily)
Bbre1456|CDS|CDS	1.7	0.3	22.5	R	COG0661	Predicted unusual protein kinase
TS28Fae19049|CDS|CDS	13.5	4.0	15.3	R	COG0670	Integral membrane protein, interacts with FtsH
Clep1251|CDS|CDS	7.5	0.5	68.1	R	COG0673	Predicted dehydrogenases and related proteins
TS28Clo06642|CDS|CDS	8.5	1.0	38.6	R	COG0673	Predicted dehydrogenases and related proteins
Bthe3730201|CDS|CDS	8.5	1.0	38.6	R	COG0673	Predicted dehydrogenases and related proteins
Clep1253|CDS|CDS	31.0	4.0	35.2	R	COG0673	Predicted dehydrogenases and related proteins
TS29Clo0164|CDS|CDS	121.8	24.0	23.0	R	COG0673	Predicted dehydrogenases and related proteins
TS28Clo10639|CDS|CDS	121.8	24.0	23.0	R	COG0673	Predicted dehydrogenases and related proteins
TS28Rum01838|CDS|CDS	4.0	1.0	18.2	R	COG0673	Predicted dehydrogenases and related proteins
TS29Clo0161|CDS|CDS	78.5	21.0	17.0	R	COG0673	Predicted dehydrogenases and related proteins
TS28Clo10636|CDS|CDS	78.5	21.0	17.0	R	COG0673	Predicted dehydrogenases and related proteins
Clep1250|CDS|CDS	23.5	7.0	15.2	R	COG0673	Predicted dehydrogenases and related proteins
TS28Bac2545|CDS|CDS	4.3	1.5	12.9	R	COG0673	Predicted dehydrogenases and related proteins
TS29Clo0162|CDS|CDS	114.0	50.0	10.4	R	COG0673	Predicted dehydrogenases and related proteins
TS29Rum20630|CDS|CDS	0.5	32.0	0.1	R	COG0673	Predicted dehydrogenases and related proteins
TS29Clo2120|CDS|CDS	14.0	3.7	17.3	R	COG0679	Predicted permeases
TS28Bif4771|CDS|CDS	0.3	32.2	0.0	R	COG0679	Predicted permeases
TS29Bif3358|CDS|CDS	0.3	49.2	0.0	R	COG0679	Predicted permeases
TS28Rum05915|CDS|CDS	12.0	4.0	13.6	R	COG0714	MoxR-like ATPases
RintL11183|CDS|CDS	3.0	1.0	13.6	R	COG0714	MoxR-like ATPases
Aput0430|CDS|CDS	3.0	1.0	13.6	R	COG0714	MoxR-like ATPases
TS29Rum00361|CDS|CDS	2.0	105.0	0.1	R	COG0714	MoxR-like ATPases
TS29Fae03451|CDS|CDS	1.0	87.5	0.1	R	COG0714	MoxR-like ATPases
TS29Bif0462|CDS|CDS	0.3	82.7	0.0	R	COG0728	Uncharacterized membrane protein, putative virulence factor
TS28Bif4394|CDS|CDS	0.3	100.0	0.0	R	COG0728	Uncharacterized membrane protein, putative virulence factor
TS28Rum09648|CDS|CDS	3.0	1.0	13.6	R	COG0733	Na+-dependent transporters of the SNF family
Robe0752|CDS|CDS	3.0	1.0	13.6	R	COG0733	Na+-dependent transporters of the SNF family
Dlon0654|CDS|CDS	2.5	1.0	11.3	R	COG0733	Na+-dependent transporters of the SNF family
TS28Dor2540|CDS|CDS	2.5	1.0	11.3	R	COG0733	Na+-dependent transporters of the SNF family
TS29Rum00894|CDS|CDS	1.0	82.0	0.1	R	COG0733	Na+-dependent transporters of the SNF family
TS29Rum16824|CDS|CDS	1.0	84.0	0.1	R	COG0733	Na+-dependent transporters of the SNF family
TS29Rum15134|CDS|CDS	6.0	1.0	27.2	R	COG0759	Uncharacterized conserved protein
TS28Rum14518|CDS|CDS	11.0	3.5	14.3	R	COG0779	Uncharacterized protein conserved in bacteria
TS29Fae04721|CDS|CDS	1.0	59.5	0.1	R	COG0779	Uncharacterized protein conserved in bacteria
TS28Fae07638|CDS|CDS	16.0	1.0	72.6	R	COG0802|COG3178	Predicted ATPase or kinase|Predicted phosphotransferase related to Ser/Thr protein kinases
TS29Rum00837|CDS|CDS	0.5	24.0	0.1	R	COG0802|COG3178	Predicted ATPase or kinase|Predicted phosphotransferase related to Ser/Thr protein kinases
Acac2543|CDS|CDS	3.0	1.0	13.6	R	COG0820	Predicted Fe-S-cluster redox enzyme
TS29Bac08016|CDS|CDS	0.3	26.5	0.1	R	COG0820	Predicted Fe-S-cluster redox enzyme
RintL10089|CDS|CDS	0.1	8.3	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Cbol3099|CDS|CDS	0.1	8.3	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Csci3162|CDS|CDS	0.1	8.3	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
TS29Col1597|CDS|CDS	0.5	48.0	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
CspM6211854|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Acac2258|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Rbro1726|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Ceut2208|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Cnex2282|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Acol2788|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
Dfor2027|CDS|CDS	0.1	18.1	0.0	R	COG0820	Predicted Fe-S-cluster redox enzyme
TS29RumUnc1140|CDS|CDS	7.0	3.0	10.6	R	COG0824	Predicted thioesterase
TS29Bif3994|CDS|CDS	0.5	34.5	0.1	R	COG1011	Predicted hydrolase (HAD superfamily)
TS28Bif2025|CDS|CDS	0.5	34.5	0.1	R	COG1011	Predicted hydrolase (HAD superfamily)
TS29Rum06868|CDS|CDS	1.3	0.3	18.2	R	COG1033	Predicted exporters of the RND superfamily
Clep1629|CDS|CDS	10.0	3.0	15.1	R	COG1033	Predicted exporters of the RND superfamily
Rlac0133|CDS|CDS	5.0	2.0	11.3	R	COG1033	Predicted exporters of the RND superfamily
TS28Fae09550|CDS|CDS	0.3	19.3	0.1	R	COG1033	Predicted exporters of the RND superfamily
TS28Rum10136|CDS|CDS	1.5	0.5	13.6	R	COG1073	Hydrolases of the alpha/beta superfamily
TS28Fae07359|CDS|CDS	0.5	27.5	0.1	R	COG1073	Hydrolases of the alpha/beta superfamily
TS28Fae00296|CDS|CDS	0.5	67.0	0.0	R	COG1092	Predicted SAM-dependent methyltransferases
TS28Bac2797|CDS|CDS	2.5	0.5	22.7	R	COG1106	Predicted ATPases
TS29Fae05427|CDS|CDS	1.0	125.5	0.0	R	COG1106	Predicted ATPases
TS28Fae02052|CDS|CDS	14.5	1.0	65.8	R	COG1159	GTPase
TS28Clo08749|CDS|CDS	4.0	1.0	18.2	R	COG1159	GTPase
Buni2292|CDS|CDS	4.5	2.0	10.2	R	COG1160	Predicted GTPases
TS29Bif4070|CDS|CDS	0.3	62.5	0.0	R	COG1216	Predicted glycosyltransferases
TS29Met0978|CDS|CDS	0.3	12.0	0.1	R	COG1234	Metal-dependent hydrolases of the beta-lactamase superfamily III
TS28Clo09340|CDS|CDS	4.0	1.0	18.2	R	COG1235	Metal-dependent hydrolases of the beta-lactamase superfamily I
BactD12759|CDS|CDS	2.0	0.7	13.6	R	COG1259	Uncharacterized conserved protein
TS29Bif0553|CDS|CDS	0.7	57.2	0.1	R	COG1272	Predicted membrane protein, hemolysin III homolog
TS28Fae02625|CDS|CDS	10.0	1.0	45.4	R	COG1277	ABC-type transport system involved in multi-copper enzyme maturation, permease component
TS28Bac6489|CDS|CDS	4.5	1.0	20.4	R	COG1284	Uncharacterized conserved protein
Buni0374|CDS|CDS	3.3	1.0	15.1	R	COG1284	Uncharacterized conserved protein
TS28Fae22188|CDS|CDS	0.3	16.0	0.1	R	COG1284	Uncharacterized conserved protein
TS29Col1920|CDS|CDS	0.5	32.0	0.1	R	COG1284	Uncharacterized conserved protein
TS29Col0119|CDS|CDS	0.5	34.0	0.1	R	COG1284	Uncharacterized conserved protein
Msmi751321|CDS|CDS	1.5	0.5	13.5	R	COG1287	Uncharacterized membrane protein, required for N-linked glycosylation
TS29Rum13350|CDS|CDS	1.0	48.0	0.1	R	COG1288	Predicted membrane protein
TS29Col1846|CDS|CDS	1.0	50.0	0.1	R	COG1288	Predicted membrane protein
CspM6210573|CDS|CDS	1.0	49.8	0.1	R	COG1289	Predicted membrane protein
Rlac1944|CDS|CDS	4.0	1.0	18.2	R	COG1297	Predicted membrane protein
TS28Fae21618|CDS|CDS	5.5	2.0	12.5	R	COG1297	Predicted membrane protein
Robe2864|CDS|CDS	1.5	0.5	13.6	R	COG1302	Uncharacterized protein conserved in bacteria
RintL11779|CDS|CDS	3.0	1.0	13.6	R	COG1302	Uncharacterized protein conserved in bacteria
TS28Rum12213|CDS|CDS	1.5	0.5	13.6	R	COG1302	Uncharacterized protein conserved in bacteria
TS28Bac2297|CDS|CDS	2.3	0.3	31.8	R	COG1322	Uncharacterized protein conserved in bacteria
TS28Fae00267|CDS|CDS	9.5	3.0	14.4	R	COG1322	Uncharacterized protein conserved in bacteria
Buni1811|CDS|CDS	2.3	0.8	12.7	R	COG1322	Uncharacterized protein conserved in bacteria
Aput1312|CDS|CDS	7.0	3.0	10.6	R	COG1322	Uncharacterized protein conserved in bacteria
TS28Fae22036|CDS|CDS	0.3	38.5	0.0	R	COG1322	Uncharacterized protein conserved in bacteria

TS28Fae22712|CDS|CDS	6.0	2.0	13.6	R	COG1323	Predicted nucleotidyltransferase
TS29Rum20187|CDS|CDS	1.0	48.0	0.1	R	COG1323	Predicted nucleotidyltransferase
TS29Fae08290|CDS|CDS	1.0	46.0	0.1	R	COG1357	Uncharacterized low-complexity proteins
Bxyl3405|CDS|CDS	0.2	8.5	0.1	R	COG1357	Uncharacterized low-complexity proteins
Bova3364|CDS|CDS	1.5	0.3	20.4	R	COG1373	Predicted ATPase (AAA+ superfamily)
BactD10311|CDS|CDS	1.4	0.5	12.7	R	COG1373	Predicted ATPase (AAA+ superfamily)
BactD21418|CDS|CDS	3.0	1.3	10.9	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS28Met0533|CDS|CDS	0.6	0.3	10.6	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS29Bac10327|CDS|CDS	0.3	13.0	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
Bova2362|CDS|CDS	0.3	15.3	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS29Rum19432|CDS|CDS	1.0	73.0	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS28Fae17497|CDS|CDS	0.5	36.5	0.1	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS29Bif0492|CDS|CDS	0.4	38.2	0.0	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS28Bif4446|CDS|CDS	0.4	38.2	0.0	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS29Bac09301|CDS|CDS	0.3	37.0	0.0	R	COG1373	Predicted ATPase (AAA+ superfamily)
TS29Fae06001|CDS|CDS	0.5	89.5	0.0	R	COG1373	Predicted ATPase (AAA+ superfamily)
Robe0623|CDS|CDS	131.7	6.0	99.6	R	COG1376	Uncharacterized protein conserved in bacteria
TS29Rum04349|CDS|CDS	156.7	29.0	24.5	R	COG1376	Uncharacterized protein conserved in bacteria
Cbol0432|CDS|CDS	7.0	3.0	10.6	R	COG1376	Uncharacterized protein conserved in bacteria
TS28Rum11191|CDS|CDS	13.7	2.0	31.0	R	COG1399	Predicted metal-binding, possibly nucleic acid-binding protein
Cbol2666|CDS|CDS	5.0	2.0	11.3	R	COG1399	Predicted metal-binding, possibly nucleic acid-binding protein
Cbol5678|CDS|CDS	7.0	2.0	15.9	R	COG1408	Predicted phosphohydrolases
TS29Fae03159|CDS|CDS	1.5	112.0	0.1	R	COG1408	Predicted phosphohydrolases
TS28Clo00068|CDS|CDS	11.0	3.0	16.6	R	COG1409	Predicted phosphohydrolases
TS28Rum01184|CDS|CDS	0.5	50.0	0.0	R	COG1409	Predicted phosphohydrolases
TS29Rum11482|CDS|CDS	0.5	86.0	0.0	R	COG1409	Predicted phosphohydrolases
Bthe7331937|CDS|CDS	7.5	0.5	67.9	R	COG1418	Predicted HD superfamily hydrolase
Aput1081|CDS|CDS	4.5	1.0	20.4	R	COG1418	Predicted HD superfamily hydrolase
BFych463602|CDS|phosphodiesterase	4.2	1.0	18.9	R	COG1418	Predicted HD superfamily hydrolase
Rtor2444|CDS|CDS	20.3	5.0	18.5	R	COG1418	Predicted HD superfamily hydrolase
Ehal2323|CDS|CDS	4.0	1.0	18.2	R	COG1418	Predicted HD superfamily hydrolase
Bsp1162686|CDS|CDS	1.9	0.5	17.2	R	COG1418	Predicted HD superfamily hydrolase
Rgna1663|CDS|CDS	8.5	2.5	15.4	R	COG1418	Predicted HD superfamily hydrolase
Rlac1515|CDS|CDS	3.3	1.0	15.1	R	COG1418	Predicted HD superfamily hydrolase
TS29Rum18607|CDS|CDS	1.5	0.5	13.6	R	COG1418	Predicted HD superfamily hydrolase
Csym2272|CDS|CDS	11.0	4.0	12.5	R	COG1418	Predicted HD superfamily hydrolase
TS28Fae00280|CDS|CDS	18.5	7.0	12.0	R	COG1418	Predicted HD superfamily hydrolase
TS29Clo3530|CDS|CDS	9.0	3.0	13.6	R	COG1451	Predicted metal-dependent hydrolase
Msmi740407|CDS|CDS	2.5	0.8	15.1	R	COG1460	Uncharacterized protein conserved in archaea
Msmi751270|CDS|CDS	2.5	0.8	15.1	R	COG1460	Uncharacterized protein conserved in archaea
TS28Met0721|CDS|CDS	2.5	0.8	15.1	R	COG1460	Uncharacterized protein conserved in archaea
Bcap1102|CDS|CDS	9.0	1.0	40.9	R	COG1461	Predicted kinase related to dihydroxyacetone kinase
Cram1128|CDS|CDS	3.0	0.5	27.2	R	COG1461	Predicted kinase related to dihydroxyacetone kinase
Clep2103|CDS|CDS	1.0	0.3	13.6	R	COG1461	Predicted kinase related to dihydroxyacetone kinase
TS29RumUnc0232|CDS|CDS	1.0	46.0	0.1	R	COG1461|COG1307	Predicted kinase related to dihydroxyacetone kinase|Uncharacterized protein conserved in bacteria
TS28Fae16695|CDS|CDS	0.3	18.0	0.1	R	COG1461|COG1307	Predicted kinase related to dihydroxyacetone kinase|Uncharacterized protein conserved in bacteria
TS29Bif2512|CDS|CDS	2.0	135.3	0.1	R	COG1479	Uncharacterized conserved protein
TS28Rum16074|CDS|CDS	30.3	6.0	23.0	R	COG1481	Uncharacterized protein conserved in bacteria
TS29Fae03943|CDS|CDS	9.5	4.0	10.8	R	COG1481	Uncharacterized protein conserved in bacteria
Clep0876|CDS|CDS	1.0	0.3	13.6	R	COG1496	Uncharacterized conserved protein
TS28Rum14615|CDS|CDS	1.0	0.3	13.6	R	COG1511	Predicted membrane protein
TS29Bif1087|CDS|CDS	1.5	76.0	0.1	R	COG1511	Predicted membrane protein
TS29Bif0655|CDS|CDS	2.2	143.8	0.1	R	COG1511	Predicted membrane protein
TS28Bif4537|CDS|CDS	1.0	107.1	0.0	R	COG1511	Predicted membrane protein
TS29Bif3533|CDS|CDS	1.0	152.1	0.0	R	COG1511	Predicted membrane protein
TS28Rum13337|CDS|CDS	22.5	3.0	34.0	R	COG1511|COG2409	Predicted membrane protein|Predicted drug exporters of the RND superfamily
TS28Clo00153|CDS|CDS	6.0	0.5	54.5	R	COG1546|COG1058	Uncharacterized protein (competence- and mitomycin-induced)|Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA
Clep0065|CDS|CDS	5.0	0.5	45.4	R	COG1546|COG1058	Uncharacterized protein (competence- and mitomycin-induced)|Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA
TS29Bif2965|CDS|CDS	0.3	72.8	0.0	R	COG1559	Predicted periplasmic solute-binding protein
Rtor0419|CDS|CDS	2.5	1.0	11.3	R	COG1561	Uncharacterized stress-induced protein
TS28Rum09135|CDS|CDS	2.5	1.0	11.3	R	COG1561	Uncharacterized stress-induced protein
Buni1574|CDS|CDS	19.5	4.5	19.7	R	COG1579	Zn-ribbon protein, possibly nucleic acid-binding
TS28Rum16082|CDS|CDS	5.5	0.5	49.9	R	COG1606	ATP-utilizing enzymes of the PP-loop superfamily
TS28Rum10243|CDS|CDS	4.0	1.0	18.2	R	COG1606	ATP-utilizing enzymes of the PP-loop superfamily
TS29Bif3306|CDS|CDS	0.8	97.8	0.0	R	COG1615	Uncharacterized conserved protein
TS28Bif4708|CDS|CDS	0.8	97.8	0.0	R	COG1615	Uncharacterized conserved protein
TS28Fae17147|CDS|CDS	0.3	28.0	0.1	R	COG1649	Uncharacterized protein conserved in bacteria
TS28Fae06125|CDS|CDS	4.0	1.0	18.2	R	COG1660	Predicted P-loop-containing kinase
BactD24266|CDS|CDS	7.0	3.0	10.6	R	COG1672	Predicted ATPase (AAA+ superfamily)
RintL13113|CDS|CDS	4.0	1.0	18.2	R	COG1699	Uncharacterized protein conserved in bacteria
Bova0527|CDS|CDS	4.5	1.0	20.4	R	COG1721	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)
TS29Bac07353|CDS|CDS	0.3	16.8	0.1	R	COG1721	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)
TS29Bif3757|CDS|CDS	0.3	39.5	0.0	R	COG1739	Uncharacterized conserved protein
TS28Bif0867|CDS|CDS	0.3	39.5	0.0	R	COG1739	Uncharacterized conserved protein
Buni3473|CDS|CDS	3.5	1.5	10.6	R	COG1741	Pirin-related protein
BactD12109|CDS|CDS	3.1	1.3	10.4	R	COG1741	Pirin-related protein
FpraM2121018|CDS|CDS	17.3	1.5	52.5	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
Bcap2813|CDS|CDS	7.0	1.0	31.8	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS28Fae02012|CDS|CDS	6.0	1.5	18.2	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS28Clo05844|CDS|CDS	11.0	3.0	16.6	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS29Col0068|CDS|CDS	1.0	67.0	0.1	R	COG1744	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
TS29RumUnc0256|CDS|CDS	1.0	50.0	0.1	R	COG1752|COG4667	Predicted esterase of the alpha-beta hydrolase superfamily|Predicted esterase of the alpha-beta hydrolase superfamily

Buni1876|CDS|CDS	4.5	0.5	40.9	R	COG1774	Uncharacterized homolog of PSP1
BactD12361|CDS|CDS	2.6	0.5	23.5	R	COG1774	Uncharacterized homolog of PSP1
Aput0899|CDS|CDS	15.0	4.0	17.0	R	COG1774	Uncharacterized homolog of PSP1
TS28Dor0588|CDS|CDS	1.5	0.5	13.6	R	COG1774	Uncharacterized homolog of PSP1
Dfor2707|CDS|CDS	2.5	1.0	11.3	R	COG1774	Uncharacterized homolog of PSP1
TS28Rum10394|CDS|CDS	5.2	1.5	15.7	R	COG1799	Uncharacterized protein conserved in bacteria
TS28Rum12599|CDS|CDS	3.0	1.0	13.6	R	COG1799	Uncharacterized protein conserved in bacteria
TS28Col1399|CDS|CDS	3.0	1.0	13.6	R	COG1799	Uncharacterized protein conserved in bacteria
TS29Clo3603|CDS|CDS	5.0	2.0	11.3	R	COG1799	Uncharacterized protein conserved in bacteria
Bxyl2321|CDS|CDS	0.2	10.8	0.1	R	COG1808	Predicted membrane protein
TS29Bac09534|CDS|CDS	0.2	10.8	0.1	R	COG1808	Predicted membrane protein
TS29Rum19888|CDS|CDS	1.0	45.5	0.1	R	COG1811	Uncharacterized membrane protein, possible Na+ channel or pump
Bsp1161111|CDS|CDS	2.5	1.0	11.3	R	COG1814	Uncharacterized membrane protein
Msmi750740|CDS|CDS	1.0	0.3	13.6	R	COG1821	Predicted ATP-utilizing enzyme (ATP-grasp superfamily)
Rgna1052|CDS|CDS	2.0	0.5	18.2	R	COG1837	Predicted RNA-binding protein (contains KH domain)
TS29Rum06889|CDS|CDS	2.0	0.5	18.2	R	COG1837	Predicted RNA-binding protein (contains KH domain)
Buni3475|CDS|CDS	3.3	1.0	15.1	R	COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
TS28Bac3072|CDS|CDS	3.3	1.0	15.1	R	COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
BactD11706|CDS|CDS	3.3	1.0	15.1	R	COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
BactD12106|CDS|CDS	2.0	0.7	13.6	R	COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
TS29Bac02465|CDS|CDS	4.5	2.0	10.2	R	COG1895	Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN
Bxyl4080|CDS|CDS	4.5	2.0	10.2	R	COG1895	Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN
Dlon1057|CDS|CDS	3.0	1.0	13.6	R	COG1896	Predicted hydrolases of HD superfamily
Msmi750736|CDS|CDS	2.7	0.3	36.3	R	COG1907	Predicted archaeal sugar kinases
TS28Met1381|CDS|CDS	2.7	0.3	36.3	R	COG1907	Predicted archaeal sugar kinases
RintL12972|CDS|CDS	5.0	2.0	11.3	R	COG1917	Uncharacterized conserved protein, contains double-stranded beta-helix domain
TS29Rum06208|CDS|CDS	5.8	1.0	26.5	R	COG2001	Uncharacterized protein conserved in bacteria
TS29Rum19264|CDS|CDS	36.0	10.0	16.3	R	COG2001	Uncharacterized protein conserved in bacteria
Rtor2549|CDS|CDS	6.0	2.0	13.6	R	COG2001	Uncharacterized protein conserved in bacteria
TS28Rum13912|CDS|CDS	0.5	26.5	0.1	R	COG2005|COG2068	N-terminal domain of molybdenum-binding protein|Uncharacterized MobA-related protein
TS28Rum01566|CDS|CDS	3.5	0.5	31.8	R	COG2052	Uncharacterized protein conserved in bacteria
TS28Rum01869|CDS|CDS	1.5	0.5	13.6	R	COG2068	Uncharacterized MobA-related protein
TS28Rum12482|CDS|CDS	4.5	1.5	13.6	R	COG2068	Uncharacterized MobA-related protein
TS29Clo0590|CDS|CDS	13.0	3.0	19.7	R	COG2070	Dioxygenases related to 2-nitropropane dioxygenase
TS29Fae08257|CDS|CDS	1.0	62.5	0.1	R	COG2081	Predicted flavoproteins
Rgna1119|CDS|CDS	4.0	1.0	18.2	R	COG2096|COG3193	Uncharacterized conserved protein|Uncharacterized protein, possibly involved in utilization of glycolate and propanediol
TS29Fae07152|CDS|CDS	0.5	42.0	0.1	R	COG2110	Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1
Msmi740349|CDS|CDS	1.3	0.5	11.3	R	COG2118	DNA-binding protein
Msmi751328|CDS|CDS	1.3	0.5	11.3	R	COG2118	DNA-binding protein
TS28Met1556|CDS|CDS	1.3	0.5	11.3	R	COG2118	DNA-binding protein
TS28Met0737|CDS|CDS	0.8	0.3	13.6	R	COG2129	Predicted phosphoesterases, related to the Icc protein
Msmi741001|CDS|CDS	0.8	0.3	13.6	R	COG2129	Predicted phosphoesterases, related to the Icc protein
Aput1275|CDS|CDS	22.0	3.0	33.3	R	COG2166	SufE protein probably involved in Fe-S center assembly
TS28Dor1043|CDS|CDS	50.0	7.0	32.4	R	COG2234	Predicted aminopeptidases
TS29Col1806|CDS|CDS	1.0	46.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS29RumUnc1649|CDS|CDS	1.0	57.0	0.1	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
TS29Fae01251|CDS|CDS	1.0	98.0	0.0	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid
Robe1287|CDS|CDS	5.5	2.0	12.5	R	COG2252	Permeases
TS29Bif1314|CDS|CDS	0.8	39.0	0.1	R	COG2252	Permeases
TS29Fae07280|CDS|CDS	1.0	97.0	0.0	R	COG2253	Uncharacterized conserved protein
Bcap1868|CDS|CDS	11.0	2.0	25.0	R	COG2262	GTPases
Buni1546|CDS|CDS	4.0	1.5	12.1	R	COG2304	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
TS28Rum02146|CDS|CDS	4.0	1.0	18.2	R	COG2316	Predicted hydrolase (HD superfamily)
TS29Fae01872|CDS|CDS	0.5	25.5	0.1	R	COG2323	Predicted membrane protein
Cbol1185|CDS|CDS	4.3	1.0	19.7	R	COG2326	Uncharacterized conserved protein
TS28Rum11117|CDS|CDS	3.0	1.0	13.6	R	COG2327	Uncharacterized conserved protein
TS28Fae13829|CDS|CDS	1.5	0.5	13.6	R	COG2333	Predicted hydrolase (metallo-beta-lactamase superfamily)
Buni2325|CDS|CDS	3.5	1.0	15.9	R	COG2344	AT-rich DNA-binding protein
ShigspD92361|CDS|CDS	17.0	3.0	25.7	R	COG2373	Large extracellular alpha-helical protein
TS29Bac12202|CDS|CDS	0.3	20.5	0.1	R	COG2425	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Buni1864|CDS|CDS	6.0	0.5	54.5	R	COG2509	Uncharacterized FAD-dependent dehydrogenases
TS28Fae18733|CDS|CDS	3.0	1.0	13.6	R	COG2509	Uncharacterized FAD-dependent dehydrogenases
TS29Rum19250|CDS|CDS	6.0	2.0	13.6	R	COG2738	Predicted Zn-dependent protease
TS28Fae19473|CDS|CDS	1.0	62.0	0.1	R	COG2819	Predicted hydrolase of the alpha/beta superfamily
TS28Col1474|CDS|CDS	4.0	1.0	18.2	R	COG2848	Uncharacterized conserved protein
Dfor1385|CDS|CDS	7.0	2.0	15.9	R	COG2848	Uncharacterized conserved protein
Dlon1087|CDS|CDS	3.0	1.0	13.6	R	COG2860	Predicted membrane protein
TS28Bif4515|CDS|CDS	0.5	49.0	0.0	R	COG2898	Uncharacterized conserved protein
TS29Bif0544|CDS|CDS	0.5	130.3	0.0	R	COG2898	Uncharacterized conserved protein
Buni0159|CDS|CDS	6.0	1.5	18.2	R	COG2908	Uncharacterized protein conserved in bacteria
TS29Fae06188|CDS|CDS	74.0	21.0	16.0	R	COG2929	Uncharacterized protein conserved in bacteria
TS28Dor0654|CDS|CDS	15.0	4.0	17.0	R	COG2936	Predicted acyl esterases
Buni1112|CDS|CDS	1.2	0.5	10.6	R	COG2985	Predicted permease
Cbol3129|CDS|CDS	6.0	2.0	13.6	R	COG3034	Uncharacterized protein conserved in bacteria
TS28Rum01371|CDS|CDS	6.5	1.5	19.7	R	COG3044	Predicted ATPase of the ABC class
BactD11356|CDS|CDS	3.0	1.0	13.6	R	COG3093	Plasmid maintenance system antidote protein
TS29Fae02873|CDS|CDS	6.0	1.0	27.2	R	COG3177	Uncharacterized conserved protein
TS28Fae21213|CDS|CDS	0.5	23.0	0.1	R	COG3177	Uncharacterized conserved protein
TS28Bac7420|CDS|CDS	1.3	73.5	0.1	R	COG3177	Uncharacterized conserved protein
TS28Fae15478|CDS|CDS	3.0	1.0	13.6	R	COG3236	Uncharacterized protein conserved in bacteria
TS29Rum20151|CDS|CDS	1.0	89.0	0.1	R	COG3291	FOG: PKD repeat
TS29Rum14035|CDS|CDS	1.0	82.0	0.1	R	COG3291|COG5263	FOG: PKD repeat|FOG: Glucan-binding domain (YG repeat)
TS28Rum09611|CDS|CDS	0.5	26.8	0.1	R	COG3314	Uncharacterized protein conserved in bacteria
TS28Rum06272|CDS|CDS	3.0	1.0	13.6	R	COG3341	Predicted double-stranded RNA/RNA-DNA hybrid binding protein

TS29Bac09107|CDS|CDS	2.5	1.0	11.3	R	COG3382	Uncharacterized conserved protein
Bthe7332327|CDS|CDS	7.5	1.0	34.0	R	COG3391	Uncharacterized conserved protein
Bsp1161685|CDS|CDS	5.0	2.0	11.3	R	COG3391	Uncharacterized conserved protein
Bsp1162034|CDS|CDS	0.7	0.3	10.7	R	COG3391	Uncharacterized conserved protein
Bova3767|CDS|CDS	23.2	9.5	11.1	R	COG3401	Fibronectin type 3 domain-containing protein
Bxyl2994|CDS|CDS	9.0	4.0	10.2	R	COG3401	Fibronectin type 3 domain-containing protein
Cbol4824|CDS|CDS	12.0	3.0	18.2	R	COG3412	Uncharacterized protein conserved in bacteria
TS28Dor1343|CDS|CDS	2.5	0.5	22.7	R	COG3533	Uncharacterized protein conserved in bacteria
TS29Bif3570|CDS|CDS	3.3	149.6	0.1	R	COG3533	Uncharacterized protein conserved in bacteria
TS29Bac01686|CDS|CDS	2.0	0.7	13.6	R	COG3550	Uncharacterized protein related to capsule biosynthesis enzymes
Begg0951|CDS|CDS	3.0	1.0	13.6	R	COG3550	Uncharacterized protein related to capsule biosynthesis enzymes
TS29Fae02237|CDS|CDS	0.3	16.0	0.1	R	COG3581	Uncharacterized protein conserved in bacteria
TS29Rum06401|CDS|CDS	26.0	2.0	59.0	R	COG3610	Uncharacterized conserved protein
Acac2873|CDS|CDS	3.0	1.0	13.6	R	COG3610	Uncharacterized conserved protein
TS29Fae09808|CDS|CDS	0.3	20.0	0.1	R	COG3641	Predicted membrane protein, putative toxin regulator
TS29Rum11497|CDS|CDS	1.0	76.0	0.1	R	COG3681	Uncharacterized conserved protein
Buni2020|CDS|CDS	5.5	0.5	49.9	R	COG3735	Uncharacterized protein conserved in bacteria
BactD12311|CDS|CDS	1.5	0.5	13.6	R	COG3831	Uncharacterized conserved protein
TS29Bif2823|CDS|CDS	0.3	14.8	0.1	R	COG3856	Uncharacterized conserved protein (small basic protein)
TS28Bif1881|CDS|CDS	0.3	14.8	0.1	R	COG3856	Uncharacterized conserved protein (small basic protein)
TS28Dor1460|CDS|CDS	2.5	1.0	11.3	R	COG3858	Predicted glycosyl hydrolase
Cbol4820|CDS|CDS	7.0	2.0	15.9	R	COG3862	Uncharacterized protein with conserved CXXC pairs
TS29Fae05330|CDS|CDS	1.0	83.0	0.1	R	COG3872	Predicted metal-dependent enzyme
TS28Eub1795|CDS|CDS	1.5	0.5	13.6	R	COG3875	Uncharacterized conserved protein
TS29Fae05457|CDS|CDS	1.0	104.0	0.0	R	COG3876	Uncharacterized protein conserved in bacteria
TS29Bif2822|CDS|CDS	0.3	21.3	0.1	R	COG3879	Uncharacterized protein conserved in bacteria
TS28Bif1882|CDS|CDS	0.3	41.9	0.0	R	COG3879	Uncharacterized protein conserved in bacteria
TS28Eub5272|CDS|CDS	9.0	4.0	10.2	R	COG3880	Uncharacterized protein with conserved CXXC pairs
TS28Rum15429|CDS|CDS	6.0	0.5	54.5	R	COG3894	Uncharacterized metal-binding protein
TS29Bif0455|CDS|CDS	1.7	138.0	0.1	R	COG3942|COG3583	Surface antigen|Uncharacterized protein conserved in bacteria
TS29Fae05982|CDS|CDS	0.5	83.0	0.0	R	COG3943	Virulence protein
TS28EntUnc063|CDS|CDS	9.0	2.0	20.4	R	COG3950	Predicted ATP-binding protein involved in virulence
TS28Bif0221|CDS|CDS	1.0	69.8	0.1	R	COG3956|COG1694	Protein containing tetrapyrrole methyltransferase domain and MazG-like (predicted pyrophosphatase) domain|Predicted pyrophosphatase
TS29Bif2938|CDS|CDS	0.5	36.3	0.1	R	COG3956|COG1694	Protein containing tetrapyrrole methyltransferase domain and MazG-like (predicted pyrophosphatase) domain|Predicted pyrophosphatase
Bxyl3199|CDS|CDS	3.8	0.5	34.4	R	COG3968	Uncharacterized protein related to glutamine synthetase
TS28Fae02780|CDS|CDS	4.7	1.0	21.2	R	COG3968	Uncharacterized protein related to glutamine synthetase
Buni0452|CDS|CDS	5.0	0.5	45.4	R	COG3969	Predicted phosphoadenosine phosphosulfate sulfotransferase
TS28Bif3124|CDS|CDS	0.5	24.7	0.1	R	COG3973	Superfamily I DNA and RNA helicases
TS29Bif2285|CDS|CDS	0.5	44.7	0.1	R	COG3973	Superfamily I DNA and RNA helicases
Bova3115|CDS|CDS	1.3	0.5	11.3	R	COG3979	Uncharacterized protein contain chitin-binding domain type 3
Bxyl2958|CDS|CDS	5.5	2.3	10.7	R	COG3979	Uncharacterized protein contain chitin-binding domain type 3
TS29Rum00141|CDS|CDS	297.0	70.0	19.3	R	COG4086	Predicted secreted protein
TS28Rum09180|CDS|CDS	6.3	1.5	19.2	R	COG4086	Predicted secreted protein
TS29Rum03113|CDS|CDS	14.0	4.0	15.9	R	COG4086	Predicted secreted protein
BWH24168|CDS|CDS	121.5	48.0	11.5	R	COG4104|COG5529	Uncharacterized conserved protein|Pyocin large subunit
TS28Fae22058|CDS|CDS	7.5	2.0	17.0	R	COG4115	Uncharacterized protein conserved in bacteria
Bcap0708|CDS|CDS	7.0	2.0	15.9	R	COG4120	ABC-type uncharacterized transport system, permease component
TS29Col0062|CDS|CDS	0.5	42.0	0.1	R	COG4120	ABC-type uncharacterized transport system, permease component
TS28Rum03708|CDS|CDS	4.5	1.0	20.4	R	COG4122	Predicted O-methyltransferase
BactD22877|CDS|CDS	0.9	0.3	12.5	R	COG4122	Predicted O-methyltransferase
Robe1619|CDS|CDS	5.0	2.0	11.3	R	COG4122	Predicted O-methyltransferase
TS28Fae16421|CDS|CDS	0.5	59.0	0.0	R	COG4123	Predicted O-methyltransferase
Aput0331|CDS|CDS	26.0	2.0	59.0	R	COG4198	Uncharacterized conserved protein
TS29Bac07234|CDS|CDS	5.5	2.0	12.5	R	COG4198	Uncharacterized conserved protein
TS29Bac08875|CDS|CDS	11.0	3.5	14.3	R	COG4225	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins
BactD11404|CDS|CDS	1.0	0.3	13.6	R	COG4225	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins
Buni2555|CDS|CDS	1.0	0.3	13.6	R	COG4225	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins
TS28Bac3674|CDS|CDS	1.0	0.3	13.6	R	COG4225	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins
Bxyl2992|CDS|CDS	1.4	0.5	12.7	R	COG4225	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins
TS28Rum16394|CDS|CDS	22.5	2.0	51.1	R	COG4260	Putative virion core protein (lumpy skin disease virus)
TS29Bac09907|CDS|CDS	0.3	13.9	0.1	R	COG4292	Predicted membrane protein
TS29Bif2400|CDS|CDS	0.3	66.3	0.0	R	COG4320	Uncharacterized protein conserved in bacteria
CspSS21632|CDS|CDS	0.2	11.8	0.1	R	COG4422	Bacteriophage protein gp37
TS29Fae10356|CDS|CDS	0.5	31.0	0.1	R	COG4474	Uncharacterized protein conserved in bacteria
TS29Fae01471|CDS|CDS	0.5	37.0	0.1	R	COG4474	Uncharacterized protein conserved in bacteria
BactD12509|CDS|CDS	2.7	1.0	12.1	R	COG4552	Predicted acetyltransferase involved in intracellular survival and related acetyltransferases
TS28Rum03210|CDS|CDS	5.0	0.5	45.4	R	COG4603	ABC-type uncharacterized transport system, permease component
Aput1055|CDS|CDS	6.0	2.0	13.6	R	COG4624	Iron only hydrogenase large subunit, C-terminal domain
TS29Bif4160|CDS|CDS	1.9	96.1	0.1	R	COG4716	Myosin-crossreactive antigen
TS28Fae21398|CDS|CDS	0.3	33.0	0.0	R	COG4716	Myosin-crossreactive antigen
TS29Rum01365|CDS|CDS	0.5	24.0	0.1	R	COG4717	Uncharacterized conserved protein
TS29Bif1298|CDS|CDS	0.5	46.0	0.0	R	COG4733	Phage-related protein, tail component
Bova3587|CDS|CDS	2.3	0.3	40.9	R	COG4804	Uncharacterized conserved protein
Bthe7332279|CDS|CDS	2.3	0.3	40.9	R	COG4804	Uncharacterized conserved protein
TS29Bif3091|CDS|CDS	0.8	55.5	0.1	R	COG4832	Uncharacterized conserved protein
TS29Clo3450|CDS|CDS	3.0	1.0	13.6	R	COG4857	Predicted kinase
TS29Rum20833|CDS|CDS	1.0	96.0	0.0	R	COG4878	Uncharacterized protein conserved in bacteria
RintL14039|CDS|CDS	3.0	1.0	13.6	R	COG4880	Secreted protein containing C-terminal beta-propeller domain distantly related to WD-40 repeats
Rtor0725|CDS|CDS	12.8	3.3	17.5	R	COG4886	Leucine-rich repeat (LRR) protein
TS29Bif0656|CDS|CDS	0.8	62.2	0.1	R	COG4905	Predicted membrane protein
TS28Bif1101|CDS|CDS	0.8	62.2	0.1	R	COG4905	Predicted membrane protein
TS29Fae08550|CDS|CDS	0.5	82.0	0.0	R	COG4905	Predicted membrane protein
TS28Fae15121|CDS|CDS	2.5	0.5	22.7	R	COG4947	Uncharacterized protein conserved in bacteria
TS29Fae00873|CDS|CDS	0.5	31.0	0.1	R	COG5015	Uncharacterized conserved protein
Csym0810|CDS|CDS	16.7	6.0	12.6	R	COG5263	FOG: Glucan-binding domain (YG repeat)
Cbol1236|CDS|CDS	29.0	12.0	11.0	R	COG5263	FOG: Glucan-binding domain (YG repeat)
Casp5886|CDS|CDS	1.0	74.0	0.1	R	COG5281	Phage-related minor tail protein

TS29Bif4120|CDS|CDS	1.0	102.8	0.0	R	COG5282	Uncharacterized conserved protein
TS29Eub2074|CDS|CDS	1.0	99.0	0.0	R	COG5283	Phage-related tail protein
TS28Bif4969|CDS|CDS	0.7	49.0	0.1	R	COG5283|COG3942|COG3583|COG3584	Phage-related tail protein|Surface antigen|Uncharacterized protein conserved in bacteria|Uncharacterized protein conserved in bacteria
Bado0737|CDS|CDS	0.3	32.5	0.0	R	COG5324	Uncharacterized conserved protein
TS29Bif3017|CDS|CDS	0.3	103.5	0.0	R	COG5324	Uncharacterized conserved protein
Bxyl2623|CDS|CDS	1.0	0.3	13.6	R	COG5368	Uncharacterized protein conserved in bacteria
Bthe7330671|CDS|CDS	12.5	5.0	11.3	R	COG5464	Uncharacterized conserved protein
TS29Bac07909|CDS|CDS	4.5	2.0	10.2	R	COG5464	Uncharacterized conserved protein
Buni0939|CDS|CDS	3.0	1.0	13.6	R	COG5495	Uncharacterized conserved protein
TS29Rum19562|CDS|CDS	1.0	51.3	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
TS28Clo10778|CDS|CDS	0.3	15.3	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Rtor1345|CDS|CDS	0.3	20.0	0.1	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Cnex2744|CDS|CDS	1.0	126.9	0.0	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
FpraM2120212|CDS|CDS	0.3	38.3	0.0	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Rbro1714|CDS|CDS	0.3	59.7	0.0	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
Ceut1813|CDS|CDS	0.5	148.2	0.0	R	COG5545	Predicted P-loop ATPase and inactivated derivatives
BFych462748|CDS|hypothetical	1,965.2	2.0	4,460.7	NA	NA	hypothetical protein
TS29Fae01517|CDS|CDS	5,766.0	10.0	2,617.6	NA	NA	hypothetical protein
Ccom1560|CDS|CDS	527.9	1.0	2,396.4	NA	NA	hypothetical protein
Cbol1796|CDS|CDS	485.5	1.0	2,204.1	NA	NA	hypothetical protein
TS29Rum16879|CDS|CDS	1,496.5	4.0	1,698.4	NA	NA	hypothetical protein
TS29Fae05351|CDS|CDS	654.8	2.0	1,486.4	NA	NA	hypothetical protein
TS28Fae18841|CDS|CDS	654.8	2.0	1,486.4	NA	NA	hypothetical protein
TS29Fae01516|CDS|CDS	1,800.0	5.5	1,485.7	NA	NA	hypothetical protein
TS29Fae05352|CDS|CDS	1,288.0	4.0	1,461.8	NA	NA	hypothetical protein
Bxyl0898|CDS|CDS	91.8	0.3	1,250.7	NA	NA	hypothetical protein
BVU2636|CDS|hypothetical	777.5	3.0	1,176.6	NA	NA	hypothetical protein
BDI0370|CDS|hypothetical	237.0	1.0	1,075.9	NA	NA	hypothetical protein
TS29Fae05350|CDS|CDS	5,133.0	22.0	1,059.2	NA	NA	hypothetical protein
Robe2147|CDS|CDS	630.4	3.0	953.9	NA	NA	hypothetical protein
TS29Rum18029|CDS|CDS	719.0	4.0	816.0	NA	NA	hypothetical protein
BFych461128|CDS|hypothetical	244.5	1.5	740.0	NA	NA	hypothetical protein
BFnctc1040|CDS|hypothetical	244.5	1.5	740.0	NA	NA	hypothetical protein
TS29Fae00793|CDS|CDS	639.0	4.0	725.2	NA	NA	hypothetical protein
TS29Rum18028|CDS|CDS	605.0	4.0	686.6	NA	NA	hypothetical protein
BT1747|CDS|pyruvate-flavodoxin	22.0	0.2	600.0	NA	NA	hypothetical protein
TS28Rum04305|CDS|CDS	128.0	1.0	581.1	NA	NA	hypothetical protein
TS29Fae09565|CDS|CDS	1,283.5	11.0	529.7	NA	NA	hypothetical protein
TS28Rum04833|CDS|CDS	113.0	1.0	513.0	NA	NA	hypothetical protein
Rtor0713|CDS|CDS	113.0	1.0	513.0	NA	NA	hypothetical protein
BDI0681|CDS|heat	450.0	4.0	510.7	NA	NA	hypothetical protein
TS29Fae02024|CDS|CDS	199.3	2.0	452.5	NA	NA	hypothetical protein
TS28Fae12331|CDS|CDS	195.0	2.0	442.6	NA	NA	hypothetical protein
TS29Fae04279|CDS|CDS	1,586.0	16.5	436.4	NA	NA	hypothetical protein
TS28Rum13907|CDS|CDS	368.3	4.0	418.0	NA	NA	hypothetical protein
TS29Rum16880|CDS|CDS	368.3	4.0	418.0	NA	NA	hypothetical protein
BT2790|CDS|phosphoenolpyruvate	98.1	1.1	411.1	NA	NA	hypothetical protein
BactD21199|CDS|CDS	90.2	1.0	409.3	NA	NA	hypothetical protein
Bste1270|CDS|CDS	134.5	1.5	407.1	NA	NA	hypothetical protein
TS29Bac03469|CDS|CDS	134.5	1.5	407.1	NA	NA	hypothetical protein
BDI1997|CDS|chaperone	716.0	8.0	406.3	NA	NA	hypothetical protein
BDI2637|CDS|hypothetical	176.0	2.0	399.5	NA	NA	hypothetical protein
TS28Fae13891|CDS|CDS	86.0	1.0	390.4	NA	NA	hypothetical protein
Bado0002|CDS|CDS	77.0	1.0	349.6	NA	NA	hypothetical protein
BFych461742|CDS|chaperone	37.9	0.5	344.3	NA	NA	hypothetical protein
BFnctc2646|CDS|putative	74.5	1.0	338.2	NA	NA	hypothetical protein
Ccom0898|CDS|CDS	71.0	1.0	322.3	NA	NA	hypothetical protein
Bfra31121812|CDS|CDS	70.7	1.0	320.8	NA	NA	hypothetical protein
TS29Rum18027|CDS|CDS	408.0	6.0	308.7	NA	NA	hypothetical protein
BDI1223|CDS|endopeptidase	925.5	15.0	280.1	NA	NA	hypothetical protein
BFych462625|CDS|small	61.5	1.0	279.2	NA	NA	hypothetical protein
BFnctc2347|CDS|hypothetical	30.0	0.5	272.4	NA	NA	hypothetical protein
TS28Rum01717|CDS|CDS	30.0	0.5	272.4	NA	NA	hypothetical protein
BFych462253|CDS|hypothetical	30.0	0.5	272.4	NA	NA	hypothetical protein
BFnctc1172|CDS|putative	116.9	2.0	265.4	NA	NA	hypothetical protein
BDI0101|CDS|small	230.5	4.0	261.6	NA	NA	hypothetical protein
Rgna2950|CDS|CDS	19.0	0.3	258.8	NA	NA	hypothetical protein
BDI0408|CDS|RNA	102.0	2.0	231.5	NA	NA	hypothetical protein
BT2704|CDS|30S	8.5	0.2	231.5	NA	NA	hypothetical protein
RintL12461|CDS|CDS	98.0	2.0	222.4	NA	NA	hypothetical protein
Cbol0049|CDS|CDS	49.0	1.0	222.4	NA	NA	hypothetical protein
TS29Rum00092|CDS|CDS	146.0	3.0	220.9	NA	NA	hypothetical protein
RintL13107|CDS|CDS	47.0	1.0	213.4	NA	NA	hypothetical protein
TS28Clo06847|CDS|CDS	47.0	1.0	213.4	NA	NA	hypothetical protein
Bthe7330385|CDS|CDS	15.3	0.3	208.3	NA	NA	hypothetical protein
BFnctc3222|CDS|chaperonin	68.2	1.5	206.3	NA	NA	hypothetical protein
BDI0100|CDS|ferritin	133.0	3.0	201.3	NA	NA	hypothetical protein
Bthe3732190|CDS|CDS	8.4	0.2	191.2	NA	NA	hypothetical protein
Bple3428|CDS|CDS	8.4	0.2	191.2	NA	NA	hypothetical protein
TS28Ali0161|CDS|CDS	41.5	1.0	188.4	NA	NA	hypothetical protein
BFych461225|CDS|molecular	82.1	2.0	186.4	NA	NA	hypothetical protein
TS28Fae02116|CDS|CDS	152.5	4.0	173.1	NA	NA	hypothetical protein
Msmi740907|CDS|CDS	18.9	0.5	171.5	NA	NA	hypothetical protein
BDI2363|CDS|30S	37.0	1.0	168.0	NA	NA	hypothetical protein
BDI3786|CDS|co-chaperonin	73.5	2.0	166.8	NA	NA	hypothetical protein
Msm1017|CDS|methyl-coenzyme	18.0	0.5	163.4	NA	NA	hypothetical protein
BDI0288|CDS|hypothetical	72.0	2.0	163.4	NA	NA	hypothetical protein
BDI3787|CDS|chaperonin	356.7	10.0	161.9	NA	NA	hypothetical protein
Dfor0627|CDS|CDS	69.0	2.0	156.6	NA	NA	hypothetical protein
TS29Bac04550|CDS|CDS	68.0	2.0	154.4	NA	NA	hypothetical protein
TS28Col1110|CDS|CDS	67.0	2.0	152.1	NA	NA	hypothetical protein
TS28Fae18234|CDS|CDS	83.0	2.5	150.7	NA	NA	hypothetical protein
BDI3677|CDS|hypothetical	66.0	2.0	149.8	NA	NA	hypothetical protein
TS28Fae14056|CDS|CDS	82.0	2.5	148.9	NA	NA	hypothetical protein
BFnctc1819|CDS|putative	32.5	1.0	147.5	NA	NA	hypothetical protein

Rgna2691|CDS|CDS	472.8	15.0	143.1	NA	NA	hypothetical protein
TS28Fae21630|CDS|CDS	62.5	2.0	141.9	NA	NA	hypothetical protein
BFych464199|CDS|elongation	46.8	1.5	141.8	NA	NA	hypothetical protein
Bova2062|CDS|CDS	10.3	0.3	139.6	NA	NA	hypothetical protein
Cbol2418|CDS|CDS	184.5	6.0	139.6	NA	NA	hypothetical protein
BDI1240|CDS|putative	91.0	3.0	137.7	NA	NA	hypothetical protein
BDI0076|CDS|putative	30.0	1.0	136.2	NA	NA	hypothetical protein
BDI3726|CDS|ribosomal	30.0	1.0	136.2	NA	NA	hypothetical protein
TS29Rum02298|CDS|CDS	87.0	3.0	131.7	NA	NA	hypothetical protein
BactD11217|CDS|CDS	19.0	0.7	129.1	NA	NA	hypothetical protein
BT2712|CDS|50S	42.6	1.5	129.0	NA	NA	hypothetical protein
TS28Rum14886|CDS|CDS	14.0	0.5	127.1	NA	NA	hypothetical protein
TS28Rum13616|CDS|CDS	55.5	2.0	126.0	NA	NA	hypothetical protein
BFych461743|CDS|GrpE	27.5	1.0	124.8	NA	NA	hypothetical protein
TS29Dor0588|CDS|CDS	54.7	2.0	124.1	NA	NA	hypothetical protein
BactD11445|CDS|CDS	13.7	0.5	124.1	NA	NA	hypothetical protein
FpraM2121275|CDS|CDS	27.0	1.0	122.6	NA	NA	hypothetical protein
BT1920|CDS|hypothetical	80.0	3.0	121.1	NA	NA	hypothetical protein
Buni1048|CDS|CDS	8.8	0.3	120.3	NA	NA	hypothetical protein
BFych461205|CDS|endopeptidase	131.9	5.0	119.8	NA	NA	hypothetical protein
TS29Fae08440|CDS|CDS	26.2	1.0	118.8	NA	NA	hypothetical protein
Msm1019|CDS|methyl-coenzyme	19.6	0.8	118.5	NA	NA	hypothetical protein
BDI3783|CDS|hypothetical	26.0	1.0	118.0	NA	NA	hypothetical protein
HPAG11388|CDS|hypothetical	26.0	1.0	118.0	NA	NA	hypothetical protein
TS28Bac4910|CDS|CDS	63.0	2.5	114.4	NA	NA	hypothetical protein
BT3970|CDS|hypothetical	6.2	0.3	111.7	NA	NA	hypothetical protein
Bthe3730991|CDS|CDS	6.2	0.3	111.7	NA	NA	hypothetical protein
Bsp1162283|CDS|CDS	6.2	0.3	111.7	NA	NA	hypothetical protein
Bthe7332579|CDS|CDS	6.2	0.3	111.7	NA	NA	hypothetical protein
TS28Fae17706|CDS|CDS	24.5	1.0	111.2	NA	NA	hypothetical protein
BDI3733|CDS|MotA/TolQ/ExbB	24.5	1.0	111.2	NA	NA	hypothetical protein
TS29Rum03899|CDS|CDS	49.0	2.0	111.2	NA	NA	hypothetical protein
BactD11416|CDS|CDS	8.1	0.3	110.1	NA	NA	hypothetical protein
BT3359|CDS|acyl	16.0	0.7	109.0	NA	NA	hypothetical protein
BFych460402|CDS|hypothetical	24.0	1.0	109.0	NA	NA	hypothetical protein
BDI3730|CDS|hypothetical	24.0	1.0	109.0	NA	NA	hypothetical protein
BFych462409|CDS|heat	36.0	1.5	109.0	NA	NA	hypothetical protein
BFnctc1818|CDS|putative	58.9	2.5	107.0	NA	NA	hypothetical protein
b3530|CDS|cellulose	11.5	0.5	104.4	NA	NA	hypothetical protein
Bxyl1866|CDS|CDS	23.0	1.0	104.4	NA	NA	hypothetical protein
BFych464175|CDS|30S	11.3	0.5	102.9	NA	NA	hypothetical protein
Buni0847|CDS|CDS	11.3	0.5	102.9	NA	NA	hypothetical protein
BLD0741|CDS|Pyruvate	5.7	0.3	102.6	NA	NA	hypothetical protein
BFych463299|CDS|fructose-bisphosphate	7.5	0.3	102.1	NA	NA	hypothetical protein
Cbol6279|CDS|CDS	22.5	1.0	102.1	NA	NA	hypothetical protein
Aput1086|CDS|CDS	45.0	2.0	102.1	NA	NA	hypothetical protein
TS29Bac01331|CDS|CDS	11.2	0.5	101.4	NA	NA	hypothetical protein
Bxyl1535|CDS|CDS	11.2	0.5	101.4	NA	NA	hypothetical protein
TS29Fae08439|CDS|CDS	44.5	2.0	101.0	NA	NA	hypothetical protein
TS28Fae17838|CDS|CDS	22.0	1.0	99.9	NA	NA	hypothetical protein
Robe0608|CDS|CDS	32.5	1.5	98.4	NA	NA	hypothetical protein
BFnctc3483|CDS|hypothetical	43.0	2.0	97.6	NA	NA	hypothetical protein
TS29Fae10503|CDS|CDS	85.0	4.0	96.5	NA	NA	hypothetical protein
BFych463033|CDS|hypothetical	6.9	0.3	96.4	NA	NA	hypothetical protein
TS29Rum12974|CDS|CDS	7.0	0.3	95.3	NA	NA	hypothetical protein
Dfor1979|CDS|CDS	7.0	0.3	95.3	NA	NA	hypothetical protein
Msm1018|CDS|methyl-coenzyme	5.3	0.3	95.3	NA	NA	hypothetical protein
TS29Bac05127|CDS|CDS	14.0	0.7	95.3	NA	NA	hypothetical protein
BDI2620|CDS|hypothetical	30.5	1.5	92.3	NA	NA	hypothetical protein
TS29Par397|CDS|CDS	30.5	1.5	92.3	NA	NA	hypothetical protein
TS28Bac4094|CDS|CDS	6.7	0.3	90.8	NA	NA	hypothetical protein
TS28Fae18813|CDS|CDS	10.0	0.5	90.8	NA	NA	hypothetical protein
BDI2362|CDS|50S	10.0	0.5	90.8	NA	NA	hypothetical protein
BAD0533|CDS|elongation	3.3	0.2	90.4	NA	NA	hypothetical protein
TS28Rum07935|CDS|CDS	29.5	1.5	89.3	NA	NA	hypothetical protein
BFych464171|CDS|50S	9.8	0.5	88.7	NA	NA	hypothetical protein
BFych463396|CDS|co-chaperonin	19.1	1.0	86.9	NA	NA	hypothetical protein
BFnctc3223|CDS|co-chaperonin	19.1	1.0	86.9	NA	NA	hypothetical protein
TS29Ali032|CDS|CDS	19.0	1.0	86.3	NA	NA	hypothetical protein
TS29Fae03670|CDS|CDS	38.0	2.0	86.3	NA	NA	hypothetical protein
Msm0213|CDS|histone,	9.5	0.5	86.3	NA	NA	hypothetical protein
Buni0612|CDS|CDS	19.0	1.0	86.3	NA	NA	hypothetical protein
BDI0954|CDS|hypothetical	19.0	1.0	86.3	NA	NA	hypothetical protein
TS29Bac04313|CDS|CDS	132.0	7.0	85.6	NA	NA	hypothetical protein
TS28Rum13670|CDS|CDS	28.2	1.5	85.2	NA	NA	hypothetical protein
BDI0147|CDS|hypothetical	56.0	3.0	84.7	NA	NA	hypothetical protein
Rbro0053|CDS|CDS	36.8	2.0	83.6	NA	NA	hypothetical protein
BDI1241|CDS|molecular	55.0	3.0	83.2	NA	NA	hypothetical protein
BFych460022|CDS|L-aspartate	9.0	0.5	81.7	NA	NA	hypothetical protein
TS29Bac08257|CDS|CDS	18.0	1.0	81.7	NA	NA	hypothetical protein
BDI0941|CDS|recognition	18.0	1.0	81.7	NA	NA	hypothetical protein
BFych463395|CDS|chaperonin	80.5	4.5	81.2	NA	NA	hypothetical protein
Buni0658|CDS|CDS	35.8	2.0	81.2	NA	NA	hypothetical protein
BDI2380|CDS|50S	17.9	1.0	81.1	NA	NA	hypothetical protein
TS29Clo4951|CDS|CDS	122.0	7.0	79.1	NA	NA	hypothetical protein
BactD11318|CDS|CDS	5.7	0.3	79.1	NA	NA	hypothetical protein
TS28Par0021|CDS|CDS	5.7	0.3	79.1	NA	NA	hypothetical protein
Bfin1131|CDS|CDS	5.7	0.3	79.1	NA	NA	hypothetical protein
Bste0643|CDS|CDS	5.7	0.3	79.1	NA	NA	hypothetical protein
Bcoproc1927|CDS|CDS	5.7	0.3	79.1	NA	NA	hypothetical protein
Buni2208|CDS|CDS	5.7	0.3	79.1	NA	NA	hypothetical protein
TS29Bif2869|CDS|CDS	8.7	0.5	78.7	NA	NA	hypothetical protein
TS28Bif1828|CDS|CDS	8.7	0.5	78.7	NA	NA	hypothetical protein
TS28Fae15050|CDS|CDS	26.0	1.5	78.7	NA	NA	hypothetical protein
Aput0549|CDS|CDS	34.5	2.0	78.3	NA	NA	hypothetical protein

Bxyl2861|CDS|CDS	8.6	0.5	77.9	NA	NA	hypothetical protein
BFych464195|CDS|50S	8.6	0.5	77.8	NA	NA	hypothetical protein
TS29Fae08068|CDS|CDS	17.0	1.0	77.2	NA	NA	hypothetical protein
TS28Rum14116|CDS|CDS	8.5	0.5	77.2	NA	NA	hypothetical protein
BDI2366|CDS|30S	17.0	1.0	77.2	NA	NA	hypothetical protein
TS29Bac07362|CDS|CDS	34.0	2.0	77.2	NA	NA	hypothetical protein
BDI1603|CDS|putative	17.0	1.0	77.2	NA	NA	hypothetical protein
TS29Rum04357|CDS|CDS	17.0	1.0	77.2	NA	NA	hypothetical protein
b2678|CDS|glycine	16.8	1.0	76.4	NA	NA	hypothetical protein
FpraM2121587|CDS|CDS	33.5	2.0	76.0	NA	NA	hypothetical protein
TS29Rum00547|CDS|CDS	448.0	27.0	75.3	NA	NA	hypothetical protein
Cbol1700|CDS|CDS	33.0	2.0	74.9	NA	NA	hypothetical protein
BFych464196|CDS|50S	8.2	0.5	74.9	NA	NA	hypothetical protein
BFnctc4019|CDS|50S	8.2	0.5	74.9	NA	NA	hypothetical protein
TS28Fae10754|CDS|CDS	41.2	2.5	74.8	NA	NA	hypothetical protein
TS29Fae09687|CDS|CDS	41.2	2.5	74.8	NA	NA	hypothetical protein
TS29Fae10194|CDS|CDS	5.4	0.3	73.8	NA	NA	hypothetical protein
Bxyl0984|CDS|CDS	8.1	0.5	73.5	NA	NA	hypothetical protein
BDI1709|CDS|30S	16.0	1.0	72.6	NA	NA	hypothetical protein
BDI0598|CDS|putative	48.0	3.0	72.6	NA	NA	hypothetical protein
BDI3791|CDS|hypothetical	16.0	1.0	72.6	NA	NA	hypothetical protein
TS29Par109|CDS|CDS	8.0	0.5	72.6	NA	NA	hypothetical protein
BFnctc2491|CDS|heat	40.0	2.5	72.6	NA	NA	hypothetical protein
FpraM2120928|CDS|CDS	8.0	0.5	72.6	NA	NA	hypothetical protein
BDI1838|CDS|UDP-bacillosamine	32.0	2.0	72.6	NA	NA	hypothetical protein
BT2711|CDS|50S	23.8	1.5	72.1	NA	NA	hypothetical protein
Bxyl1094|CDS|CDS	5.3	0.3	71.5	NA	NA	hypothetical protein
BDI0359|CDS|serine	78.5	5.0	71.3	NA	NA	hypothetical protein
Dfor0045|CDS|CDS	47.0	3.0	71.1	NA	NA	hypothetical protein
BFych462744|CDS|serine	15.5	1.0	70.4	NA	NA	hypothetical protein
BFych461892|CDS|pyruvate	7.7	0.5	69.6	NA	NA	hypothetical protein
BDI2377|CDS|50S	15.3	1.0	69.6	NA	NA	hypothetical protein
BLD1839|CDS|1,3-propanediol	7.7	0.5	69.5	NA	NA	hypothetical protein
TS28Dor0215|CDS|CDS	15.1	1.0	68.4	NA	NA	hypothetical protein
TS28Bac1553|CDS|CDS	5.0	0.3	68.1	NA	NA	hypothetical protein
Bxyl1121|CDS|CDS	5.0	0.3	68.1	NA	NA	hypothetical protein
HPAG10370|CDS|high	15.0	1.0	68.1	NA	NA	hypothetical protein
TS29Par418|CDS|CDS	15.0	1.0	68.1	NA	NA	hypothetical protein
BDI2375|CDS|50S	30.0	2.0	68.1	NA	NA	hypothetical protein
Robe1420|CDS|CDS	7.5	0.5	68.1	NA	NA	hypothetical protein
TS29Rum15481|CDS|CDS	15.0	1.0	68.1	NA	NA	hypothetical protein
TS29Fae10144|CDS|CDS	22.5	1.5	68.1	NA	NA	hypothetical protein
Bado0652|CDS|CDS	2.5	0.2	67.7	NA	NA	hypothetical protein
Buni2830|CDS|CDS	14.8	1.0	67.3	NA	NA	hypothetical protein
TS28Bac0307|CDS|CDS	9.8	0.7	67.0	NA	NA	hypothetical protein
TS28Fae02028|CDS|CDS	14.5	1.0	65.8	NA	NA	hypothetical protein
Bxyl3701|CDS|CDS	14.3	1.0	65.1	NA	NA	hypothetical protein
BactD10742|CDS|CDS	23.8	1.7	64.9	NA	NA	hypothetical protein
BDI0287|CDS|glyceraldehyde	14.2	1.0	64.5	NA	NA	hypothetical protein
TS29Rum11835|CDS|CDS	28.3	2.0	64.3	NA	NA	hypothetical protein
BactD14466|CDS|CDS	11.8	0.8	64.2	NA	NA	hypothetical protein
Bxyl1667|CDS|CDS	11.8	0.8	64.2	NA	NA	hypothetical protein
BDI1893|CDS|hypothetical	14.0	1.0	63.6	NA	NA	hypothetical protein
BDI2434|CDS|GTP-binding	7.0	0.5	63.6	NA	NA	hypothetical protein
TS28Fae12272|CDS|CDS	14.0	1.0	63.6	NA	NA	hypothetical protein
Bfin3068|CDS|CDS	14.0	1.0	63.6	NA	NA	hypothetical protein
BDI2436|CDS|3-oxoacyl-[acyl-carrier-protein]	14.0	1.0	63.6	NA	NA	hypothetical protein
Dfor0628|CDS|CDS	14.0	1.0	63.6	NA	NA	hypothetical protein
EUBREC1884|CDS|hypothetical	7.0	0.5	63.6	NA	NA	hypothetical protein
BDI3701|CDS|cationic	7.0	0.5	63.6	NA	NA	hypothetical protein
TS28Bif4358|CDS|CDS	14.0	1.0	63.6	NA	NA	hypothetical protein
BDI1089|CDS|negative	83.0	6.0	62.8	NA	NA	hypothetical protein
Bxyl1462|CDS|CDS	34.4	2.5	62.4	NA	NA	hypothetical protein
TS29Bac03595|CDS|CDS	34.4	2.5	62.4	NA	NA	hypothetical protein
Aput1491|CDS|CDS	41.0	3.0	62.0	NA	NA	hypothetical protein
Bbre0206|CDS|CDS	4.7	0.3	61.8	NA	NA	hypothetical protein
BFnctc3993|CDS|50S	6.8	0.5	61.5	NA	NA	hypothetical protein
TS29Rum04456|CDS|CDS	4.5	0.3	61.3	NA	NA	hypothetical protein
BFnctc0198|CDS|putative	13.5	1.0	61.3	NA	NA	hypothetical protein
BFych460241|CDS|RNA	13.5	1.0	61.3	NA	NA	hypothetical protein
TS28Rum13782|CDS|CDS	13.5	1.0	61.3	NA	NA	hypothetical protein
Cbol4929|CDS|CDS	26.3	2.0	59.8	NA	NA	hypothetical protein
Cbol6475|CDS|CDS	26.3	2.0	59.8	NA	NA	hypothetical protein
TS29Rum04358|CDS|CDS	52.5	4.0	59.6	NA	NA	hypothetical protein
BactD13935|CDS|CDS	39.3	3.0	59.5	NA	NA	hypothetical protein
Bxyl2795|CDS|CDS	6.6	0.5	59.5	NA	NA	hypothetical protein
b3593|CDS|rhsA	6.5	0.5	59.0	NA	NA	hypothetical protein
BFych464493|CDS|hypothetical	4.3	0.3	59.0	NA	NA	hypothetical protein
BFych460111|CDS|hypothetical	3.3	0.3	59.0	NA	NA	hypothetical protein
Bsp1161733|CDS|CDS	6.5	0.5	59.0	NA	NA	hypothetical protein
b0507|CDS|glyoxylate	6.5	0.5	59.0	NA	NA	hypothetical protein
BDI2693|CDS|GTP	13.0	1.0	59.0	NA	NA	hypothetical protein
b2660|CDS|predicted	6.5	0.5	59.0	NA	NA	hypothetical protein
TS29Bac01746|CDS|CDS	3.3	0.3	59.0	NA	NA	hypothetical protein
TS28Fae10699|CDS|CDS	6.5	0.5	59.0	NA	NA	hypothetical protein
Bint0735|CDS|CDS	3.3	0.3	59.0	NA	NA	hypothetical protein
TS29Dor1172|CDS|CDS	13.0	1.0	59.0	NA	NA	hypothetical protein
BDI3397|CDS|alkyl	13.0	1.0	59.0	NA	NA	hypothetical protein
HPAG11496|CDS|leucyl-tRNA	13.0	1.0	59.0	NA	NA	hypothetical protein
BDI3461|CDS|putative	13.0	1.0	59.0	NA	NA	hypothetical protein
BFnctc1189|CDS|molecular	90.1	7.0	58.4	NA	NA	hypothetical protein
Bxyl1100|CDS|CDS	21.3	1.7	57.9	NA	NA	hypothetical protein
FpraM2120511|CDS|CDS	6.4	0.5	57.8	NA	NA	hypothetical protein
BFych461659|CDS|hypothetical	6.3	0.5	57.5	NA	NA	hypothetical protein
BFnctc1667|CDS|hypothetical	6.3	0.5	57.5	NA	NA	hypothetical protein

Bxyl0982|CDS|CDS	3.2	0.3	57.2	NA	NA	hypothetical protein
TS29Par701|CDS|CDS	12.5	1.0	56.7	NA	NA	hypothetical protein
BDI2369|CDS|50S	25.0	2.0	56.7	NA	NA	hypothetical protein
TS29Par548|CDS|CDS	12.5	1.0	56.7	NA	NA	hypothetical protein
TS28Rum14109|CDS|CDS	49.5	4.0	56.2	NA	NA	hypothetical protein
b4034|CDS|maltose	18.5	1.5	56.0	NA	NA	hypothetical protein
TS28Rum00324|CDS|CDS	18.5	1.5	56.0	NA	NA	hypothetical protein
TS29Fae01328|CDS|CDS	24.5	2.0	55.6	NA	NA	hypothetical protein
BDI0722|CDS|hypothetical	49.0	4.0	55.6	NA	NA	hypothetical protein
TS28Bac1461|CDS|CDS	40.7	3.3	55.4	NA	NA	hypothetical protein
TS28Bac3848|CDS|CDS	22.2	1.8	55.0	NA	NA	hypothetical protein
TS28Clo08157|CDS|CDS	12.0	1.0	54.5	NA	NA	hypothetical protein
BDI1447|CDS|hypothetical	12.0	1.0	54.5	NA	NA	hypothetical protein
BFnctc3579|CDS|hypothetical	6.0	0.5	54.5	NA	NA	hypothetical protein
TS29Fae09217|CDS|CDS	12.0	1.0	54.5	NA	NA	hypothetical protein
TS28Fae22740|CDS|CDS	6.0	0.5	54.5	NA	NA	hypothetical protein
Aput0055|CDS|CDS	24.0	2.0	54.5	NA	NA	hypothetical protein
BDI0537|CDS|two-component	12.0	1.0	54.5	NA	NA	hypothetical protein
BFych464509|CDS|putative	6.0	0.5	54.5	NA	NA	hypothetical protein
Buni1203|CDS|CDS	6.0	0.5	54.5	NA	NA	hypothetical protein
b4277|CDS|KpLE2	12.0	1.0	54.5	NA	NA	hypothetical protein
Cbol4140|CDS|CDS	12.0	1.0	54.5	NA	NA	hypothetical protein
BDI0386|CDS|integrase	12.0	1.0	54.5	NA	NA	hypothetical protein
TS29Rum13499|CDS|CDS	24.0	2.0	54.5	NA	NA	hypothetical protein
TS29Rum20937|CDS|CDS	12.0	1.0	54.5	NA	NA	hypothetical protein
TS28Fae22761|CDS|CDS	24.0	2.0	54.5	NA	NA	hypothetical protein
BFnctc2551|CDS|putative	6.0	0.5	54.5	NA	NA	hypothetical protein
TS28Rum12480|CDS|CDS	6.0	0.5	54.5	NA	NA	hypothetical protein
BFnctc4303|CDS|putative	6.0	0.5	54.5	NA	NA	hypothetical protein
BFnctc1691|CDS|peptide	6.0	0.5	54.5	NA	NA	hypothetical protein
TS28Ali0765|CDS|CDS	12.0	1.0	54.5	NA	NA	hypothetical protein
Aput1485|CDS|CDS	12.0	1.0	54.5	NA	NA	hypothetical protein
Bsp1163738|CDS|CDS	11.9	1.0	54.1	NA	NA	hypothetical protein
TS28Met0541|CDS|CDS	9.9	0.8	53.8	NA	NA	hypothetical protein
Msmi750779|CDS|CDS	9.9	0.8	53.8	NA	NA	hypothetical protein
BactD13599|CDS|CDS	11.9	1.0	53.8	NA	NA	hypothetical protein
BFych464201|CDS|tyrosine	5.8	0.5	53.0	NA	NA	hypothetical protein
BDI3706|CDS|hypothetical	35.0	3.0	53.0	NA	NA	hypothetical protein
Bxyl1827|CDS|CDS	5.8	0.5	52.8	NA	NA	hypothetical protein
TS28Fae08084|CDS|CDS	23.2	2.0	52.7	NA	NA	hypothetical protein
BFnctc3997|CDS|30S	17.3	1.5	52.5	NA	NA	hypothetical protein
TS28Fae07399|CDS|CDS	11.5	1.0	52.2	NA	NA	hypothetical protein
Aput1695|CDS|CDS	11.5	1.0	52.2	NA	NA	hypothetical protein
BFych463377|CDS|putative	11.5	1.0	52.2	NA	NA	hypothetical protein
BDI2383|CDS|30S	34.5	3.0	52.2	NA	NA	hypothetical protein
BFnctc1661|CDS|putative	11.5	1.0	52.2	NA	NA	hypothetical protein
BactD13115|CDS|CDS	5.7	0.5	52.1	NA	NA	hypothetical protein
Bxyl1368|CDS|CDS	5.7	0.5	52.1	NA	NA	hypothetical protein
TS28Fae22762|CDS|CDS	68.0	6.0	51.5	NA	NA	hypothetical protein
Ldb2187|CDS|hypothetical	11.3	1.0	51.1	NA	NA	hypothetical protein
Bcac0639|CDS|CDS	11.2	1.0	50.8	NA	NA	hypothetical protein
BDI2464|CDS|hypothetical	67.0	6.0	50.7	NA	NA	hypothetical protein
TS28Bac0462|CDS|CDS	7.4	0.7	50.5	NA	NA	hypothetical protein
Buni0964|CDS|CDS	3.7	0.3	49.9	NA	NA	hypothetical protein
Bthe7335684|CDS|CDS	3.7	0.3	49.9	NA	NA	hypothetical protein
TS28Bac5501|CDS|CDS	3.7	0.3	49.9	NA	NA	hypothetical protein
TS28Bac2302|CDS|CDS	3.7	0.3	49.9	NA	NA	hypothetical protein
b3482|CDS|rhsB	5.5	0.5	49.9	NA	NA	hypothetical protein
b3071|CDS|predicted	11.0	1.0	49.9	NA	NA	hypothetical protein
TS28Fae16863|CDS|CDS	11.0	1.0	49.9	NA	NA	hypothetical protein
BDI0097|CDS|glycine	11.0	1.0	49.9	NA	NA	hypothetical protein
Bxyl1605|CDS|CDS	5.5	0.5	49.9	NA	NA	hypothetical protein
Sinf0611|CDS|CDS	11.0	1.0	49.9	NA	NA	hypothetical protein
TS28Bif5274|CDS|CDS	11.0	1.0	49.9	NA	NA	hypothetical protein
TS29Fae02222|CDS|CDS	11.0	1.0	49.9	NA	NA	hypothetical protein
Bbre0642|CDS|CDS	2.2	0.2	49.9	NA	NA	hypothetical protein
Msm0623|CDS|50S	2.2	0.2	49.9	NA	NA	hypothetical protein
TS29Clo2082|CDS|CDS	11.0	1.0	49.9	NA	NA	hypothetical protein
BFych464017|CDS|ribosomal	5.5	0.5	49.9	NA	NA	hypothetical protein
TS28Fae01757|CDS|CDS	5.5	0.5	49.9	NA	NA	hypothetical protein
Aput0614|CDS|CDS	88.0	8.0	49.9	NA	NA	hypothetical protein
TS28Rum03178|CDS|CDS	5.5	0.5	49.9	NA	NA	hypothetical protein
TS29Rum12358|CDS|CDS	11.0	1.0	49.9	NA	NA	hypothetical protein
Caer1715|CDS|CDS	5.5	0.5	49.9	NA	NA	hypothetical protein
TS29Fae06303|CDS|CDS	131.0	12.0	49.6	NA	NA	hypothetical protein
TS29Bac02016|CDS|CDS	43.5	4.0	49.4	NA	NA	hypothetical protein
BFnctc4280|CDS|hypothetical	10.9	1.0	49.3	NA	NA	hypothetical protein
TS29Bac09424|CDS|CDS	54.3	5.0	49.3	NA	NA	hypothetical protein
BDI1698|CDS|hypothetical	76.0	7.0	49.3	NA	NA	hypothetical protein
Msm0542|CDS|methylenetetrahydromethanopterin	10.8	1.0	49.2	NA	NA	hypothetical protein
BT4453|CDS|6-pyruvoyl-tetrahydropterin	10.8	1.0	49.2	NA	NA	hypothetical protein
BT2629|CDS|putative	9.0	0.8	48.9	NA	NA	hypothetical protein
TS28Rum14325|CDS|CDS	21.5	2.0	48.8	NA	NA	hypothetical protein
Bova2295|CDS|CDS	10.7	1.0	48.4	NA	NA	hypothetical protein
TS28Fae18997|CDS|CDS	32.0	3.0	48.4	NA	NA	hypothetical protein
TS28Fae17789|CDS|CDS	63.8	6.0	48.3	NA	NA	hypothetical protein
BDI3380|CDS|hypothetical	42.5	4.0	48.2	NA	NA	hypothetical protein
TS28Fae07504|CDS|CDS	42.5	4.0	48.2	NA	NA	hypothetical protein
Robe1900|CDS|CDS	10.5	1.0	47.7	NA	NA	hypothetical protein
TS29Dor1173|CDS|CDS	21.0	2.0	47.7	NA	NA	hypothetical protein
TS29Rum14639|CDS|CDS	21.0	2.0	47.7	NA	NA	hypothetical protein
BDI0237|CDS|N-acetylglucosamine-6-phosphate	21.0	2.0	47.7	NA	NA	hypothetical protein
Bthe7333178|CDS|CDS	10.5	1.0	47.7	NA	NA	hypothetical protein

FpraM2121475|CDS|CDS	5.3	0.5	47.7	NA	NA	hypothetical protein
BWH23807|CDS|CDS	20.8	2.0	47.3	NA	NA	hypothetical protein
TS28Fae10232|CDS|CDS	3.4	0.3	46.7	NA	NA	hypothetical protein
Msm0884|CDS|adhesin-like	8.6	0.8	46.6	NA	NA	hypothetical protein
TS29Rum11874|CDS|CDS	86.0	8.5	45.9	NA	NA	hypothetical protein
TS28Fae03126|CDS|CDS	10.1	1.0	45.9	NA	NA	hypothetical protein
BactD10370|CDS|CDS	10.0	1.0	45.4	NA	NA	hypothetical protein
b4058|CDS|ATPase	5.0	0.5	45.4	NA	NA	hypothetical protein
BDI3462|CDS|hypothetical	40.0	4.0	45.4	NA	NA	hypothetical protein
BDI0725|CDS|hypothetical	10.0	1.0	45.4	NA	NA	hypothetical protein
TS29Col1522|CDS|CDS	10.0	1.0	45.4	NA	NA	hypothetical protein
b4230|CDS|predicted	10.0	1.0	45.4	NA	NA	hypothetical protein
BFych462178|CDS|F0F1	5.0	0.5	45.4	NA	NA	hypothetical protein
Bfin0259|CDS|CDS	10.0	1.0	45.4	NA	NA	hypothetical protein
Aput0986|CDS|CDS	20.0	2.0	45.4	NA	NA	hypothetical protein
TS28Rum09032|CDS|CDS	10.0	1.0	45.4	NA	NA	hypothetical protein
TS28Fae13469|CDS|CDS	10.0	1.0	45.4	NA	NA	hypothetical protein
BFnctc3199|CDS|hypothetical	10.0	1.0	45.4	NA	NA	hypothetical protein
Rtor0640|CDS|CDS	20.0	2.0	45.4	NA	NA	hypothetical protein
BFych463755|CDS|aconitate	5.0	0.5	45.4	NA	NA	hypothetical protein
b4059|CDS|single-stranded	10.0	1.0	45.4	NA	NA	hypothetical protein

BDI3400|CDS|sugar	20.0	2.0	45.4	NA	NA	hypothetical protein
BDI0692|CDS|50S	10.0	1.0	45.4	NA	NA	hypothetical protein
TS29Dor1445|CDS|CDS	20.0	2.0	45.4	NA	NA	hypothetical protein
RintL13117|CDS|CDS	10.0	1.0	45.4	NA	NA	hypothetical protein
Buni0230|CDS|CDS	5.0	0.5	45.4	NA	NA	hypothetical protein
BDI0935|CDS|putative	10.0	1.0	45.4	NA	NA	hypothetical protein
TS28Fae12041|CDS|CDS	5.0	0.5	45.4	NA	NA	hypothetical protein
M23Apeg1149|CDS|Glycerol-3-phosphate	10.0	1.0	45.4	NA	NA	hypothetical protein
BFnctc1299|CDS|putative	5.0	0.5	45.4	NA	NA	hypothetical protein
BDI0353|CDS|putative	30.0	3.0	45.4	NA	NA	hypothetical protein
Aput1548|CDS|CDS	30.0	3.0	45.4	NA	NA	hypothetical protein
TS29Fae07012|CDS|CDS	84.0	8.5	44.9	NA	NA	hypothetical protein
Robe0624|CDS|CDS	93.3	9.5	44.6	NA	NA	hypothetical protein
TS28Fae22763|CDS|CDS	29.3	3.0	44.4	NA	NA	hypothetical protein
TS28Fae08675|CDS|CDS	34.2	3.5	44.3	NA	NA	hypothetical protein
b4065|CDS|predicted	9.7	1.0	43.9	NA	NA	hypothetical protein
TS29Bac03137|CDS|CDS	29.0	3.0	43.9	NA	NA	hypothetical protein
BDI1874|CDS|ATP-dependent	67.5	7.0	43.8	NA	NA	hypothetical protein
Aput1547|CDS|CDS	77.0	8.0	43.7	NA	NA	hypothetical protein
BactD13776|CDS|CDS	9.5	1.0	43.3	NA	NA	hypothetical protein
Buni2847|CDS|CDS	23.8	2.5	43.3	NA	NA	hypothetical protein
BDI1933|CDS|putative	19.0	2.0	43.1	NA	NA	hypothetical protein
BLD0100|CDS|Cystathionine	4.8	0.5	43.1	NA	NA	hypothetical protein
Aput0034|CDS|CDS	19.0	2.0	43.1	NA	NA	hypothetical protein
TS28Clo00072|CDS|CDS	19.0	2.0	43.1	NA	NA	hypothetical protein
TS29Fae05353|CDS|CDS	323.0	34.0	43.1	NA	NA	hypothetical protein
TS28Eub5220|CDS|CDS	3.2	0.3	43.1	NA	NA	hypothetical protein
BFych464167|CDS|30S	4.7	0.5	42.9	NA	NA	hypothetical protein
Begg0846|CDS|CDS	3.1	0.3	42.8	NA	NA	hypothetical protein
Bxyl1213|CDS|CDS	3.1	0.3	42.8	NA	NA	hypothetical protein
Bthe7332532|CDS|CDS	3.1	0.3	42.8	NA	NA	hypothetical protein
Bthe3733902|CDS|CDS	3.1	0.3	42.8	NA	NA	hypothetical protein
BT2731|CDS|30S	37.4	4.0	42.5	NA	NA	hypothetical protein
TS28Rum10552|CDS|CDS	4.7	0.5	42.4	NA	NA	hypothetical protein
BDI0580|CDS|carbamyl	28.0	3.0	42.4	NA	NA	hypothetical protein
TS29Dor1174|CDS|CDS	56.0	6.0	42.4	NA	NA	hypothetical protein
BDI2272|CDS|elongation	46.5	5.0	42.2	NA	NA	hypothetical protein
TS29Col1331|CDS|CDS	130.0	14.0	42.2	NA	NA	hypothetical protein
Buni0627|CDS|CDS	9.3	1.0	42.0	NA	NA	hypothetical protein
BDI0385|CDS|hypothetical	37.0	4.0	42.0	NA	NA	hypothetical protein
BDI1697|CDS|hypothetical	37.0	4.0	42.0	NA	NA	hypothetical protein
TS28Clo06858|CDS|CDS	18.5	2.0	42.0	NA	NA	hypothetical protein
FpraM2121530|CDS|CDS	36.5	4.0	41.4	NA	NA	hypothetical protein
TS28Bac6131|CDS|CDS	6.1	0.7	41.3	NA	NA	hypothetical protein
Buni0317|CDS|CDS	6.1	0.7	41.3	NA	NA	hypothetical protein
Bxyl1122|CDS|CDS	9.0	1.0	41.0	NA	NA	hypothetical protein
Bxyl0225|CDS|CDS	3.0	0.3	40.9	NA	NA	hypothetical protein
Bxyl3699|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
Cste0815|CDS|CDS	1.8	0.2	40.9	NA	NA	hypothetical protein
BDI3797|CDS|hypothetical	9.0	1.0	40.9	NA	NA	hypothetical protein
TS28Rum11077|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
TS28Fae11890|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
TS29Fae06995|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
b1919|CDS|D-cysteine	4.5	0.5	40.9	NA	NA	hypothetical protein
BDI2266|CDS|50S	18.0	2.0	40.9	NA	NA	hypothetical protein
TS28Clo09605|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
TS29Rum15434|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
TS28Rum13633|CDS|CDS	4.5	0.5	40.9	NA	NA	hypothetical protein
BFych461876|CDS|cytochrome	4.5	0.5	40.9	NA	NA	hypothetical protein
BFych464091|CDS|hypothetical	4.5	0.5	40.9	NA	NA	hypothetical protein
Aput1934|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
TS29Rum15065|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
BDI0664|CDS|RNA	9.0	1.0	40.9	NA	NA	hypothetical protein
BFych464127|CDS|hypothetical	4.5	0.5	40.9	NA	NA	hypothetical protein
Cbol1695|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
BFych463740|CDS|hypothetical	4.5	0.5	40.9	NA	NA	hypothetical protein
TS29Rum15984|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
TS29RumUnc1195|CDS|CDS	9.0	1.0	40.9	NA	NA	hypothetical protein
BDI2376|CDS|30S	9.0	1.0	40.9	NA	NA	hypothetical protein
BFnctc3528|CDS|hypothetical	4.5	0.5	40.9	NA	NA	hypothetical protein
TS29RumUnc1713|CDS|CDS	80.0	9.0	40.4	NA	NA	hypothetical protein
BactD12101|CDS|CDS	2.9	0.3	39.7	NA	NA	hypothetical protein
BFnctc1566|CDS|putative	4.4	0.5	39.6	NA	NA	hypothetical protein
Buni0933|CDS|CDS	104.5	12.0	39.5	NA	NA	hypothetical protein
TS28Bac7847|CDS|CDS	8.7	1.0	39.3	NA	NA	hypothetical protein
TS29Rum13815|CDS|CDS	26.0	3.0	39.3	NA	NA	hypothetical protein
TS29Fae08295|CDS|CDS	13.0	1.5	39.3	NA	NA	hypothetical protein
Robe0465|CDS|CDS	4.3	0.5	39.3	NA	NA	hypothetical protein
TS28Rum15068|CDS|CDS	4.3	0.5	39.3	NA	NA	hypothetical protein
BactD12816|CDS|CDS	4.3	0.5	39.3	NA	NA	hypothetical protein
TS28Clo01897|CDS|CDS	17.2	2.0	39.0	NA	NA	hypothetical protein
TS29Bac10303|CDS|CDS	17.0	2.0	38.6	NA	NA	hypothetical protein
b4095|CDS|carbon-phosphorus	8.5	1.0	38.6	NA	NA	hypothetical protein
TS29Rum03344|CDS|CDS	17.0	2.0	38.6	NA	NA	hypothetical protein
BDI3339|CDS|putative	8.5	1.0	38.6	NA	NA	hypothetical protein
Bova1180|CDS|CDS	8.5	1.0	38.6	NA	NA	hypothetical protein
BDI0828|CDS|V-type	21.0	2.5	38.1	NA	NA	hypothetical protein
TS29Fae01039|CDS|CDS	88.0	10.5	38.0	NA	NA	hypothetical protein
BFych460776|CDS|hypothetical	8.3	1.0	37.8	NA	NA	hypothetical protein
BDI2384|CDS|30S	8.3	1.0	37.8	NA	NA	hypothetical protein
TS28Bac7643|CDS|CDS	2.7	0.3	37.2	NA	NA	hypothetical protein
TS29Bac08805|CDS|CDS	41.0	5.0	37.2	NA	NA	hypothetical protein
TS28Fae17686|CDS|CDS	49.0	6.0	37.1	NA	NA	hypothetical protein
TS29Rum02227|CDS|CDS	56.0	7.0	36.3	NA	NA	hypothetical protein
BFnctc2970|CDS|hypothetical	4.0	0.5	36.3	NA	NA	hypothetical protein

BFych463239|CDS|aminoacyl-histidine	4.0	0.5	36.3	NA	NA	hypothetical protein
BDI0581|CDS|hypothetical	8.0	1.0	36.3	NA	NA	hypothetical protein
b2664|CDS|DNA-binding	4.0	0.5	36.3	NA	NA	hypothetical protein
FpraM2121796|CDS|CDS	4.0	0.5	36.3	NA	NA	hypothetical protein
Aput1931|CDS|CDS	16.0	2.0	36.3	NA	NA	hypothetical protein
BDI3562|CDS|putative	8.0	1.0	36.3	NA	NA	hypothetical protein
b4117|CDS|biodegradative	4.0	0.5	36.3	NA	NA	hypothetical protein
BDI0272|CDS|putative	8.0	1.0	36.3	NA	NA	hypothetical protein
BFnctc0328|CDS|putative	4.0	0.5	36.3	NA	NA	hypothetical protein
TS28Ali0722|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
TS28Clo05687|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
TS29Fae07332|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
b0414|CDS|fused	4.0	0.5	36.3	NA	NA	hypothetical protein
BFych460302|CDS|cell	4.0	0.5	36.3	NA	NA	hypothetical protein
BLD0252|CDS|ABC-type	4.0	0.5	36.3	NA	NA	hypothetical protein
TS29Fae10268|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
BDI2277|CDS|sigma-54	8.0	1.0	36.3	NA	NA	hypothetical protein
TS29Bac07622|CDS|CDS	40.0	5.0	36.3	NA	NA	hypothetical protein
BFych460510|CDS|orotate	8.0	1.0	36.3	NA	NA	hypothetical protein
TS29Fae00210|CDS|CDS	4.0	0.5	36.3	NA	NA	hypothetical protein
FpraM2121543|CDS|CDS	4.0	0.5	36.3	NA	NA	hypothetical protein
TS29Rum07999|CDS|CDS	16.0	2.0	36.3	NA	NA	hypothetical protein
Aput1411|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
TS29Met0800|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
TS29Fae00892|CDS|CDS	4.0	0.5	36.3	NA	NA	hypothetical protein
TS28Rum15992|CDS|CDS	4.0	0.5	36.3	NA	NA	hypothetical protein
TS29Bac01992|CDS|CDS	92.0	11.5	36.3	NA	NA	hypothetical protein
Bova3955|CDS|CDS	2.0	0.3	36.3	NA	NA	hypothetical protein
BLD0065|CDS|hypothetical	2.0	0.3	36.3	NA	NA	hypothetical protein
BactD12836|CDS|CDS	2.0	0.3	36.3	NA	NA	hypothetical protein
TS28Bac3972|CDS|CDS	8.0	1.0	36.3	NA	NA	hypothetical protein
BactD10210|CDS|CDS	2.7	0.3	36.3	NA	NA	hypothetical protein
Bxyl4254|CDS|CDS	2.7	0.3	36.3	NA	NA	hypothetical protein
TS29Bac02045|CDS|CDS	408.7	51.5	36.0	NA	NA	hypothetical protein
TS28Fae12708|CDS|CDS	78.5	10.0	35.6	NA	NA	hypothetical protein
TS29Bac09094|CDS|CDS	35.0	4.5	35.3	NA	NA	hypothetical protein
BactD13772|CDS|CDS	2.6	0.3	35.2	NA	NA	hypothetical protein
TS28Fae14068|CDS|CDS	15.5	2.0	35.2	NA	NA	hypothetical protein
EUBREC1017|CDS|3-hydroxybutyryl-coA	15.5	2.0	35.2	NA	NA	hypothetical protein
Aput1440|CDS|CDS	15.5	2.0	35.2	NA	NA	hypothetical protein
BactD22267|CDS|CDS	3.9	0.5	35.2	NA	NA	hypothetical protein
Bxyl1397|CDS|CDS	3.9	0.5	35.1	NA	NA	hypothetical protein
BFnctc4018|CDS|50S	11.6	1.5	35.0	NA	NA	hypothetical protein
b3931|CDS|molecular	3.8	0.5	34.8	NA	NA	hypothetical protein
Msm0783|CDS|tungsten	3.8	0.5	34.8	NA	NA	hypothetical protein
Buni0291|CDS|CDS	20.3	2.7	34.6	NA	NA	hypothetical protein
TS28Bac1538|CDS|CDS	20.3	2.7	34.6	NA	NA	hypothetical protein
TS29Rum04366|CDS|CDS	49.5	6.5	34.6	NA	NA	hypothetical protein
Bcac0198|CDS|CDS	7.6	1.0	34.5	NA	NA	hypothetical protein
TS29Bac12093|CDS|CDS	3.8	0.5	34.4	NA	NA	hypothetical protein
TS29Fae04643|CDS|CDS	22.7	3.0	34.3	NA	NA	hypothetical protein
BFych464170|CDS|50S	7.6	1.0	34.3	NA	NA	hypothetical protein
BFnctc3992|CDS|50S	7.6	1.0	34.3	NA	NA	hypothetical protein
CspL21862|CDS|CDS	67.8	9.0	34.2	NA	NA	hypothetical protein
Bova3649|CDS|CDS	6.9	0.9	34.2	NA	NA	hypothetical protein
BFnctc2233|CDS|F0F1	7.5	1.0	34.0	NA	NA	hypothetical protein
BFych464369|CDS|hypothetical	7.5	1.0	34.0	NA	NA	hypothetical protein
TS29Fae04365|CDS|CDS	15.0	2.0	34.0	NA	NA	hypothetical protein
BFych462177|CDS|F0F1	7.5	1.0	34.0	NA	NA	hypothetical protein
BDI3376|CDS|ribosome	15.0	2.0	34.0	NA	NA	hypothetical protein
Bxyl2686|CDS|CDS	7.5	1.0	34.0	NA	NA	hypothetical protein
BFych461706|CDS|N-acetylneuraminate	3.8	0.5	34.0	NA	NA	hypothetical protein
BDI0711|CDS|malate	15.0	2.0	34.0	NA	NA	hypothetical protein
BDI2306|CDS|hypothetical	15.0	2.0	34.0	NA	NA	hypothetical protein
b1015|CDS|proline:sodium	7.5	1.0	34.0	NA	NA	hypothetical protein
TS28Fae18896|CDS|CDS	15.0	2.0	34.0	NA	NA	hypothetical protein
BDI2283|CDS|putative	30.0	4.0	34.0	NA	NA	hypothetical protein
Ccom0260|CDS|CDS	7.5	1.0	34.0	NA	NA	hypothetical protein
TS29Par523|CDS|CDS	15.0	2.0	34.0	NA	NA	hypothetical protein
BFych464174|CDS|50S	11.1	1.5	33.7	NA	NA	hypothetical protein
BFnctc3996|CDS|50S	11.1	1.5	33.7	NA	NA	hypothetical protein
TS28Clo10254|CDS|CDS	111.3	15.0	33.7	NA	NA	hypothetical protein
BFnctc3045|CDS|hypothetical	3.7	0.5	33.5	NA	NA	hypothetical protein
TS28Fae21943|CDS|CDS	7.4	1.0	33.4	NA	NA	hypothetical protein
BFych464013|CDS|50S	3.7	0.5	33.3	NA	NA	hypothetical protein
BLD0185|CDS|hypothetical	3.7	0.5	33.3	NA	NA	hypothetical protein
TS29Bac02508|CDS|CDS	33.0	4.5	33.3	NA	NA	hypothetical protein
Bxyl4368|CDS|CDS	3.7	0.5	33.3	NA	NA	hypothetical protein
TS29Rum09928|CDS|CDS	11.0	1.5	33.3	NA	NA	hypothetical protein
BDI2382|CDS|elongation	51.3	7.0	33.2	NA	NA	hypothetical protein
FpraM2122295|CDS|CDS	18.3	2.5	33.1	NA	NA	hypothetical protein
BDI2483|CDS|cell	14.5	2.0	32.9	NA	NA	hypothetical protein
Buni0308|CDS|CDS	6.0	0.8	32.7	NA	NA	hypothetical protein
Bxyl2079|CDS|CDS	1.8	0.3	32.7	NA	NA	hypothetical protein
BDI0770|CDS|PhoH-like	18.0	2.5	32.7	NA	NA	hypothetical protein
Msm0622|CDS|50S	6.2	0.9	32.7	NA	NA	hypothetical protein
BL0198|CDS|hypothetical	3.6	0.5	32.5	NA	NA	hypothetical protein
TS29Bac05128|CDS|CDS	59.7	8.3	32.5	NA	NA	hypothetical protein
BDI2723|CDS|hypothetical	50.0	7.0	32.4	NA	NA	hypothetical protein
Msm1404|CDS|formate	10.6	1.5	32.1	NA	NA	hypothetical protein
Bthe7335529|CDS|CDS	2.3	0.3	31.8	NA	NA	hypothetical protein
BDI1236|CDS|epimerase/reductase,	14.0	2.0	31.8	NA	NA	hypothetical protein
BFnctc1360|CDS|hypothetical	3.5	0.5	31.8	NA	NA	hypothetical protein
BFnctc3893|CDS|ATP-dependent	3.5	0.5	31.8	NA	NA	hypothetical protein

TS29Clo0994|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
Cbol4552|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
Aput0544|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
b3338|CDS|periplasmic	7.0	1.0	31.8	NA	NA	hypothetical protein
Buni1939|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
BFnctc3963|CDS|putative	3.5	0.5	31.8	NA	NA	hypothetical protein
BFych464141|CDS|cation	3.5	0.5	31.8	NA	NA	hypothetical protein
Dfor2465|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
TS28Rum02210|CDS|CDS	3.5	0.5	31.8	NA	NA	hypothetical protein
TS29Fae05927|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
TS28Fae05841|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
EUBREC0423|CDS|50S	3.5	0.5	31.8	NA	NA	hypothetical protein
BFnctc4153|CDS|putative	3.5	0.5	31.8	NA	NA	hypothetical protein
Cbol4555|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
BDI0416|CDS|hypothetical	14.0	2.0	31.8	NA	NA	hypothetical protein
BFnctc3397|CDS|hypothetical	3.5	0.5	31.8	NA	NA	hypothetical protein
TS29Clo3497|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
BDI0168|CDS|putative	7.0	1.0	31.8	NA	NA	hypothetical protein
BFych461469|CDS|nicotinate-nucleotide	3.5	0.5	31.8	NA	NA	hypothetical protein
Buni1595|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
TS29Clo1361|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
BDI0647|CDS|putative	7.0	1.0	31.8	NA	NA	hypothetical protein
TS29Par887|CDS|CDS	10.5	1.5	31.8	NA	NA	hypothetical protein
TS29Rum12352|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
BFnctc1400|CDS|putative	3.5	0.5	31.8	NA	NA	hypothetical protein
BDI1527|CDS|putative	7.0	1.0	31.8	NA	NA	hypothetical protein
TS28Fae13138|CDS|CDS	3.5	0.5	31.8	NA	NA	hypothetical protein
BactD23944|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
TS28Fae18458|CDS|CDS	3.5	0.5	31.8	NA	NA	hypothetical protein
EUBREC0534|CDS|hypoxanthine	7.0	1.0	31.8	NA	NA	hypothetical protein
BFnctc2334|CDS|hypothetical	3.5	0.5	31.8	NA	NA	hypothetical protein
BL1681|CDS|hypoxanthine-guanine	3.5	0.5	31.8	NA	NA	hypothetical protein
BDI2278|CDS|tyrosine	28.0	4.0	31.8	NA	NA	hypothetical protein
BFych463763|CDS|dihydroxy-acid	3.5	0.5	31.8	NA	NA	hypothetical protein
b3789|CDS|glucose-1-phosphate	3.5	0.5	31.8	NA	NA	hypothetical protein
BFych462564|CDS|hypothetical	3.5	0.5	31.8	NA	NA	hypothetical protein
TS29Bac11505|CDS|CDS	3.5	0.5	31.8	NA	NA	hypothetical protein
Aput1838|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
TS29Rum20164|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
b2413|CDS|predicted	3.5	0.5	31.8	NA	NA	hypothetical protein
Buni0613|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
Msm0758|CDS|30S	3.5	0.5	31.8	NA	NA	hypothetical protein
TS28Fae22220|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
Bova0529|CDS|CDS	3.5	0.5	31.8	NA	NA	hypothetical protein
BDI1476|CDS|conserved	70.0	10.0	31.8	NA	NA	hypothetical protein
BDI0723|CDS|hypothetical	35.0	5.0	31.8	NA	NA	hypothetical protein
Robe1223|CDS|CDS	2.3	0.3	31.8	NA	NA	hypothetical protein
TS28Rum10495|CDS|CDS	2.3	0.3	31.8	NA	NA	hypothetical protein
TS28Bac6134|CDS|CDS	2.3	0.3	31.8	NA	NA	hypothetical protein
Clep0902|CDS|CDS	2.3	0.3	31.8	NA	NA	hypothetical protein
Bxyl4375|CDS|CDS	7.0	1.0	31.8	NA	NA	hypothetical protein
TS29Bac09452|CDS|CDS	4.6	0.7	31.5	NA	NA	hypothetical protein
BactD14458|CDS|CDS	4.6	0.7	31.5	NA	NA	hypothetical protein
Bxyl1677|CDS|CDS	4.6	0.7	31.5	NA	NA	hypothetical protein
Caer1507|CDS|CDS	20.7	3.0	31.3	NA	NA	hypothetical protein
TS28Clo10637|CDS|CDS	102.0	15.0	30.9	NA	NA	hypothetical protein
TS29Bac05748|CDS|CDS	68.0	10.0	30.9	NA	NA	hypothetical protein
BDI0210|CDS|glycoside	34.0	5.0	30.9	NA	NA	hypothetical protein
Bxyl1820|CDS|CDS	2.3	0.3	30.6	NA	NA	hypothetical protein
TS28Fae01719|CDS|CDS	13.5	2.0	30.6	NA	NA	hypothetical protein
Bxyl0419|CDS|CDS	2.2	0.3	30.4	NA	NA	hypothetical protein
BFych462788|CDS|tyrosine	2.2	0.3	30.4	NA	NA	hypothetical protein
TS28Bac3047|CDS|CDS	1.7	0.3	30.3	NA	NA	hypothetical protein
Buni0275|CDS|CDS	6.7	1.0	30.3	NA	NA	hypothetical protein
FpraM2120746|CDS|CDS	3.3	0.5	30.3	NA	NA	hypothetical protein
TS28Rum09604|CDS|CDS	10.0	1.5	30.3	NA	NA	hypothetical protein
Aput2363|CDS|CDS	20.0	3.0	30.3	NA	NA	hypothetical protein
TS29Clo0433|CDS|CDS	10.0	1.5	30.3	NA	NA	hypothetical protein
TS28Col0352|CDS|CDS	13.3	2.0	30.3	NA	NA	hypothetical protein
BFnctc2496|CDS|putative	3.3	0.5	30.3	NA	NA	hypothetical protein
BFych461853|CDS|6-phosphogluconate	3.3	0.5	30.3	NA	NA	hypothetical protein
BFych462414|CDS|hypothetical	3.3	0.5	30.3	NA	NA	hypothetical protein
EFER0050|CDS|putative	3.3	0.5	30.3	NA	NA	hypothetical protein
BFnctc0920|CDS|putative	3.3	0.5	30.3	NA	NA	hypothetical protein
BFych460999|CDS|putative	3.3	0.5	30.3	NA	NA	hypothetical protein
BLD0478|CDS|ATP	2.2	0.3	30.0	NA	NA	hypothetical protein
b1474|CDS|formate	3.3	0.5	30.0	NA	NA	hypothetical protein
BDI2313|CDS|hypothetical	33.0	5.0	30.0	NA	NA	hypothetical protein
BDI0661|CDS|translation	13.2	2.0	29.9	NA	NA	hypothetical protein
TS29Fae00068|CDS|CDS	6.6	1.0	29.9	NA	NA	hypothetical protein
BFych461000|CDS|putative	6.5	1.0	29.5	NA	NA	hypothetical protein
TS28Col1416|CDS|CDS	6.5	1.0	29.5	NA	NA	hypothetical protein
Aput0248|CDS|CDS	6.5	1.0	29.5	NA	NA	hypothetical protein
TS29Clo3365|CDS|CDS	6.5	1.0	29.5	NA	NA	hypothetical protein
TS28Fae21699|CDS|CDS	6.5	1.0	29.5	NA	NA	hypothetical protein
BDI0463|CDS|electron	13.0	2.0	29.5	NA	NA	hypothetical protein
Aput0802|CDS|CDS	13.0	2.0	29.5	NA	NA	hypothetical protein
Buni1376|CDS|CDS	6.5	1.0	29.5	NA	NA	hypothetical protein
BFnctc3677|CDS|hypothetical	6.5	1.0	29.5	NA	NA	hypothetical protein
Buni1549|CDS|CDS	6.5	1.0	29.5	NA	NA	hypothetical protein
b4263|CDS|predicted	13.0	2.0	29.5	NA	NA	hypothetical protein
BDI0164|CDS|lactoylglutathione	13.0	2.0	29.5	NA	NA	hypothetical protein
BL1343|CDS|glucosamine-6-phosphate	4.3	0.7	29.5	NA	NA	hypothetical protein
Buni0932|CDS|CDS	44.2	6.8	29.3	NA	NA	hypothetical protein
Bova0532|CDS|CDS	64.6	10.0	29.3	NA	NA	hypothetical protein

BFnctc0108|CDS|putative	9.7	1.5	29.3	NA	NA	hypothetical protein
TS29Fae08624|CDS|CDS	96.5	15.0	29.2	NA	NA	hypothetical protein
BFnctc4022|CDS|elongation	48.0	7.5	29.1	NA	NA	hypothetical protein
Aput0496|CDS|CDS	16.0	2.5	29.1	NA	NA	hypothetical protein
Msm1016|CDS|methyl-coenzyme	14.8	2.3	28.9	NA	NA	hypothetical protein
TS28Rum13807|CDS|CDS	9.5	1.5	28.9	NA	NA	hypothetical protein
BactD23874|CDS|CDS	3.2	0.5	28.8	NA	NA	hypothetical protein
BFnctc3195|CDS|hypothetical	3.2	0.5	28.8	NA	NA	hypothetical protein
BFych463320|CDS|excinuclease	3.2	0.5	28.8	NA	NA	hypothetical protein
Bova4219|CDS|CDS	3.2	0.5	28.8	NA	NA	hypothetical protein
BFych461478|CDS|phosphoglucomutase	9.5	1.5	28.8	NA	NA	hypothetical protein
BDI2379|CDS|50S	19.0	3.0	28.8	NA	NA	hypothetical protein
BDI3819|CDS|hypothetical	19.0	3.0	28.8	NA	NA	hypothetical protein
b3212|CDS|glutamate	6.3	1.0	28.8	NA	NA	hypothetical protein
TS28Rum13612|CDS|CDS	22.0	3.5	28.5	NA	NA	hypothetical protein
BT3833|CDS|50S	12.6	2.0	28.5	NA	NA	hypothetical protein
TS29Bac04216|CDS|CDS	31.0	5.0	28.1	NA	NA	hypothetical protein
Bxyl0239|CDS|CDS	5.2	0.8	28.1	NA	NA	hypothetical protein
TS28Rum01135|CDS|CDS	6.2	1.0	28.0	NA	NA	hypothetical protein
Aput0975|CDS|CDS	37.0	6.0	28.0	NA	NA	hypothetical protein
BFnctc2235|CDS|F0F1	3.1	0.5	27.9	NA	NA	hypothetical protein
Buni1280|CDS|CDS	46.0	7.5	27.8	NA	NA	hypothetical protein
BactD14372|CDS|CDS	1.5	0.3	27.8	NA	NA	hypothetical protein
BFych463801|CDS|methylmalonyl-CoA	8.2	1.3	27.8	NA	NA	hypothetical protein
TS29Bac02507|CDS|CDS	82.5	13.5	27.7	NA	NA	hypothetical protein
BFnctc2227|CDS|F0F1	9.1	1.5	27.6	NA	NA	hypothetical protein
Buni3320|CDS|CDS	2.0	0.3	27.2	NA	NA	hypothetical protein
Bxyl4317|CDS|CDS	2.0	0.3	27.2	NA	NA	hypothetical protein
TS28Bac0967|CDS|CDS	2.0	0.3	27.2	NA	NA	hypothetical protein
BLD0020|CDS|ABC-type	2.0	0.3	27.2	NA	NA	hypothetical protein
BFych464019|CDS|beta-galactosidase	2.0	0.3	27.2	NA	NA	hypothetical protein
Msm0001|CDS|exoribonuclease	2.0	0.3	27.2	NA	NA	hypothetical protein
FpraM2121454|CDS|CDS	12.0	2.0	27.2	NA	NA	hypothetical protein
Bfra31123232|CDS|CDS	12.0	2.0	27.2	NA	NA	hypothetical protein
BFych463426|CDS|AraC	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI2020|CDS|putative	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Bac07229|CDS|CDS	24.0	4.0	27.2	NA	NA	hypothetical protein
b3704|CDS|protein	6.0	1.0	27.2	NA	NA	hypothetical protein
BFych461409|CDS|hypothetical	3.0	0.5	27.2	NA	NA	hypothetical protein
FpraM2122635|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
Bova1673|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Ali203|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI2941|CDS|probable	30.0	5.0	27.2	NA	NA	hypothetical protein
BDI2685|CDS|hypothetical	24.0	4.0	27.2	NA	NA	hypothetical protein
TS28Fae22445|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
Bxyl3876|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
BDI3968|CDS|30S	6.0	1.0	27.2	NA	NA	hypothetical protein
BFnctc3248|CDS|AraC	6.0	1.0	27.2	NA	NA	hypothetical protein
b2976|CDS|malate	3.0	0.5	27.2	NA	NA	hypothetical protein
TS28Rum14250|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
TS29Bac03632|CDS|CDS	12.0	2.0	27.2	NA	NA	hypothetical protein
TS28Bac4598|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI2358|CDS|translation	6.0	1.0	27.2	NA	NA	hypothetical protein
BFych460464|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI1210|CDS|RNA	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI2027|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
Aput1133|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
Msm1431|CDS|30S	1.5	0.3	27.2	NA	NA	hypothetical protein
TS29Rum18437|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
str1734|CDS|sucrose-specific	3.0	0.5	27.2	NA	NA	hypothetical protein
BFych462861|CDS|hypothetical	3.0	0.5	27.2	NA	NA	hypothetical protein
BFnctc1345|CDS|hypothetical	3.0	0.5	27.2	NA	NA	hypothetical protein
BFych462241|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
FpraM2122253|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
Robe2888|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
b2507|CDS|GMP	3.0	0.5	27.2	NA	NA	hypothetical protein
Cbol3714|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
Robe3355|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI0265|CDS|ATP	6.0	1.0	27.2	NA	NA	hypothetical protein
BFych463739|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI1749|CDS|ROK	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI0206|CDS|deoxycytidylate	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Clo3168|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
TS28Rum12399|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
BDI1816|CDS|glycerol	6.0	1.0	27.2	NA	NA	hypothetical protein
TS28Clo05858|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Fae02471|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI2638|CDS|putative	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Fae06405|CDS|CDS	24.0	4.0	27.2	NA	NA	hypothetical protein
TS29Clo0894|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
Acac2673|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI3818|CDS|hypothetical	12.0	2.0	27.2	NA	NA	hypothetical protein
TS29Rum20884|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
Aput0350|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI3802|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
Buni2609|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI0459|CDS|putative	6.0	1.0	27.2	NA	NA	hypothetical protein
BDI2308|CDS|type	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Rum16564|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
b3266|CDS|multidrug	3.0	0.5	27.2	NA	NA	hypothetical protein
TS29Clo1425|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BFnctc3231|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Met0801|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
b3741|CDS|glucose-inhibited	3.0	0.5	27.2	NA	NA	hypothetical protein
TS29Rum06302|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein

BDI3595|CDS|two-component	6.0	1.0	27.2	NA	NA	hypothetical protein
Cint333|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BFnctc3542|CDS|putative	6.0	1.0	27.2	NA	NA	hypothetical protein
TS29Fae09748|CDS|CDS	3.0	0.5	27.2	NA	NA	hypothetical protein
BDI2753|CDS|peptide	6.0	1.0	27.2	NA	NA	hypothetical protein
Aput1493|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
BFnctc3527|CDS|hypothetical	6.0	1.0	27.2	NA	NA	hypothetical protein
BactD21559|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
TS28Clo07103|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
TS28Clo06234|CDS|CDS	6.0	1.0	27.2	NA	NA	hypothetical protein
b3818|CDS|predicted	6.0	1.0	27.2	NA	NA	hypothetical protein
TS28Rum13653|CDS|CDS	9.0	1.5	27.2	NA	NA	hypothetical protein
BFnctc1409|CDS|putative	9.0	1.5	27.2	NA	NA	hypothetical protein
TS29Fae04314|CDS|CDS	36.0	6.0	27.2	NA	NA	hypothetical protein
TS29Fae00037|CDS|CDS	18.0	3.0	27.2	NA	NA	hypothetical protein
TS28Bac5793|CDS|CDS	18.0	3.0	27.2	NA	NA	hypothetical protein
TS29Clo1421|CDS|CDS	9.0	1.5	27.2	NA	NA	hypothetical protein
BDI2365|CDS|50S	18.0	3.0	27.2	NA	NA	hypothetical protein
BDI1203|CDS|superoxide	18.0	3.0	27.2	NA	NA	hypothetical protein
TS29Bac08221|CDS|CDS	18.0	3.0	27.2	NA	NA	hypothetical protein
Bxyl4361|CDS|CDS	9.0	1.5	27.1	NA	NA	hypothetical protein
TS29Met0524|CDS|CDS	70.8	12.0	26.8	NA	NA	hypothetical protein
BFych464177|CDS|30S	11.8	2.0	26.7	NA	NA	hypothetical protein
BFnctc3999|CDS|30S	11.8	2.0	26.7	NA	NA	hypothetical protein
TS28Rum13671|CDS|CDS	23.5	4.0	26.7	NA	NA	hypothetical protein
TS29Rum13371|CDS|CDS	23.5	4.0	26.7	NA	NA	hypothetical protein
BDI3496|CDS|putative	47.0	8.0	26.7	NA	NA	hypothetical protein
Msm0051|CDS|adhesin-like	58.7	10.0	26.6	NA	NA	hypothetical protein
BactD10931|CDS|CDS	1.5	0.3	26.6	NA	NA	hypothetical protein
Bcac2197|CDS|CDS	1.5	0.3	26.6	NA	NA	hypothetical protein
Bova3213|CDS|CDS	5.8	1.0	26.5	NA	NA	hypothetical protein
Aput1549|CDS|CDS	35.0	6.0	26.5	NA	NA	hypothetical protein
BFych464176|CDS|50S	8.7	1.5	26.2	NA	NA	hypothetical protein
TS29Bac12273|CDS|CDS	46.0	8.0	26.1	NA	NA	hypothetical protein
TS29Rum08912|CDS|CDS	7.7	1.3	26.1	NA	NA	hypothetical protein
Buni1024|CDS|CDS	28.6	5.0	26.0	NA	NA	hypothetical protein
TS29RumUnc0851|CDS|CDS	74.4	13.0	26.0	NA	NA	hypothetical protein
TS29Bac11676|CDS|CDS	11.4	2.0	25.9	NA	NA	hypothetical protein
Bxyl4373|CDS|CDS	5.7	1.0	25.7	NA	NA	hypothetical protein
b3792|CDS|O-antigen	5.7	1.0	25.7	NA	NA	hypothetical protein
TS29Bac06581|CDS|CDS	5.7	1.0	25.7	NA	NA	hypothetical protein
TS28Fae10209|CDS|CDS	5.7	1.0	25.7	NA	NA	hypothetical protein
BDI0209|CDS|glycosyltransferase	17.0	3.0	25.7	NA	NA	hypothetical protein
TS28Clo07027|CDS|CDS	17.0	3.0	25.7	NA	NA	hypothetical protein
BDI3222|CDS|hypothetical	34.0	6.0	25.7	NA	NA	hypothetical protein
TS29Dor1206|CDS|CDS	17.0	3.0	25.7	NA	NA	hypothetical protein
BDI0145|CDS|sugar	17.0	3.0	25.7	NA	NA	hypothetical protein
TS29RumUnc0461|CDS|CDS	22.5	4.0	25.5	NA	NA	hypothetical protein
TS28Bac1477|CDS|CDS	19.7	3.5	25.5	NA	NA	hypothetical protein
Buni3535|CDS|CDS	19.7	3.5	25.5	NA	NA	hypothetical protein
Bova2383|CDS|CDS	5.6	1.0	25.5	NA	NA	hypothetical protein
Msm1414|CDS|tungsten	1.4	0.3	25.4	NA	NA	hypothetical protein
TS29Bac09992|CDS|CDS	28.0	5.0	25.4	NA	NA	hypothetical protein
TS29Rum01496|CDS|CDS	28.0	5.0	25.4	NA	NA	hypothetical protein
BDI2647|CDS|putative	50.0	9.0	25.2	NA	NA	hypothetical protein
FpraM2120034|CDS|CDS	13.8	2.5	25.1	NA	NA	hypothetical protein
TS28Rum14402|CDS|CDS	19.3	3.5	25.1	NA	NA	hypothetical protein
TS29Bac04437|CDS|CDS	19.3	3.5	25.1	NA	NA	hypothetical protein
BFnctc4020|CDS|putative	11.0	2.0	25.0	NA	NA	hypothetical protein
BFych464197|CDS|transcription	11.0	2.0	25.0	NA	NA	hypothetical protein
ShigspD91533|CDS|CDS	5.5	1.0	25.0	NA	NA	hypothetical protein
TS28Clo05832|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
Robe1927|CDS|CDS	5.5	1.0	25.0	NA	NA	hypothetical protein
TS28Clo02843|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
BFych461858|CDS|hypothetical	11.0	2.0	25.0	NA	NA	hypothetical protein
BDI2104|CDS|UDP-3-O-[3-hydroxymyristoyl]	11.0	2.0	25.0	NA	NA	hypothetical protein
Buni0610|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
EFER4119|CDS|putative	5.5	1.0	25.0	NA	NA	hypothetical protein
TS29Rum18423|CDS|CDS	22.0	4.0	25.0	NA	NA	hypothetical protein
TS28Fae17013|CDS|CDS	5.5	1.0	25.0	NA	NA	hypothetical protein
b0977|CDS|protein	5.5	1.0	25.0	NA	NA	hypothetical protein
TS29Rum04739|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
Aput0526|CDS|CDS	22.0	4.0	25.0	NA	NA	hypothetical protein
TS28Col1485|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
TS28Fae18730|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
TS28Eub2055|CDS|CDS	5.5	1.0	25.0	NA	NA	hypothetical protein
b4325|CDS|predicted	5.5	1.0	25.0	NA	NA	hypothetical protein
BDI1339|CDS|glycoside	11.0	2.0	25.0	NA	NA	hypothetical protein
BDI3487|CDS|50S	11.0	2.0	25.0	NA	NA	hypothetical protein
TS28Fae14843|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
Aput1177|CDS|CDS	11.0	2.0	25.0	NA	NA	hypothetical protein
TS28Fae00238|CDS|CDS	5.5	1.0	25.0	NA	NA	hypothetical protein
BDI2634|CDS|hypothetical	11.0	2.0	25.0	NA	NA	hypothetical protein
BDI2051|CDS|hypothetical	11.0	2.0	25.0	NA	NA	hypothetical protein
TS29Par799|CDS|CDS	5.5	1.0	25.0	NA	NA	hypothetical protein
BFnctc3811|CDS|putative	5.5	1.0	25.0	NA	NA	hypothetical protein
TS29Rum08882|CDS|CDS	55.0	10.0	25.0	NA	NA	hypothetical protein
BDI3804|CDS|glutamate	33.0	6.0	25.0	NA	NA	hypothetical protein
TS29Fae08573|CDS|CDS	120.5	22.0	24.9	NA	NA	hypothetical protein
CspL21861|CDS|CDS	30.0	5.5	24.8	NA	NA	hypothetical protein
TS29Bac11989|CDS|CDS	65.3	12.0	24.7	NA	NA	hypothetical protein
Msm1409|CDS|tungsten	3.8	0.7	24.6	NA	NA	hypothetical protein
BFych463742|CDS|putative	5.4	1.0	24.6	NA	NA	hypothetical protein
BDI1206|CDS|hypothetical	27.0	5.0	24.5	NA	NA	hypothetical protein
TS28Rum09603|CDS|CDS	56.5	10.5	24.4	NA	NA	hypothetical protein

Caer1380|CDS|CDS	9.8	1.8	24.3	NA	NA	hypothetical protein
BFych462988|CDS|2-amino-3-ketobutyrate	2.7	0.5	24.2	NA	NA	hypothetical protein
TS29Rum02179|CDS|CDS	2.7	0.5	24.2	NA	NA	hypothetical protein
Bxyl4147|CDS|CDS	5.3	1.0	24.2	NA	NA	hypothetical protein
BFnctc0153|CDS|UDP-N-acetylglucosamine	2.7	0.5	24.2	NA	NA	hypothetical protein
BFych464466|CDS|acyl-CoA	2.7	0.5	24.2	NA	NA	hypothetical protein
EUBREC3013|CDS|hypothetical	10.7	2.0	24.2	NA	NA	hypothetical protein
TS29Rum15345|CDS|CDS	29.3	5.5	24.2	NA	NA	hypothetical protein
BDI2299|CDS|hypothetical	16.0	3.0	24.2	NA	NA	hypothetical protein
TS28Rum08239|CDS|CDS	8.0	1.5	24.2	NA	NA	hypothetical protein
TS29Clo3119|CDS|CDS	8.0	1.5	24.2	NA	NA	hypothetical protein
BDI2370|CDS|50S	16.0	3.0	24.2	NA	NA	hypothetical protein
Casp1293|CDS|CDS	5.3	1.0	24.2	NA	NA	hypothetical protein
BFych463746|CDS|TonB	5.3	1.0	24.2	NA	NA	hypothetical protein
TS29Rum13707|CDS|CDS	5.3	1.0	24.2	NA	NA	hypothetical protein
Chyl2948|CDS|CDS	5.3	1.0	24.2	NA	NA	hypothetical protein
BDI0493|CDS|putative	37.0	7.0	24.0	NA	NA	hypothetical protein
TS28Fae01389|CDS|CDS	1.8	0.3	23.8	NA	NA	hypothetical protein
TS28Fae12405|CDS|CDS	10.5	2.0	23.8	NA	NA	hypothetical protein
BFnctc3995|CDS|50S	2.6	0.5	23.8	NA	NA	hypothetical protein
TS29Dor2150|CDS|CDS	21.0	4.0	23.8	NA	NA	hypothetical protein
BFych464173|CDS|50S	2.6	0.5	23.8	NA	NA	hypothetical protein
BDI3732|CDS|hypothetical	21.0	4.0	23.8	NA	NA	hypothetical protein
Buni2118|CDS|CDS	10.5	2.0	23.8	NA	NA	hypothetical protein
BDI0660|CDS|threonyl-tRNA	31.5	6.0	23.8	NA	NA	hypothetical protein
Buni3150|CDS|CDS	36.5	7.0	23.7	NA	NA	hypothetical protein
Msm1336|CDS|heterodisulfide	13.0	2.5	23.7	NA	NA	hypothetical protein
BactD13254|CDS|CDS	5.2	1.0	23.6	NA	NA	hypothetical protein
Aput1619|CDS|CDS	26.0	5.0	23.6	NA	NA	hypothetical protein
TS29Fae08133|CDS|CDS	5.2	1.0	23.5	NA	NA	hypothetical protein
BFych463269|CDS|phosphoglycerate	10.3	2.0	23.5	NA	NA	hypothetical protein
BFnctc3107|CDS|phosphoglycerate	10.3	2.0	23.5	NA	NA	hypothetical protein
Msmi741407|CDS|CDS	61.7	12.0	23.3	NA	NA	hypothetical protein
TS28Fae18610|CDS|CDS	44.5	8.7	23.3	NA	NA	hypothetical protein
TS29Fae08167|CDS|CDS	44.5	8.7	23.3	NA	NA	hypothetical protein
Bxyl1101|CDS|CDS	3.4	0.7	23.0	NA	NA	hypothetical protein
Robe0613|CDS|CDS	95.5	19.0	22.8	NA	NA	hypothetical protein
b3903|CDS|L-rhamnose	1.7	0.3	22.7	NA	NA	hypothetical protein
TS28Bac4653|CDS|CDS	1.7	0.3	22.7	NA	NA	hypothetical protein
BactD14369|CDS|CDS	1.7	0.3	22.7	NA	NA	hypothetical protein
BFnctc1216|CDS|putative	1.7	0.3	22.7	NA	NA	hypothetical protein
Bxyl0237|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
TS29Rum18157|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI0650|CDS|putative	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI1191|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28Clo06689|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
Bxyl0403|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
BFnctc0443|CDS|gamma-glutamyl	2.5	0.5	22.7	NA	NA	hypothetical protein
BDI3969|CDS|50S	5.0	1.0	22.7	NA	NA	hypothetical protein
BFych460498|CDS|gamma-glutamyl	2.5	0.5	22.7	NA	NA	hypothetical protein
TS28Ali0708|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI1042|CDS|NADP-reducing	5.0	1.0	22.7	NA	NA	hypothetical protein
Bcap2910|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFnctc0936|CDS|2-dehydro-3-deoxyphosphooctonate	2.5	0.5	22.7	NA	NA	hypothetical protein
CspM6211506|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
Cbol4770|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
b3376|CDS|conserved	2.5	0.5	22.7	NA	NA	hypothetical protein
BDI1800|CDS|indolepyruvate	10.0	2.0	22.7	NA	NA	hypothetical protein
BFnctc1587|CDS|hypothetical	2.5	0.5	22.7	NA	NA	hypothetical protein
BFnctc2393|CDS|ATP-dependent	10.0	2.0	22.7	NA	NA	hypothetical protein
BDI0662|CDS|50S	5.0	1.0	22.7	NA	NA	hypothetical protein
BT2617|CDS|reverse	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28Rum01613|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFych461632|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
b3473|CDS|predicted	2.5	0.5	22.7	NA	NA	hypothetical protein
BFych464478|CDS|hypothetical	2.5	0.5	22.7	NA	NA	hypothetical protein
TS28Rum01638|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
BDI2121|CDS|uncharacterized	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI1730|CDS|putative	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28Rum08484|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
TS29Col0581|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFnctc1665|CDS|hypothetical	2.5	0.5	22.7	NA	NA	hypothetical protein
BFnctc4030|CDS|glutamyl-tRNA	2.5	0.5	22.7	NA	NA	hypothetical protein
Dfor0626|CDS|CDS	20.0	4.0	22.7	NA	NA	hypothetical protein
TS29Rum18454|CDS|CDS	10.0	2.0	22.7	NA	NA	hypothetical protein
BFnctc3052|CDS|transcription	5.0	1.0	22.7	NA	NA	hypothetical protein
b2547|CDS|fused	10.0	2.0	22.7	NA	NA	hypothetical protein
TS29Bac03818|CDS|CDS	20.0	4.0	22.7	NA	NA	hypothetical protein
TS29Bac02857|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
BFych461199|CDS|putative	2.5	0.5	22.7	NA	NA	hypothetical protein
BDI0488|CDS|putative	5.0	1.0	22.7	NA	NA	hypothetical protein
TS29Clo3169|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFych460962|CDS|putative	2.5	0.5	22.7	NA	NA	hypothetical protein
BFych461573|CDS|hypothetical	2.5	0.5	22.7	NA	NA	hypothetical protein
BFnctc3393|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI0072|CDS|putative	5.0	1.0	22.7	NA	NA	hypothetical protein
BFnctc4164|CDS|4-hydroxy-3-methylbut 2-en-1-yl	2.5	0.5	22.7	NA	NA	hypothetical protein
M23Apeg3590|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
Begg1010|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
Clep0607|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
TS29Par352|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
BLD1581|CDS|2-keto-4-pentenoate	1.3	0.3	22.7	NA	NA	hypothetical protein

BFych463530|CDS|putative	2.5	0.5	22.7	NA	NA	hypothetical protein
TS29Dor2149|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
Rgna1524|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFych461657|CDS|hypothetical	2.5	0.5	22.7	NA	NA	hypothetical protein
TS28Ali1906|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28Rum04611|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI2357|CDS|30S	5.0	1.0	22.7	NA	NA	hypothetical protein
BactD13755|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
TS29Rum21176|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFnctc1698|CDS|putative	2.5	0.5	22.7	NA	NA	hypothetical protein
BDI2195|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
TS29Rum02734|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI0099|CDS|hypothetical	10.0	2.0	22.7	NA	NA	hypothetical protein
BFych464160|CDS|methionine	5.0	1.0	22.7	NA	NA	hypothetical protein
Rumhyd3688|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
TS29Fae03719|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
TS29Dor1169|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI3690|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
b2800|CDS|L-fuculose-1-phosphate	5.0	1.0	22.7	NA	NA	hypothetical protein
Robe3513|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFych461691|CDS|hypothetical	2.5	0.5	22.7	NA	NA	hypothetical protein
TS28Clo04778|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BDI3799|CDS|hypothetical	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28Rum05914|CDS|CDS	10.0	2.0	22.7	NA	NA	hypothetical protein
TS29Rum11525|CDS|CDS	10.0	2.0	22.7	NA	NA	hypothetical protein
TS28Fae16577|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
Buni1274|CDS|CDS	2.5	0.5	22.7	NA	NA	hypothetical protein
Cbol0250|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28Rum05667|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
Bfin3199|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
TS28RumUnc0148|CDS|CDS	5.0	1.0	22.7	NA	NA	hypothetical protein
BFnctc3791|CDS|putative	7.5	1.5	22.7	NA	NA	hypothetical protein
TS29Fae02437|CDS|CDS	15.0	3.0	22.7	NA	NA	hypothetical protein
TS28Fae00495|CDS|CDS	7.5	1.5	22.7	NA	NA	hypothetical protein
BDI3533|CDS|transcription	15.0	3.0	22.7	NA	NA	hypothetical protein
TS29Fae00359|CDS|CDS	7.5	1.5	22.7	NA	NA	hypothetical protein
BDI3383|CDS|enoyl-[acyl-carrier-protein]	15.0	3.0	22.7	NA	NA	hypothetical protein
Bxyl0016|CDS|CDS	15.0	3.0	22.7	NA	NA	hypothetical protein
Aput0871|CDS|CDS	15.0	3.0	22.7	NA	NA	hypothetical protein
BDI1515|CDS|hypothetical	15.0	3.0	22.7	NA	NA	hypothetical protein
TS29Rum17529|CDS|CDS	7.5	1.5	22.7	NA	NA	hypothetical protein
BFnctc2761|CDS|putative	15.0	3.0	22.7	NA	NA	hypothetical protein
TS29Fae07330|CDS|CDS	7.5	1.5	22.7	NA	NA	hypothetical protein
TS28Bac2609|CDS|CDS	3.3	0.7	22.7	NA	NA	hypothetical protein
BFych463034|CDS|hypothetical	9.9	2.0	22.5	NA	NA	hypothetical protein
BT1958|CDS|hypothetical	9.9	2.0	22.5	NA	NA	hypothetical protein
BFnctc3138|CDS|fructose-bisphosphate	16.5	3.3	22.5	NA	NA	hypothetical protein
BFnctc0219|CDS|translation	14.8	3.0	22.4	NA	NA	hypothetical protein
BactD10051|CDS|CDS	2.5	0.5	22.4	NA	NA	hypothetical protein
BLD1723|CDS|Ribosomal	2.5	0.5	22.2	NA	NA	hypothetical protein
TS29Rum00140|CDS|CDS	122.0	25.0	22.2	NA	NA	hypothetical protein
Bsp1162556|CDS|CDS	9.8	2.0	22.1	NA	NA	hypothetical protein
Bsp1162031|CDS|CDS	0.7	0.1	22.0	NA	NA	hypothetical protein
Buni0341|CDS|CDS	2.4	0.5	21.9	NA	NA	hypothetical protein
Ccom1704|CDS|CDS	19.3	4.0	21.9	NA	NA	hypothetical protein
BFych461217|CDS|hypothetical	4.8	1.0	21.9	NA	NA	hypothetical protein
BFnctc4015|CDS|DNA-directed	24.2	5.0	21.9	NA	NA	hypothetical protein
TS28Rum02365|CDS|CDS	12.0	2.5	21.8	NA	NA	hypothetical protein
Robe3564|CDS|CDS	24.0	5.0	21.8	NA	NA	hypothetical protein
TS28Rum14880|CDS|CDS	21.5	4.5	21.7	NA	NA	hypothetical protein
TS29Rum16475|CDS|CDS	14.3	3.0	21.7	NA	NA	hypothetical protein
BFnctc3243|CDS|adenylosuccinate	4.8	1.0	21.7	NA	NA	hypothetical protein
BT2631|CDS|putative	2.4	0.5	21.6	NA	NA	hypothetical protein
BDI1271|CDS|serine	19.0	4.0	21.6	NA	NA	hypothetical protein
FpraM2120128|CDS|CDS	9.5	2.0	21.6	NA	NA	hypothetical protein
Buni2619|CDS|CDS	19.8	4.2	21.5	NA	NA	hypothetical protein
Robe0609|CDS|CDS	42.5	9.0	21.4	NA	NA	hypothetical protein
BFnctc4004|CDS|30S	2.4	0.5	21.4	NA	NA	hypothetical protein
BDI1854|CDS|AAA-metalloprotease	33.0	7.0	21.4	NA	NA	hypothetical protein
BFych462020|CDS|hypothetical	14.1	3.0	21.4	NA	NA	hypothetical protein
Bxyl2888|CDS|CDS	6.3	1.3	21.3	NA	NA	hypothetical protein
TS29Bac02765|CDS|CDS	23.4	5.0	21.2	NA	NA	hypothetical protein
FpraM2120521|CDS|CDS	4.7	1.0	21.2	NA	NA	hypothetical protein
BFych460188|CDS|UDP-N-acetylglucosamine	4.7	1.0	21.2	NA	NA	hypothetical protein
BDI1397|CDS|ATP-dependent	14.0	3.0	21.2	NA	NA	hypothetical protein
TS28Fae21330|CDS|CDS	2.3	0.5	21.2	NA	NA	hypothetical protein
Msm0202|CDS|translation	3.5	0.8	21.2	NA	NA	hypothetical protein
BFnctc0714|CDS|hypothetical	14.0	3.0	21.2	NA	NA	hypothetical protein
Aput1932|CDS|CDS	28.0	6.0	21.2	NA	NA	hypothetical protein
TS28Bac0366|CDS|CDS	2.3	0.5	21.2	NA	NA	hypothetical protein
BDI0672|CDS|phosphoglycerate	14.0	3.0	21.2	NA	NA	hypothetical protein
TS29Rum03193|CDS|CDS	14.0	3.0	21.2	NA	NA	hypothetical protein
Bxyl2186|CDS|CDS	9.3	2.0	21.2	NA	NA	hypothetical protein
Ehal1623|CDS|CDS	2.3	0.5	21.2	NA	NA	hypothetical protein
Bfra31120443|CDS|CDS	2.3	0.5	21.2	NA	NA	hypothetical protein
Clep0205|CDS|CDS	34.2	7.3	21.2	NA	NA	hypothetical protein
TS29Rum17007|CDS|CDS	64.8	14.0	21.0	NA	NA	hypothetical protein
Ccom1703|CDS|CDS	23.0	5.0	20.9	NA	NA	hypothetical protein
BDI0507|CDS|hypothetical	23.0	5.0	20.9	NA	NA	hypothetical protein
TS29Rum18034|CDS|CDS	23.0	5.0	20.9	NA	NA	hypothetical protein
TS29Rum14197|CDS|CDS	23.0	5.0	20.9	NA	NA	hypothetical protein
TS28Fae07391|CDS|CDS	11.5	2.5	20.9	NA	NA	hypothetical protein
BFnctc3998|CDS|50S	6.9	1.5	20.8	NA	NA	hypothetical protein
BFnctc3111|CDS|hypothetical	16.0	3.5	20.8	NA	NA	hypothetical protein

TS28RumUnc1234|CDS|CDS	16.0	3.5	20.8	NA	NA	hypothetical protein
TS29Bac02770|CDS|CDS	16.8	3.7	20.7	NA	NA	hypothetical protein
Buni0214|CDS|CDS	38.5	8.5	20.6	NA	NA	hypothetical protein
BactD11684|CDS|CDS	4.9	1.1	20.5	NA	NA	hypothetical protein
TS29Fae03990|CDS|CDS	49.7	11.0	20.5	NA	NA	hypothetical protein
Msm1413|CDS|tungsten	8.1	1.8	20.5	NA	NA	hypothetical protein
TS29Bac07473|CDS|CDS	13.5	3.0	20.5	NA	NA	hypothetical protein
TS29Rum05541|CDS|CDS	3.0	0.7	20.4	NA	NA	hypothetical protein
TS28Met1060|CDS|CDS	1.5	0.3	20.4	NA	NA	hypothetical protein
stu1596|CDS|cation-P-type	1.5	0.3	20.4	NA	NA	hypothetical protein
stu0252|CDS|diaminopimelate	1.5	0.3	20.4	NA	NA	hypothetical protein
stu1569|CDS|CorA	3.0	0.7	20.4	NA	NA	hypothetical protein
str1596|CDS|cation	1.5	0.3	20.4	NA	NA	hypothetical protein
str1569|CDS|cation	3.0	0.7	20.4	NA	NA	hypothetical protein
TS28Fae18233|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
TS29Fae03420|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
TS29Bac01551|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
Aput1501|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
TS29Rum04206|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
Rbro0857|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
BDI3914|CDS|conserved	9.0	2.0	20.4	NA	NA	hypothetical protein
Bova3371|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
BDI0792|CDS|sulfite	18.0	4.0	20.4	NA	NA	hypothetical protein
TS29Bac08223|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
TS28Fae22735|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
BDI1474|CDS|hypothetical	9.0	2.0	20.4	NA	NA	hypothetical protein
TS29Clo4791|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
Dlon2487|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
TS29Col0157|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
BDI1400|CDS|hypothetical	18.0	4.0	20.4	NA	NA	hypothetical protein
TS28Fae09488|CDS|CDS	18.0	4.0	20.4	NA	NA	hypothetical protein
TS29Par386|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
TS29Fae09384|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
BLD1558|CDS|SalY-type	2.3	0.5	20.4	NA	NA	hypothetical protein
BDI1548|CDS|TonB-like	9.0	2.0	20.4	NA	NA	hypothetical protein
TS29Rum17853|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
TS29Bac11570|CDS|CDS	18.0	4.0	20.4	NA	NA	hypothetical protein
TS28Rum03410|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
BDI1829|CDS|bifunctional	18.0	4.0	20.4	NA	NA	hypothetical protein
TS29Rum15436|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
BDI1291|CDS|hypothetical	9.0	2.0	20.4	NA	NA	hypothetical protein
Rtor1158|CDS|CDS	4.5	1.0	20.4	NA	NA	hypothetical protein
Acac2900|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
Bste1256|CDS|CDS	2.3	0.5	20.4	NA	NA	hypothetical protein
Aput1132|CDS|CDS	9.0	2.0	20.4	NA	NA	hypothetical protein
BDI3815|CDS|hypothetical	9.0	2.0	20.4	NA	NA	hypothetical protein
BDI3489|CDS|30S	13.5	3.0	20.4	NA	NA	hypothetical protein
Buni0293|CDS|CDS	53.2	11.8	20.4	NA	NA	hypothetical protein
BDI2805|CDS|phosphoenolpyruvate	40.3	9.0	20.3	NA	NA	hypothetical protein
TS29Fae08622|CDS|CDS	49.0	11.0	20.2	NA	NA	hypothetical protein
Msm0999|CDS|methyl	16.3	3.7	20.2	NA	NA	hypothetical protein
BFych464165|CDS|50S	11.1	2.5	20.2	NA	NA	hypothetical protein
BFnctc3987|CDS|50S	11.1	2.5	20.2	NA	NA	hypothetical protein
BactD24581|CDS|CDS	2.2	0.5	20.1	NA	NA	hypothetical protein
TS29Bac05519|CDS|CDS	31.0	7.0	20.1	NA	NA	hypothetical protein
BFych462742|CDS|RNA	4.4	1.0	20.1	NA	NA	hypothetical protein
BFnctc2759|CDS|putative	4.4	1.0	20.1	NA	NA	hypothetical protein
Buni1133|CDS|CDS	8.8	2.0	20.1	NA	NA	hypothetical protein
TS29Bac07251|CDS|CDS	17.7	4.0	20.1	NA	NA	hypothetical protein
Msm0438|CDS|vacuolar-type	2.4	0.5	20.0	NA	NA	hypothetical protein
TS29Par766|CDS|CDS	88.1	20.0	20.0	NA	NA	hypothetical protein
Msmi750581|CDS|CDS	1.5	0.3	20.0	NA	NA	hypothetical protein
TS28Met0711|CDS|CDS	1.5	0.3	20.0	NA	NA	hypothetical protein
BactD20051|CDS|CDS	2.2	0.5	20.0	NA	NA	hypothetical protein
BL0751|CDS|ATP	2.2	0.5	20.0	NA	NA	hypothetical protein
TS29Fae08380|CDS|CDS	11.0	2.5	20.0	NA	NA	hypothetical protein
BDI2356|CDS|30S	11.0	2.5	20.0	NA	NA	hypothetical protein
Bova0737|CDS|CDS	2.2	0.5	20.0	NA	NA	hypothetical protein
TS29Rum21191|CDS|CDS	37.0	8.5	19.8	NA	NA	hypothetical protein
BL1101|CDS|hypothetical	95.5	22.0	19.7	NA	NA	hypothetical protein
FpraM2122061|CDS|CDS	69.4	16.0	19.7	NA	NA	hypothetical protein
Clep0216|CDS|CDS	6.5	1.5	19.7	NA	NA	hypothetical protein
TS29Par417|CDS|CDS	6.5	1.5	19.7	NA	NA	hypothetical protein
TS29Rum00755|CDS|CDS	13.0	3.0	19.7	NA	NA	hypothetical protein
TS29Par319|CDS|CDS	13.0	3.0	19.7	NA	NA	hypothetical protein
TS29Bac08806|CDS|CDS	13.0	3.0	19.7	NA	NA	hypothetical protein
TS28Clo03058|CDS|CDS	13.0	3.0	19.7	NA	NA	hypothetical protein
Clep2099|CDS|CDS	13.0	3.0	19.7	NA	NA	hypothetical protein
BDI1098|CDS|Xaa-Pro	13.0	3.0	19.7	NA	NA	hypothetical protein
BDI0940|CDS|carboxynorspermidine	13.0	3.0	19.7	NA	NA	hypothetical protein
TS28Clo02774|CDS|CDS	65.0	15.0	19.7	NA	NA	hypothetical protein
Msmi750379|CDS|CDS	1.1	0.3	19.7	NA	NA	hypothetical protein
BDI2378|CDS|50S	4.3	1.0	19.7	NA	NA	hypothetical protein
Msm1411|CDS|tungsten	4.3	1.0	19.5	NA	NA	hypothetical protein
BL0549|CDS|adenylosuccinate	2.2	0.5	19.5	NA	NA	hypothetical protein
BDI1031|CDS|pyruvate	30.0	7.0	19.5	NA	NA	hypothetical protein
BFnctc3437|CDS|glutamate	15.0	3.5	19.5	NA	NA	hypothetical protein
FpraM2120613|CDS|CDS	47.8	11.2	19.4	NA	NA	hypothetical protein
FpraM2120129|CDS|CDS	47.8	11.2	19.4	NA	NA	hypothetical protein
Msm0621|CDS|acidic	5.0	1.2	19.4	NA	NA	hypothetical protein
BFych464485|CDS|hypothetical	17.0	4.0	19.3	NA	NA	hypothetical protein
Aput0210|CDS|CDS	8.5	2.0	19.3	NA	NA	hypothetical protein
BDI2646|CDS|hypothetical	17.0	4.0	19.3	NA	NA	hypothetical protein
Buni1273|CDS|CDS	8.5	2.0	19.3	NA	NA	hypothetical protein
Aput2026|CDS|CDS	8.5	2.0	19.3	NA	NA	hypothetical protein
BL1582|CDS|30S	1.1	0.3	19.2	NA	NA	hypothetical protein

BLD1711|CDS|Ribosomal	1.1	0.3	19.2	NA	NA	hypothetical protein
TS28Fae16376|CDS|CDS	12.7	3.0	19.2	NA	NA	hypothetical protein
Bden1243|CDS|CDS	2.1	0.5	19.1	NA	NA	hypothetical protein
BFnctc4129|CDS|polynucleotide	10.5	2.5	19.1	NA	NA	hypothetical protein
TS28Fae02282|CDS|CDS	21.0	5.0	19.1	NA	NA	hypothetical protein
BFych462412|CDS|TPR	10.5	2.5	19.1	NA	NA	hypothetical protein
BT2700|CDS|50S	4.2	1.0	19.1	NA	NA	hypothetical protein
TS29Fae00241|CDS|CDS	12.5	3.0	18.9	NA	NA	hypothetical protein
BDI0163|CDS|methylmalonyl-CoA	25.0	6.0	18.9	NA	NA	hypothetical protein
Bfin0932|CDS|CDS	6.0	1.5	18.8	NA	NA	hypothetical protein
BFych464551|CDS|fumarate	1.4	0.3	18.8	NA	NA	hypothetical protein
BactD11211|CDS|CDS	5.5	1.3	18.7	NA	NA	hypothetical protein
BDI3033|CDS|L-aspartate	20.5	5.0	18.6	NA	NA	hypothetical protein
BDI3816|CDS|putative	20.5	5.0	18.6	NA	NA	hypothetical protein
BFnctc0179|CDS|putative	2.0	0.5	18.5	NA	NA	hypothetical protein
BFych460220|CDS|acyl	2.0	0.5	18.5	NA	NA	hypothetical protein
BDI1517|CDS|putative	57.0	14.0	18.5	NA	NA	hypothetical protein
Msm1117|CDS|cobalamin	59.0	14.5	18.5	NA	NA	hypothetical protein
TS29Rum04348|CDS|CDS	107.3	26.5	18.4	NA	NA	hypothetical protein
Bova0264|CDS|CDS	4.0	1.0	18.3	NA	NA	hypothetical protein
BactD23742|CDS|CDS	4.0	1.0	18.3	NA	NA	hypothetical protein
BFych464192|CDS|DNA-directed	24.2	6.0	18.3	NA	NA	hypothetical protein
TS28Clo00205|CDS|CDS	5.4	1.3	18.3	NA	NA	hypothetical protein
BFych462850|CDS|putative	64.5	16.1	18.2	NA	NA	hypothetical protein
TS28Bac6125|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Bsp1162035|CDS|CDS	0.3	0.1	18.2	NA	NA	hypothetical protein
TS29Bac02077|CDS|CDS	28.0	7.0	18.2	NA	NA	hypothetical protein
BFych463273|CDS|hypothetical	14.0	3.5	18.2	NA	NA	hypothetical protein
BFych463635|CDS|glutamate	14.0	3.5	18.2	NA	NA	hypothetical protein
TS28Fae21577|CDS|CDS	14.0	3.5	18.2	NA	NA	hypothetical protein
BDI1124|CDS|Na(+)-translocating	4.0	1.0	18.2	NA	NA	hypothetical protein
BFych462230|CDS|putative	6.0	1.5	18.2	NA	NA	hypothetical protein
TS28Rum13322|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Cbol4716|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Fae13123|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Clep0351|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Fae00262|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
TS29Rum03712|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI0313|CDS|hypothetical	8.0	2.0	18.2	NA	NA	hypothetical protein
BDI3843|CDS|hypothetical	8.0	2.0	18.2	NA	NA	hypothetical protein
Ehal2607|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Bxyl2835|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFych463959|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
BFych463178|CDS|putative	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Col0078|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
TS28Rum06435|CDS|CDS	6.0	1.5	18.2	NA	NA	hypothetical protein
TS28Fae12104|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum03308|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Rum05635|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFych462632|CDS|hypothetical	2.0	0.5	18.2	NA	NA	hypothetical protein
TS29Rum08493|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
FpraM2120876|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Fae05286|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Rum09716|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI3377|CDS|ribosome-associated	8.0	2.0	18.2	NA	NA	hypothetical protein
TS28Clo07310|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
HPAG10815|CDS|inositol-5-monophosphate	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI2355|CDS|30S	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI0987|CDS|pyruvate	8.0	2.0	18.2	NA	NA	hypothetical protein
FpraM2120841|CDS|CDS	6.0	1.5	18.2	NA	NA	hypothetical protein
FpraM2121307|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
BFych461325|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Rum05381|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFych461583|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
BFych462294|CDS|hypothetical	2.0	0.5	18.2	NA	NA	hypothetical protein
BFych460298|CDS|30S	2.0	0.5	18.2	NA	NA	hypothetical protein
TS29Clo4224|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Dor1170|CDS|CDS	12.0	3.0	18.2	NA	NA	hypothetical protein
BFnctc4025|CDS|30S	2.0	0.5	18.2	NA	NA	hypothetical protein
Aput1508|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
TS29Clo3173|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
BFnctc2383|CDS|hypothetical	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Clo04150|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
TS29Ali429|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Rtor0190|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Aput1617|CDS|CDS	24.0	6.0	18.2	NA	NA	hypothetical protein
TS29Clo3167|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Fae09966|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI1119|CDS|hypothetical	4.0	1.0	18.2	NA	NA	hypothetical protein
M23Apeg1849|CDS|hypothetical	4.0	1.0	18.2	NA	NA	hypothetical protein
b2906|CDS|predicted	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Fae19107|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Clo04561|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BactD22375|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Buni1825|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Rgna0318|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Dfor0848|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
b3056|CDS|fused	6.0	1.5	18.2	NA	NA	hypothetical protein
b2049|CDS|mannose-1-phosphate	2.0	0.5	18.2	NA	NA	hypothetical protein
BFych460528|CDS|acetyl-coenzyme	2.0	0.5	18.2	NA	NA	hypothetical protein
Bthe7335571|CDS|CDS	1.0	0.3	18.2	NA	NA	hypothetical protein
Dfor1274|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Clo05486|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
BFych463853|CDS|methylglyoxal	2.0	0.5	18.2	NA	NA	hypothetical protein
BFnctc2564|CDS|putative	4.0	1.0	18.2	NA	NA	hypothetical protein

BFnctc3707|CDS|hypothetical	2.0	0.5	18.2	NA	NA	hypothetical protein
Aput0171|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Bthe3730719|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI0477|CDS|UDP-N-acetylglucosamine	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Fae01387|CDS|CDS	12.0	3.0	18.2	NA	NA	hypothetical protein
BFnctc1965|CDS|hypothetical	2.0	0.5	18.2	NA	NA	hypothetical protein
TS29Fae04747|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum14704|CDS|CDS	16.0	4.0	18.2	NA	NA	hypothetical protein
TS28Clo05689|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
BFych461820|CDS|hypothetical	1.0	0.3	18.2	NA	NA	hypothetical protein
BDI3540|CDS|glycoside	16.0	4.0	18.2	NA	NA	hypothetical protein
Cbol2263|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
FpraM2120130|CDS|CDS	6.0	1.5	18.2	NA	NA	hypothetical protein
BL1400|CDS|hypothetical	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI0928|CDS|Na+/H+	4.0	1.0	18.2	NA	NA	hypothetical protein
M23Apeg3634|CDS|3-hydroxybutyryl-CoA	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI1316|CDS|hypothetical	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI2097|CDS|phosphoglucomutase	16.0	4.0	18.2	NA	NA	hypothetical protein
BFnctc2109|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
TS29Bac11758|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
b3026|CDS|sensory	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Fae07802|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFnctc0455|CDS|orotate	8.0	2.0	18.2	NA	NA	hypothetical protein
BDI3125|CDS|putative	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Dor1496|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Cbol5275|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Bste2306|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI3370|CDS|acetate	12.0	3.0	18.2	NA	NA	hypothetical protein
TS28Rum07612|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
TS29Rum01315|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
BDI0825|CDS|ATP	12.0	3.0	18.2	NA	NA	hypothetical protein
BDI1817|CDS|glycerol-3-phosphate	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Bac12104|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Fae03748|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI3098|CDS|putative	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI2831|CDS|putative	8.0	2.0	18.2	NA	NA	hypothetical protein
TS29Rum16756|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Robe3278|CDS|CDS	6.0	1.5	18.2	NA	NA	hypothetical protein
TS29Bac01101|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI2059|CDS|3-isopropylmalate	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28RumUnc1535|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFych464202|CDS|30S	2.0	0.5	18.2	NA	NA	hypothetical protein
BFnctc4365|CDS|translation-associated	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Eub0234|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum18420|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
Buni0158|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
EFER2728|CDS|exonuclease	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Bac06953|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum17134|CDS|CDS	12.0	3.0	18.2	NA	NA	hypothetical protein
Bxyl3807|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Clep1276|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Acac0630|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
EUBREC0715|CDS|cell	4.0	1.0	18.2	NA	NA	hypothetical protein
M23Apeg1214|CDS|PTS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum01635|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Bac1929|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
Clep0226|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI3213|CDS|outer	12.0	3.0	18.2	NA	NA	hypothetical protein
Aput1464|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Bste1244|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI3414|CDS|galactoside	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI1482|CDS|hypothetical	4.0	1.0	18.2	NA	NA	hypothetical protein
Aput0426|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
Aput1043|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
RintL13841|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Bfra31123680|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
EUBREC2388|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI1735|CDS|hypothetical	8.0	2.0	18.2	NA	NA	hypothetical protein
BDI1428|CDS|transcriptional	8.0	2.0	18.2	NA	NA	hypothetical protein
Dfor2477|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI1288|CDS|hypothetical	4.0	1.0	18.2	NA	NA	hypothetical protein
BactD20960|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Rum00786|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFnctc0387|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28RumUnc0315|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI1453|CDS|hypothetical	4.0	1.0	18.2	NA	NA	hypothetical protein
b1510|CDS|predicted	2.0	0.5	18.2	NA	NA	hypothetical protein
BFnctc3624|CDS|methylglyoxal	2.0	0.5	18.2	NA	NA	hypothetical protein
BFnctc2388|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Rum03208|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Fae18034|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum13369|CDS|CDS	24.0	6.0	18.2	NA	NA	hypothetical protein
BDI1218|CDS|hypothetical	8.0	2.0	18.2	NA	NA	hypothetical protein
BLD0786|CDS|Threonine	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Rum13621|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Rum15202|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
Acac0958|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFnctc3620|CDS|putative	10.0	2.5	18.2	NA	NA	hypothetical protein
TS29Fae04126|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Fae20274|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
Buni0757|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
b2545|CDS|predicted	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Fae03250|CDS|CDS	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Fae02150|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein

BDI0950|CDS|conserved	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Fae07888|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BFnctc3018|CDS|putative	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI2609|CDS|putative	2.0	0.5	18.2	NA	NA	hypothetical protein
M23Apeg1351|CDS|LSU	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI3774|CDS|glycoside	4.0	1.0	18.2	NA	NA	hypothetical protein
Aput0425|CDS|CDS	12.0	3.0	18.2	NA	NA	hypothetical protein
BDI1303|CDS|redox-sensitive	4.0	1.0	18.2	NA	NA	hypothetical protein
BDI2359|CDS|methionine	2.0	0.5	18.2	NA	NA	hypothetical protein
TS28Ali1376|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS29Fae04758|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
TS28Col1444|CDS|CDS	4.0	1.0	18.2	NA	NA	hypothetical protein
BactD20009|CDS|CDS	1.0	0.3	18.2	NA	NA	hypothetical protein
BFnctc0247|CDS|30S	2.0	0.5	18.2	NA	NA	hypothetical protein
BDI3084|CDS|putative	12.0	3.0	18.2	NA	NA	hypothetical protein
Aput1894|CDS|CDS	8.0	2.0	18.2	NA	NA	hypothetical protein
BDI2257|CDS|gamma-glutamyl	4.0	1.0	18.2	NA	NA	hypothetical protein
Bsp1162553|CDS|CDS	1.3	0.3	18.2	NA	NA	hypothetical protein
TS29Rum09361|CDS|CDS	1.3	0.3	18.2	NA	NA	hypothetical protein
TS29Bac09613|CDS|CDS	1.3	0.3	18.2	NA	NA	hypothetical protein
BFych460255|CDS|L-fuculose-1-phosphate	1.3	0.3	18.2	NA	NA	hypothetical protein
Buni0276|CDS|CDS	1.3	0.3	18.2	NA	NA	hypothetical protein
TS28Clo09615|CDS|CDS	1.3	0.3	18.2	NA	NA	hypothetical protein
BT4258|CDS|putative	1.3	0.3	18.2	NA	NA	hypothetical protein
BactD11867|CDS|CDS	1.3	0.3	18.2	NA	NA	hypothetical protein
BFnctc0929|CDS|50S	2.0	0.5	18.0	NA	NA	hypothetical protein
BFych461009|CDS|50S	2.0	0.5	18.0	NA	NA	hypothetical protein
BactD10372|CDS|CDS	13.8	3.5	17.9	NA	NA	hypothetical protein
BFych462410|CDS|ATP-dependent	13.8	3.5	17.9	NA	NA	hypothetical protein
BFnctc0885|CDS|putative	7.9	2.0	17.9	NA	NA	hypothetical protein
BFych460967|CDS|glyceraldehyde	7.9	2.0	17.9	NA	NA	hypothetical protein
TS29Bac00149|CDS|CDS	39.2	10.0	17.8	NA	NA	hypothetical protein
BFnctc1955|CDS|putative	13.7	3.5	17.7	NA	NA	hypothetical protein
Bden0010|CDS|CDS	2.0	0.5	17.7	NA	NA	hypothetical protein
Msm1412|CDS|tungsten	5.3	1.4	17.7	NA	NA	hypothetical protein
BAD1290|CDS|sugar	3.3	0.8	17.7	NA	NA	hypothetical protein
TS29Rum15071|CDS|CDS	35.0	9.0	17.7	NA	NA	hypothetical protein
BDI0494|CDS|putative	35.0	9.0	17.7	NA	NA	hypothetical protein
BFnctc2474|CDS|hypothetical	2.6	0.7	17.6	NA	NA	hypothetical protein
TS28Fae01662|CDS|CDS	15.5	4.0	17.6	NA	NA	hypothetical protein
Msmi740498|CDS|CDS	31.0	8.0	17.6	NA	NA	hypothetical protein
TS29Rum17530|CDS|CDS	29.0	7.5	17.6	NA	NA	hypothetical protein
TS29Bac07995|CDS|CDS	56.0	14.5	17.5	NA	NA	hypothetical protein
Msm0704|CDS|translation	2.3	0.6	17.5	NA	NA	hypothetical protein
BDI3379|CDS|putative	73.0	19.0	17.4	NA	NA	hypothetical protein
BDI0484|CDS|preprotein	23.0	6.0	17.4	NA	NA	hypothetical protein
BDI2640|CDS|hypothetical	23.0	6.0	17.4	NA	NA	hypothetical protein
BDI0458|CDS|thiol	23.0	6.0	17.4	NA	NA	hypothetical protein
b3867|CDS|coproporphyrinogen	3.8	1.0	17.4	NA	NA	hypothetical protein
TS29Bac00719|CDS|CDS	26.8	7.0	17.4	NA	NA	hypothetical protein
BDI3747|CDS|hypothetical	88.0	23.0	17.4	NA	NA	hypothetical protein
TS29Bac09289|CDS|CDS	34.4	9.0	17.4	NA	NA	hypothetical protein
FpraM2121176|CDS|CDS	30.5	8.0	17.3	NA	NA	hypothetical protein
TS28Fae11007|CDS|CDS	9.5	2.5	17.3	NA	NA	hypothetical protein
TS28Fae14948|CDS|CDS	9.5	2.5	17.3	NA	NA	hypothetical protein
FpraM2121833|CDS|CDS	43.7	11.5	17.2	NA	NA	hypothetical protein
TS29Bac01198|CDS|CDS	15.2	4.0	17.2	NA	NA	hypothetical protein
TS28Rum00322|CDS|CDS	17.0	4.5	17.2	NA	NA	hypothetical protein
TS29Rum15231|CDS|CDS	17.0	4.5	17.2	NA	NA	hypothetical protein
Bsp1163400|CDS|CDS	1.3	0.3	17.0	NA	NA	hypothetical protein
BVU1517|CDS|hypothetical	3.8	1.0	17.0	NA	NA	hypothetical protein
BactD10916|CDS|CDS	15.0	4.0	17.0	NA	NA	hypothetical protein
TS29Bac01785|CDS|CDS	30.0	8.0	17.0	NA	NA	hypothetical protein
TS29Bac05518|CDS|CDS	30.0	8.0	17.0	NA	NA	hypothetical protein
BDI0653|CDS|outer	30.0	8.0	17.0	NA	NA	hypothetical protein
Msm0200|CDS|translation	3.4	0.9	17.0	NA	NA	hypothetical protein
Buni2824|CDS|CDS	24.3	6.5	17.0	NA	NA	hypothetical protein
BFnctc3988|CDS|50S	7.4	2.0	16.9	NA	NA	hypothetical protein
BFych464166|CDS|50S	7.4	2.0	16.9	NA	NA	hypothetical protein
BFnctc4257|CDS|hypothetical	13.0	3.5	16.9	NA	NA	hypothetical protein
TS29Bac03143|CDS|CDS	26.0	7.0	16.9	NA	NA	hypothetical protein
TS28Rum08295|CDS|CDS	8.7	2.3	16.9	NA	NA	hypothetical protein
Rtor1382|CDS|CDS	8.7	2.3	16.9	NA	NA	hypothetical protein
TS29Fae01563|CDS|CDS	37.0	10.0	16.8	NA	NA	hypothetical protein
Dlon0163|CDS|CDS	11.1	3.0	16.7	NA	NA	hypothetical protein
BFych464191|CDS|DNA-directed	29.4	8.0	16.7	NA	NA	hypothetical protein
Buni2857|CDS|CDS	9.2	2.5	16.6	NA	NA	hypothetical protein
BDI1362|CDS|putative	11.0	3.0	16.6	NA	NA	hypothetical protein
TS28Rum04805|CDS|CDS	5.5	1.5	16.6	NA	NA	hypothetical protein
TS28Fae18628|CDS|CDS	5.5	1.5	16.6	NA	NA	hypothetical protein
BDI1237|CDS|2-amino-3-ketobutyrate	11.0	3.0	16.6	NA	NA	hypothetical protein
Aput0682|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
TS29Bac05584|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
TS28Fae17702|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
BDI3673|CDS|putative	33.0	9.0	16.6	NA	NA	hypothetical protein
Aput1668|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
BDI0618|CDS|non-specific	7.3	2.0	16.6	NA	NA	hypothetical protein
Aput0384|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
b0114|CDS|pyruvate	1.8	0.5	16.6	NA	NA	hypothetical protein
Aput1484|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
BDI3589|CDS|putative	5.5	1.5	16.6	NA	NA	hypothetical protein
BDI2807|CDS|putative	11.0	3.0	16.6	NA	NA	hypothetical protein
Buni2850|CDS|CDS	16.5	4.5	16.6	NA	NA	hypothetical protein
BFnctc3905|CDS|hypothetical	5.5	1.5	16.6	NA	NA	hypothetical protein
Aput1272|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein

Aput0598|CDS|CDS	11.0	3.0	16.6	NA	NA	hypothetical protein
FpraM2122257|CDS|CDS	1.8	0.5	16.6	NA	NA	hypothetical protein
Buni0292|CDS|CDS	20.7	5.7	16.6	NA	NA	hypothetical protein
BactD11817|CDS|CDS	14.0	3.8	16.5	NA	NA	hypothetical protein
TS29Bac04870|CDS|CDS	14.0	3.8	16.5	NA	NA	hypothetical protein
BactD12028|CDS|CDS	12.7	3.5	16.5	NA	NA	hypothetical protein
TS29Bac11275|CDS|CDS	24.3	6.7	16.5	NA	NA	hypothetical protein
TS29Fae02346|CDS|CDS	29.0	8.0	16.5	NA	NA	hypothetical protein
TS29Bac06936|CDS|CDS	3.6	1.0	16.4	NA	NA	hypothetical protein
EUBREC3460|CDS|hypothetical	0.9	0.3	16.3	NA	NA	hypothetical protein
BDI0526|CDS|RNA	18.0	5.0	16.3	NA	NA	hypothetical protein
TS29RumUnc0801|CDS|CDS	18.0	5.0	16.3	NA	NA	hypothetical protein
TS29Fae06390|CDS|CDS	36.0	10.0	16.3	NA	NA	hypothetical protein
BDI2264|CDS|DNA-directed	39.5	11.0	16.3	NA	NA	hypothetical protein
Bova3030|CDS|CDS	1.8	0.5	16.2	NA	NA	hypothetical protein
BWH25667|CDS|CDS	5.3	1.5	16.1	NA	NA	hypothetical protein
Bthe3735771|CDS|CDS	5.3	1.5	16.1	NA	NA	hypothetical protein
FpraM2121103|CDS|CDS	6.5	1.8	16.1	NA	NA	hypothetical protein
BFych460562|CDS|putative	8.8	2.5	16.0	NA	NA	hypothetical protein
BFnctc0512|CDS|ROK	8.8	2.5	16.0	NA	NA	hypothetical protein
TS28Rum01975|CDS|CDS	10.0	2.8	16.0	NA	NA	hypothetical protein
TS28Rum00223|CDS|CDS	102.0	29.0	16.0	NA	NA	hypothetical protein
Bova2000|CDS|CDS	1.2	0.3	15.9	NA	NA	hypothetical protein
TS28Rum02617|CDS|CDS	1.2	0.3	15.9	NA	NA	hypothetical protein
TS29Clo1422|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
Ehal0408|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BFnctc0828|CDS|bifunctional	3.5	1.0	15.9	NA	NA	hypothetical protein
TS29Rum17364|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
EUBREC0186|CDS|ABC-type	3.5	1.0	15.9	NA	NA	hypothetical protein
BFych464512|CDS|putative	1.8	0.5	15.9	NA	NA	hypothetical protein
BDI0267|CDS|putative	7.0	2.0	15.9	NA	NA	hypothetical protein
b3469|CDS|zinc,	7.0	2.0	15.9	NA	NA	hypothetical protein
BDI0162|CDS|hypothetical	14.0	4.0	15.9	NA	NA	hypothetical protein
BFnctc2392|CDS|queuine	3.5	1.0	15.9	NA	NA	hypothetical protein
Bcap3279|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
BFnctc2916|CDS|putative	3.5	1.0	15.9	NA	NA	hypothetical protein
TS29Rum03119|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
Dfor0622|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BFnctc4151|CDS|putative	3.5	1.0	15.9	NA	NA	hypothetical protein
Aput1107|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
b0214|CDS|ribonuclease	3.5	1.0	15.9	NA	NA	hypothetical protein
TS28Rum08483|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
TS28Fae18875|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
b0833|CDS|conserved	3.5	1.0	15.9	NA	NA	hypothetical protein
TS28Eub0619|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BactD23165|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BDI0942|CDS|putative	7.0	2.0	15.9	NA	NA	hypothetical protein
TS28Met1040|CDS|CDS	1.8	0.5	15.9	NA	NA	hypothetical protein
TS29Met0453|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BDI1873|CDS|hypothetical	7.0	2.0	15.9	NA	NA	hypothetical protein
TS28Rum10914|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BFych464014|CDS|hypothetical	3.5	1.0	15.9	NA	NA	hypothetical protein
BDI0388|CDS|hypothetical	14.0	4.0	15.9	NA	NA	hypothetical protein
Aput1571|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
TS29Bac01993|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BFych462758|CDS|glutaminyl-tRNA	3.5	1.0	15.9	NA	NA	hypothetical protein
BFych462303|CDS|tRNA-guanine	3.5	1.0	15.9	NA	NA	hypothetical protein
TS29Ali283|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
TS29Par069|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
b2805|CDS|DNA-binding	3.5	1.0	15.9	NA	NA	hypothetical protein
Ccom1306|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BFnctc3788|CDS|hypothetical	3.5	1.0	15.9	NA	NA	hypothetical protein
Dfor3176|CDS|CDS	3.5	1.0	15.9	NA	NA	hypothetical protein
BDI3817|CDS|hypothetical	7.0	2.0	15.9	NA	NA	hypothetical protein
Dlon0994|CDS|CDS	7.0	2.0	15.9	NA	NA	hypothetical protein
TS28Rum01427|CDS|CDS	1.8	0.5	15.9	NA	NA	hypothetical protein
BDI1312|CDS|putative	7.0	2.0	15.9	NA	NA	hypothetical protein
BFych461633|CDS|putative	7.0	2.0	15.9	NA	NA	hypothetical protein
TS28Bac2690|CDS|CDS	2.3	0.7	15.9	NA	NA	hypothetical protein
BFnctc4005|CDS|elongation	19.2	5.5	15.8	NA	NA	hypothetical protein
TS29Bac07465|CDS|CDS	8.7	2.5	15.8	NA	NA	hypothetical protein
BFych460987|CDS|outer	9.8	2.8	15.8	NA	NA	hypothetical protein
Bfra31121758|CDS|CDS	3.5	1.0	15.7	NA	NA	hypothetical protein
TS29Par767|CDS|CDS	224.9	65.0	15.7	NA	NA	hypothetical protein
TS29Fae08625|CDS|CDS	58.5	17.0	15.6	NA	NA	hypothetical protein
BactD11585|CDS|CDS	1.7	0.5	15.6	NA	NA	hypothetical protein
BDI2052|CDS|GTP	24.0	7.0	15.6	NA	NA	hypothetical protein
TS29Bac02922|CDS|CDS	24.0	7.0	15.6	NA	NA	hypothetical protein
Aput2282|CDS|CDS	24.0	7.0	15.6	NA	NA	hypothetical protein
BFych461684|CDS|peptide	12.0	3.5	15.6	NA	NA	hypothetical protein
BFych464180|CDS|50S	5.1	1.5	15.5	NA	NA	hypothetical protein
BFnctc4002|CDS|50S	5.1	1.5	15.5	NA	NA	hypothetical protein
BactD12171|CDS|CDS	6.8	2.0	15.5	NA	NA	hypothetical protein
BDI0963|CDS|peptidase,	20.5	6.0	15.5	NA	NA	hypothetical protein
Buni2098|CDS|CDS	6.8	2.0	15.5	NA	NA	hypothetical protein
BFych464155|CDS|DNA-directed	11.9	3.5	15.5	NA	NA	hypothetical protein
BactD13477|CDS|CDS	2.8	0.8	15.4	NA	NA	hypothetical protein
Aput0220|CDS|CDS	17.0	5.0	15.4	NA	NA	hypothetical protein
BDI0418|CDS|putative	17.0	5.0	15.4	NA	NA	hypothetical protein
BDI3564|CDS|putative	8.5	2.5	15.4	NA	NA	hypothetical protein
Msm0740|CDS|50S	0.9	0.3	15.4	NA	NA	hypothetical protein
BFych462492|CDS|hypothetical	3.4	1.0	15.4	NA	NA	hypothetical protein
TS29Fae06535|CDS|CDS	1.7	0.5	15.4	NA	NA	hypothetical protein
TS29Bac01262|CDS|CDS	27.0	8.0	15.3	NA	NA	hypothetical protein
Even1735|CDS|CDS	1.1	0.3	15.3	NA	NA	hypothetical protein
Ccom2237|CDS|CDS	4.5	1.3	15.3	NA	NA	hypothetical protein

BDI2942|CDS|renin-binding	27.0	8.0	15.3	NA	NA	hypothetical protein
TS28Rum03074|CDS|CDS	13.5	4.0	15.3	NA	NA	hypothetical protein
TS28Fae17156|CDS|CDS	37.0	11.0	15.3	NA	NA	hypothetical protein
Bxyl2493|CDS|CDS	10.0	3.0	15.2	NA	NA	hypothetical protein
TS29Rum05558|CDS|CDS	1.7	0.5	15.1	NA	NA	hypothetical protein
Buni2312|CDS|CDS	1.7	0.5	15.1	NA	NA	hypothetical protein
BFnctc0984|CDS|putative	1.7	0.5	15.1	NA	NA	hypothetical protein
b4079|CDS|formate	1.7	0.5	15.1	NA	NA	hypothetical protein
Buni2886|CDS|CDS	3.3	1.0	15.1	NA	NA	hypothetical protein
BactD10380|CDS|CDS	1.7	0.5	15.1	NA	NA	hypothetical protein
TS29Rum18831|CDS|CDS	3.3	1.0	15.1	NA	NA	hypothetical protein
TS29Fae00280|CDS|CDS	15.0	4.5	15.1	NA	NA	hypothetical protein
TS28Rum15918|CDS|CDS	3.3	1.0	15.1	NA	NA	hypothetical protein
BactD10196|CDS|CDS	3.3	1.0	15.1	NA	NA	hypothetical protein
BFych461655|CDS|aldose	5.0	1.5	15.1	NA	NA	hypothetical protein
BDI2742|CDS|carboxylesterase	20.0	6.0	15.1	NA	NA	hypothetical protein
TS29RumUnc0578|CDS|CDS	5.0	1.5	15.1	NA	NA	hypothetical protein
BDI3691|CDS|orotate	10.0	3.0	15.1	NA	NA	hypothetical protein
TS28RumUnc1575|CDS|CDS	5.0	1.5	15.1	NA	NA	hypothetical protein
BDI3566|CDS|prolipoprotein	5.0	1.5	15.1	NA	NA	hypothetical protein
BDI3152|CDS|N-acetylglucosamine-6-phosphate	10.0	3.0	15.1	NA	NA	hypothetical protein
BactD21952|CDS|CDS	10.0	3.0	15.1	NA	NA	hypothetical protein
BDI1220|CDS|outer	10.0	3.0	15.1	NA	NA	hypothetical protein
TS28Rum15592|CDS|CDS	5.0	1.5	15.1	NA	NA	hypothetical protein
TS28Fae07353|CDS|CDS	10.0	3.0	15.1	NA	NA	hypothetical protein
BFnctc0481|CDS|putative	5.0	1.5	15.1	NA	NA	hypothetical protein
TS29Clo2365|CDS|CDS	10.0	3.0	15.1	NA	NA	hypothetical protein
BFych462944|CDS|hypothetical	10.0	3.0	15.1	NA	NA	hypothetical protein
TS28Clo09183|CDS|CDS	10.0	3.0	15.1	NA	NA	hypothetical protein
BDI0645|CDS|putative	10.0	3.0	15.1	NA	NA	hypothetical protein
Msm1376|CDS|DNA-directed	2.5	0.8	15.1	NA	NA	hypothetical protein
BDI1107|CDS|phosphoserine	10.0	3.0	15.1	NA	NA	hypothetical protein
TS29Bac10312|CDS|CDS	3.3	1.0	15.1	NA	NA	hypothetical protein
Bxyl1179|CDS|CDS	3.3	1.0	15.1	NA	NA	hypothetical protein
TS29Rum09521|CDS|CDS	1.7	0.5	15.1	NA	NA	hypothetical protein
BFych461264|CDS|hypothetical	1.7	0.5	15.1	NA	NA	hypothetical protein
TS29Bac06300|CDS|CDS	1.7	0.5	15.1	NA	NA	hypothetical protein
TS28Fae22716|CDS|CDS	109.0	33.0	15.0	NA	NA	hypothetical protein
Aput1806|CDS|CDS	16.5	5.0	15.0	NA	NA	hypothetical protein
Aput2021|CDS|CDS	36.0	11.0	14.9	NA	NA	hypothetical protein
BDI2767|CDS|hypothetical	49.0	15.0	14.8	NA	NA	hypothetical protein
TS29Fae05190|CDS|CDS	21.2	6.5	14.8	NA	NA	hypothetical protein
CspM6210548|CDS|CDS	6.5	2.0	14.8	NA	NA	hypothetical protein
BDI3086|CDS|hypothetical	13.0	4.0	14.8	NA	NA	hypothetical protein
BDI2069|CDS|ketol-acid	13.0	4.0	14.8	NA	NA	hypothetical protein
BFych464513|CDS|NAD-dependent	3.3	1.0	14.8	NA	NA	hypothetical protein
Dfor0044|CDS|CDS	13.0	4.0	14.8	NA	NA	hypothetical protein
Aput1134|CDS|CDS	13.0	4.0	14.8	NA	NA	hypothetical protein
BFych463388|CDS|hypothetical	6.5	2.0	14.8	NA	NA	hypothetical protein
BDI2999|CDS|putative	13.0	4.0	14.8	NA	NA	hypothetical protein
BDI0506|CDS|D-3-phosphoglycerate	13.0	4.0	14.8	NA	NA	hypothetical protein
Aput2049|CDS|CDS	13.0	4.0	14.8	NA	NA	hypothetical protein
Bint0432|CDS|CDS	4.8	1.5	14.7	NA	NA	hypothetical protein
Bple2877|CDS|CDS	16.0	5.0	14.5	NA	NA	hypothetical protein
TS29Rum00391|CDS|CDS	8.0	2.5	14.5	NA	NA	hypothetical protein
Bxyl1750|CDS|CDS	1.9	0.6	14.5	NA	NA	hypothetical protein
TS29Rum13795|CDS|CDS	102.0	32.0	14.5	NA	NA	hypothetical protein
TS28Fae12703|CDS|CDS	66.9	21.0	14.5	NA	NA	hypothetical protein
BFych463028|CDS|iron(III)	1.5	0.5	14.4	NA	NA	hypothetical protein
BT1952|CDS|Fe3+	1.5	0.5	14.4	NA	NA	hypothetical protein
FpraM2121791|CDS|CDS	3.2	1.0	14.4	NA	NA	hypothetical protein
TS29Rum03409|CDS|CDS	3.2	1.0	14.4	NA	NA	hypothetical protein
b4179|CDS|exoribonuclease	3.2	1.0	14.4	NA	NA	hypothetical protein
BFych463862|CDS|30S	3.2	1.0	14.4	NA	NA	hypothetical protein
BFnctc3632|CDS|30S	3.2	1.0	14.4	NA	NA	hypothetical protein
TS28Fae03016|CDS|CDS	9.5	3.0	14.4	NA	NA	hypothetical protein
TS29Rum20960|CDS|CDS	19.0	6.0	14.4	NA	NA	hypothetical protein
TS28Fae16391|CDS|CDS	9.5	3.0	14.4	NA	NA	hypothetical protein
BDI1516|CDS|putative	19.0	6.0	14.4	NA	NA	hypothetical protein
BT4530|CDS|ATP-dependent	3.2	1.0	14.4	NA	NA	hypothetical protein
BFnctc3636|CDS|elongation	14.2	4.5	14.3	NA	NA	hypothetical protein
Bcoproc1930|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
BT1954|CDS|putative	0.7	0.2	14.3	NA	NA	hypothetical protein
Bfin1128|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
BactD11321|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
BFych463030|CDS|putative	0.7	0.2	14.3	NA	NA	hypothetical protein
Bthe3733899|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
TS28Par0018|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
Bxyl1216|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
Bthe7332528|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
Bste0640|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
Begg0850|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
Buni2205|CDS|CDS	0.7	0.2	14.3	NA	NA	hypothetical protein
TS28Fae07518|CDS|CDS	11.0	3.5	14.3	NA	NA	hypothetical protein
BDI2619|CDS|30S	22.0	7.0	14.3	NA	NA	hypothetical protein
TS29Rum00032|CDS|CDS	429.0	137.0	14.2	NA	NA	hypothetical protein
TS28Clo02972|CDS|CDS	12.5	4.0	14.2	NA	NA	hypothetical protein
b3339|CDS|protein	2.6	0.8	14.1	NA	NA	hypothetical protein
TS28Rum14450|CDS|CDS	14.0	4.5	14.1	NA	NA	hypothetical protein
TS28Bif3719|CDS|CDS	28.0	9.0	14.1	NA	NA	hypothetical protein
TS28Bac1539|CDS|CDS	20.7	6.7	14.1	NA	NA	hypothetical protein
Bxyl1852|CDS|CDS	4.7	1.5	14.1	NA	NA	hypothetical protein
TS29Bac05580|CDS|CDS	15.5	5.0	14.1	NA	NA	hypothetical protein
Bova2063|CDS|CDS	2.6	0.8	14.1	NA	NA	hypothetical protein
BFych464158|CDS|30S	3.1	1.0	14.0	NA	NA	hypothetical protein

BFnctc3979|CDS|30S	3.1	1.0	14.0	NA	NA	hypothetical protein
FpraM2120716|CDS|CDS	6.2	2.0	14.0	NA	NA	hypothetical protein
TS28Bac2868|CDS|CDS	3.1	1.0	14.0	NA	NA	hypothetical protein
Bxyl0795|CDS|CDS	3.1	1.0	14.0	NA	NA	hypothetical protein
Bsp1160220|CDS|CDS	3.1	1.0	14.0	NA	NA	hypothetical protein
Bova1808|CDS|CDS	3.1	1.0	13.9	NA	NA	hypothetical protein
BactD20607|CDS|CDS	3.1	1.0	13.9	NA	NA	hypothetical protein
BFnctc3635|CDS|two-component	4.6	1.5	13.9	NA	NA	hypothetical protein
Buni1690|CDS|CDS	8.7	2.8	13.9	NA	NA	hypothetical protein
Bova2231|CDS|CDS	131.4	43.0	13.9	NA	NA	hypothetical protein
TS28Bac1458|CDS|CDS	6.1	2.0	13.9	NA	NA	hypothetical protein
BL1402|CDS|response	4.8	1.6	13.9	NA	NA	hypothetical protein
BFnctc2747|CDS|V-type	4.5	1.5	13.7	NA	NA	hypothetical protein
str0120|CDS|molecular	2.0	0.7	13.6	NA	NA	hypothetical protein
stu0120|CDS|molecular	2.0	0.7	13.6	NA	NA	hypothetical protein
STER0163|CDS|molecular	2.0	0.7	13.6	NA	NA	hypothetical protein
BactD10965|CDS|CDS	2.0	0.7	13.6	NA	NA	hypothetical protein
TS29Bac08870|CDS|CDS	2.0	0.7	13.6	NA	NA	hypothetical protein
Buni2773|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Begg2764|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Bova2586|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
BLD0800|CDS|Putative	1.0	0.3	13.6	NA	NA	hypothetical protein
b3340|CDS|protein	1.0	0.3	13.6	NA	NA	hypothetical protein
Buni3634|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Buni0427|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
stu1647|CDS|putative	1.0	0.3	13.6	NA	NA	hypothetical protein
str1647|CDS|putative	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bac1133|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Bxyl2960|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
BFnctc0389|CDS|putative	1.0	0.3	13.6	NA	NA	hypothetical protein
Bxyl2881|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Msm1537|CDS|predicted	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bif2241|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bac2159|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
BT4002|CDS|ATPase,	1.0	0.3	13.6	NA	NA	hypothetical protein
Bsp1162318|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Bova1186|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
BL1049|CDS|hypothetical	1.0	0.3	13.6	NA	NA	hypothetical protein
stu1748|CDS|excinuclease	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Rum06604|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
str0608|CDS|ferrous	1.0	0.3	13.6	NA	NA	hypothetical protein
Buni2968|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
TS29Rum10519|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Pmer0679|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bac1563|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Hfil2895|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
b2320|CDS|erythronate-4-phosphate	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bac2180|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
Msm1341|CDS|isoleucyl-tRNA	1.0	0.3	13.6	NA	NA	hypothetical protein
TS29Bac01685|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bac1236|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
BFych464588|CDS|putative	1.0	0.3	13.6	NA	NA	hypothetical protein
Dfor2558|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
STER0654|CDS|Fe2+	1.0	0.3	13.6	NA	NA	hypothetical protein
stu0608|CDS|ferrous	1.0	0.3	13.6	NA	NA	hypothetical protein
TS28Bac6454|CDS|CDS	1.0	0.3	13.6	NA	NA	hypothetical protein
BLD1741|CDS|hypothetical	2.0	0.7	13.6	NA	NA	hypothetical protein
b0366|CDS|taurine	1.5	0.5	13.6	NA	NA	hypothetical protein
BactD20149|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Aput2043|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
TS29Rum18531|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BactD21371|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI2710|CDS|NAD-dependent	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Fae01359|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Eub0683|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI0514|CDS|electron	6.0	2.0	13.6	NA	NA	hypothetical protein
TS29Bac03373|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Clo03129|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Fae17102|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum02547|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
Buni2172|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum09757|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Msm0243|CDS|exosome	1.5	0.5	13.6	NA	NA	hypothetical protein
Bxyl2147|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI0797|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Fae09944|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI2367|CDS|30S	3.0	1.0	13.6	NA	NA	hypothetical protein
Aste0198|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI1195|CDS|hypothetical	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Clo08150|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Cmet0659|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Rgna2178|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
Buni1101|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
Rbro0647|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
b3941|CDS|5,10-methylenetetrahydrofolate	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI1036|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI1523|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
Bcoproc0593|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28RumUnc2041|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI0166|CDS|putative	3.0	1.0	13.6	NA	NA	hypothetical protein
BactD11118|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Col1358|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Fae06200|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI3814|CDS|putative	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI1077|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein

Aput1028|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
Bxyl2365|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI0323|CDS|hypothetical	6.0	2.0	13.6	NA	NA	hypothetical protein
RintL11124|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum01194|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Fae10176|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych462647|CDS|iron-containing	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Fae22013|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Rtor0789|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Rtor1141|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc0880|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc1940|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
b3256|CDS|acetyl-CoA	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych463899|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28RumUnc1577|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFnctc0226|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc0447|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum09941|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Dfor1354|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFnctc2670|CDS|putative	6.0	2.0	13.6	NA	NA	hypothetical protein
TS29Rum00247|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
Ccom1445|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI2030|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI3744|CDS|arginine/ornithine	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum12520|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum12576|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
HPAG11487|CDS|ubiquinol	3.0	1.0	13.6	NA	NA	hypothetical protein
Cbol0269|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych461494|CDS|cytidine	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Dor1446|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
ShigspD92851|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
Buni0936|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
M23Apeg2174|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych462408|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum17969|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych460602|CDS|LuxR	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI0955|CDS|putative	15.0	5.0	13.6	NA	NA	hypothetical protein
TS28Rum13911|CDS|CDS	7.5	2.5	13.6	NA	NA	hypothetical protein
EUBREC1485|CDS|ribosomal	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Fae07331|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BFnctc1315|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych460502|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
b3052|CDS|fused	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI0312|CDS|glycine	6.0	2.0	13.6	NA	NA	hypothetical protein
BFnctc3247|CDS|putative	6.0	2.0	13.6	NA	NA	hypothetical protein
Aput0539|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
TS28Rum12867|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych461327|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum00252|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Casp0144|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI2758|CDS|transcription	6.0	2.0	13.6	NA	NA	hypothetical protein
TS29Clo2463|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Aput0686|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Fae12298|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BFnctc4084|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
BLD1715|CDS|Ribosomal	0.8	0.3	13.6	NA	NA	hypothetical protein
HPAG10287|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
b3956|CDS|phosphoenolpyruvate	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc3191|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
Aput1693|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
Bcoprop1580|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
b3502|CDS|arsenite/antimonite	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych462360|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum00379|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Aput0502|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
b2292|CDS|predicted	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI3568|CDS|glucosamine-6-phosphate	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI0761|CDS|folylpolyglutamate	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI3171|CDS|glycine	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych464543|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc0136|CDS|putative	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI2946|CDS|glycoside	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych462747|CDS|dipeptidyl	3.0	1.0	13.6	NA	NA	hypothetical protein
Msm0792|CDS|predicted	0.8	0.3	13.6	NA	NA	hypothetical protein
RintL11545|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Bthe3732252|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
RintL10676|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Fae05600|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Clo05010|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI2583|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
FpraM2120057|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Cbol0587|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Aput1434|CDS|CDS	15.0	5.0	13.6	NA	NA	hypothetical protein
TS29Fae06504|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
b0412|CDS|predicted	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum16374|CDS|CDS	15.0	5.0	13.6	NA	NA	hypothetical protein
BDI0776|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
Cbar1101|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFnctc3398|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych461331|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
Bxyl1017|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
Rgna1037|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Dor0678|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Msm1430|CDS|ribosomal	0.8	0.3	13.6	NA	NA	hypothetical protein
Msm0268|CDS|cysteinyl-tRNA	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum18572|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein

TS28Rum02626|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Clo05766|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum13304|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Ali093|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
Msm1245|CDS|DNA-binding	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI0331|CDS|putative	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI3363|CDS|putative	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum14018|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Aput0968|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
Aput0254|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Rum05014|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Fae05334|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
RintL10310|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Rgna2483|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Ali357|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BL1588|CDS|50S	0.8	0.3	13.6	NA	NA	hypothetical protein
TS29Ali240|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS29Rum12260|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum16643|CDS|CDS	15.0	5.0	13.6	NA	NA	hypothetical protein
TS29Dor0920|CDS|CDS	15.0	5.0	13.6	NA	NA	hypothetical protein
b1502|CDS|predicted	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum10744|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Clep0634|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI1140|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
Buni3333|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Par196|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Bthe3733487|CDS|CDS	16.5	5.5	13.6	NA	NA	hypothetical protein
BDI2562|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum07663|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
Clep1381|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BFnctc0486|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych460270|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
b0212|CDS|predicted	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Rum01652|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
Buni0052|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc1176|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Fae05102|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Fae21143|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI3297|CDS|putative	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych462737|CDS|two-component	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Rum12471|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI3750|CDS|putative	6.0	2.0	13.6	NA	NA	hypothetical protein
Buni1074|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Clo09439|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Bif4717|CDS|CDS	0.6	0.2	13.6	NA	NA	hypothetical protein
Rtor0382|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum05444|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Csci2017|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Met0789|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Fae03671|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych461047|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Clo09575|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BDI0798|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
b4174|CDS|modulator	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28RumUnc1927|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum20005|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Even0032|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
b2118|CDS|conserved	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29RumUnc1006|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum14457|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS29Dor1871|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Eub1208|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum04484|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
EUBREC2954|CDS|two-component	1.5	0.5	13.6	NA	NA	hypothetical protein
Cbol3415|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Rum05973|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum03515|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych463594|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI0504|CDS|recombination	15.0	5.0	13.6	NA	NA	hypothetical protein
Aput0854|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BFych464411|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Fae19327|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFych461641|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
Ccom1591|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Caer1622|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Buni0563|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Clo02716|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BFych463291|CDS|biotin	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Rum12414|CDS|CDS	33.0	11.0	13.6	NA	NA	hypothetical protein
TS28RumUnc1357|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Dfor2089|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
BFnctc0159|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
Buni0852|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
EUBREC1464|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum02103|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
EUBREC2145|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
Dfor2351|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
PRABACTJOHN3100|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI1892|CDS|hypothetical	6.0	2.0	13.6	NA	NA	hypothetical protein
BFych461878|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc3669|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
Dlon0170|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
HPAG11274|CDS|cation	3.0	1.0	13.6	NA	NA	hypothetical protein
b2154|CDS|predicted	3.0	1.0	13.6	NA	NA	hypothetical protein
EUBREC0191|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
BL0130|CDS|hypothetical	0.8	0.3	13.6	NA	NA	hypothetical protein

Dlon0829|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
M23Apeg955|CDS|Lysyl-tRNA	3.0	1.0	13.6	NA	NA	hypothetical protein
TS28Rum03008|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc0963|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
BactD23113|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
FpraM2121468|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI3548|CDS|glutamine	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Met1032|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI3210|CDS|putative	6.0	2.0	13.6	NA	NA	hypothetical protein
BFych462606|CDS|putative	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Fae15376|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFnctc3043|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
TS28Fae09585|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Met0785|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum17974|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
Pmer3259|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFych463404|CDS|hypothetical	6.0	2.0	13.6	NA	NA	hypothetical protein
TS29Met0145|CDS|CDS	12.0	4.0	13.6	NA	NA	hypothetical protein
BDI2587|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum10233|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum06777|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BFnctc0552|CDS|LuxR	1.5	0.5	13.6	NA	NA	hypothetical protein
EUBREC2887|CDS|two-component	3.0	1.0	13.6	NA	NA	hypothetical protein
BactD21951|CDS|CDS	6.0	2.0	13.6	NA	NA	hypothetical protein
TS28Eub8163|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BFnctc4156|CDS|hypothetical	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Clo2125|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum21188|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Bple1104|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
TS29Ali242|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum03532|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum17630|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum09927|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BLD1403|CDS|LacI-type	3.0	1.0	13.6	NA	NA	hypothetical protein
TS29Rum18848|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
FpraM2122044|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI2495|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
BDI2113|CDS|hypothetical	3.0	1.0	13.6	NA	NA	hypothetical protein
Aput0099|CDS|CDS	3.0	1.0	13.6	NA	NA	hypothetical protein
Robe0271|CDS|CDS	1.5	0.5	13.6	NA	NA	hypothetical protein
BDI1081|CDS|putative	9.0	3.0	13.6	NA	NA	hypothetical protein
TS28Clo02771|CDS|CDS	18.0	6.0	13.6	NA	NA	hypothetical protein
BDI1733|CDS|malic	36.0	12.0	13.6	NA	NA	hypothetical protein
BDI2353|CDS|50S	9.0	3.0	13.6	NA	NA	hypothetical protein
Aput1061|CDS|CDS	9.0	3.0	13.6	NA	NA	hypothetical protein
TS29Ali150|CDS|CDS	4.5	1.5	13.6	NA	NA	hypothetical protein
BDI2388|CDS|hypothetical	9.0	3.0	13.6	NA	NA	hypothetical protein
Caer1870|CDS|CDS	4.5	1.5	13.6	NA	NA	hypothetical protein
BDI2001|CDS|putative	9.0	3.0	13.6	NA	NA	hypothetical protein
Aput1346|CDS|CDS	9.0	3.0	13.6	NA	NA	hypothetical protein
Aput1119|CDS|CDS	4.5	1.5	13.6	NA	NA	hypothetical protein
BDI2507|CDS|hypothetical	9.0	3.0	13.6	NA	NA	hypothetical protein
TS28Fae18501|CDS|CDS	4.5	1.5	13.6	NA	NA	hypothetical protein
Caer2210|CDS|CDS	4.5	1.5	13.6	NA	NA	hypothetical protein
TS28Fae09498|CDS|CDS	9.0	3.0	13.6	NA	NA	hypothetical protein
BDI0519|CDS|CTP	9.0	3.0	13.6	NA	NA	hypothetical protein
BLD0587|CDS|Ribosomal	2.3	0.8	13.6	NA	NA	hypothetical protein
BDI0354|CDS|hypothetical	9.0	3.0	13.6	NA	NA	hypothetical protein
TS28Fae18377|CDS|CDS	9.0	3.0	13.6	NA	NA	hypothetical protein
BDI2086|CDS|nicotinate-nucleotide	9.0	3.0	13.6	NA	NA	hypothetical protein
Bxyl0201|CDS|CDS	2.0	0.7	13.6	NA	NA	hypothetical protein
BFnctc2510|CDS|50S	6.0	2.0	13.5	NA	NA	hypothetical protein
Bxyl0240|CDS|CDS	3.0	1.0	13.5	NA	NA	hypothetical protein
BFych461043|CDS|30S	8.9	3.0	13.5	NA	NA	hypothetical protein
BDI2374|CDS|30S	17.8	6.0	13.5	NA	NA	hypothetical protein
TS29Rum13372|CDS|CDS	31.2	10.5	13.5	NA	NA	hypothetical protein
BL1593|CDS|30S	3.7	1.3	13.4	NA	NA	hypothetical protein
BLD1720|CDS|Ribosomal	3.7	1.3	13.4	NA	NA	hypothetical protein
Bxyl4456|CDS|CDS	1.5	0.5	13.4	NA	NA	hypothetical protein
Rtor1548|CDS|CDS	59.0	20.0	13.4	NA	NA	hypothetical protein
BL1596|CDS|50S	2.5	0.8	13.3	NA	NA	hypothetical protein
Buni3209|CDS|CDS	5.9	2.0	13.3	NA	NA	hypothetical protein
BactD12790|CDS|CDS	3.9	1.3	13.3	NA	NA	hypothetical protein
TS29Rum15668|CDS|CDS	47.0	16.0	13.3	NA	NA	hypothetical protein
BFych462527|CDS|superoxide	5.8	2.0	13.2	NA	NA	hypothetical protein
TS28Rum14949|CDS|CDS	17.5	6.0	13.2	NA	NA	hypothetical protein
BDI2252|CDS|delta-1-pyrroline-5-carboxylate	17.5	6.0	13.2	NA	NA	hypothetical protein
BFych461552|CDS|ribonuclease	4.4	1.5	13.2	NA	NA	hypothetical protein
TS29Bac08532|CDS|CDS	3.9	1.3	13.2	NA	NA	hypothetical protein
Aput1267|CDS|CDS	29.0	10.0	13.2	NA	NA	hypothetical protein
TS29Bac11379|CDS|CDS	14.5	5.0	13.2	NA	NA	hypothetical protein
TS29Fae08572|CDS|CDS	87.0	30.0	13.2	NA	NA	hypothetical protein
Msm1122|CDS|coenzyme	2.9	1.0	13.2	NA	NA	hypothetical protein
BFnctc1919|CDS|6-phosphogluconate	4.3	1.5	13.1	NA	NA	hypothetical protein
Rgna2802|CDS|CDS	15.8	5.5	13.1	NA	NA	hypothetical protein
Rgna3025|CDS|CDS	15.8	5.5	13.1	NA	NA	hypothetical protein
BFnctc3976|CDS|DNA-directed	12.9	4.5	13.1	NA	NA	hypothetical protein
CspM6211856|CDS|CDS	1.4	0.5	13.0	NA	NA	hypothetical protein
Dfor2025|CDS|CDS	1.4	0.5	13.0	NA	NA	hypothetical protein
TS29Rum15985|CDS|CDS	31.5	11.0	13.0	NA	NA	hypothetical protein
BVU0817|CDS|50S	2.9	1.0	13.0	NA	NA	hypothetical protein
TS28Rum13299|CDS|CDS	41.5	14.5	13.0	NA	NA	hypothetical protein
BactD14398|CDS|CDS	1.7	0.6	13.0	NA	NA	hypothetical protein
Rbro0754|CDS|CDS	6.7	2.3	13.0	NA	NA	hypothetical protein
Aput0883|CDS|CDS	20.0	7.0	13.0	NA	NA	hypothetical protein

Bxyl4371|CDS|CDS	20.3	7.2	12.9	NA	NA	hypothetical protein
BFych464142|CDS|outer	2.8	1.0	12.9	NA	NA	hypothetical protein
TS29Bac09227|CDS|CDS	8.5	3.0	12.9	NA	NA	hypothetical protein
TS28Fae10681|CDS|CDS	8.5	3.0	12.9	NA	NA	hypothetical protein
BFnctc3619|CDS|putative	8.5	3.0	12.9	NA	NA	hypothetical protein
TS28Fae20999|CDS|CDS	17.0	6.0	12.9	NA	NA	hypothetical protein
TS29Fae07524|CDS|CDS	34.0	12.0	12.9	NA	NA	hypothetical protein
Bxyl1306|CDS|CDS	8.5	3.0	12.9	NA	NA	hypothetical protein
TS29Bac02966|CDS|CDS	17.0	6.0	12.9	NA	NA	hypothetical protein
b0575|CDS|copper/silver	2.8	1.0	12.9	NA	NA	hypothetical protein
TS29Bac05130|CDS|CDS	31.2	11.0	12.9	NA	NA	hypothetical protein
BFnctc0853|CDS|GFO/IDH/MOCA	2.8	1.0	12.9	NA	NA	hypothetical protein
BFnctc1033|CDS|GTPase	2.8	1.0	12.9	NA	NA	hypothetical protein
BactD21104|CDS|CDS	4.5	1.6	12.9	NA	NA	hypothetical protein
Bova2381|CDS|CDS	4.5	1.6	12.9	NA	NA	hypothetical protein
BactD20603|CDS|CDS	1.4	0.5	12.8	NA	NA	hypothetical protein
BFych464184|CDS|30S	4.2	1.5	12.8	NA	NA	hypothetical protein
BFnctc4006|CDS|30S	4.2	1.5	12.8	NA	NA	hypothetical protein
TS29Fae03277|CDS|CDS	15.5	5.5	12.8	NA	NA	hypothetical protein
TS28Fae12015|CDS|CDS	15.5	5.5	12.8	NA	NA	hypothetical protein
TS29Rum16964|CDS|CDS	98.5	35.0	12.8	NA	NA	hypothetical protein
BDI2760|CDS|polynucleotide	16.8	6.0	12.7	NA	NA	hypothetical protein
BFych464183|CDS|elongation	18.2	6.5	12.7	NA	NA	hypothetical protein
FpraM2121831|CDS|CDS	14.0	5.0	12.7	NA	NA	hypothetical protein
BDI3087|CDS|putative	14.0	5.0	12.7	NA	NA	hypothetical protein
BDI2654|CDS|hypothetical	7.0	2.5	12.7	NA	NA	hypothetical protein
BDI2437|CDS|hypothetical	7.0	2.5	12.7	NA	NA	hypothetical protein
Buni1543|CDS|CDS	7.0	2.5	12.7	NA	NA	hypothetical protein
BDI3003|CDS|hypothetical	14.0	5.0	12.7	NA	NA	hypothetical protein
BactD21953|CDS|CDS	14.0	5.0	12.7	NA	NA	hypothetical protein
BDI1125|CDS|Na(+)-translocating	14.0	5.0	12.7	NA	NA	hypothetical protein
BDI2394|CDS|ATP-dependent	28.0	10.0	12.7	NA	NA	hypothetical protein
Dfor2606|CDS|CDS	1.4	0.5	12.7	NA	NA	hypothetical protein
Msm0738|CDS|preprotein	0.7	0.3	12.7	NA	NA	hypothetical protein
FpraM2121821|CDS|CDS	16.8	6.0	12.7	NA	NA	hypothetical protein
Bxyl2955|CDS|CDS	19.5	7.0	12.6	NA	NA	hypothetical protein
BDI0409|CDS|hypothetical	12.5	4.5	12.6	NA	NA	hypothetical protein
TS28Fae12105|CDS|CDS	12.5	4.5	12.6	NA	NA	hypothetical protein
Bxyl3201|CDS|CDS	6.9	2.5	12.6	NA	NA	hypothetical protein
BFych464194|CDS|50S	5.5	2.0	12.6	NA	NA	hypothetical protein
b2283|CDS|NADH:ubiquinone	5.5	2.0	12.5	NA	NA	hypothetical protein
TS29Rum18719|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
Bsp1163983|CDS|CDS	2.8	1.0	12.5	NA	NA	hypothetical protein
Aput1496|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
BDI1524|CDS|hypothetical	11.0	4.0	12.5	NA	NA	hypothetical protein
Buni1538|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
TS29Rum14196|CDS|CDS	22.0	8.0	12.5	NA	NA	hypothetical protein
Aput1935|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
TS29Rum00263|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
TS28Met0247|CDS|CDS	2.8	1.0	12.5	NA	NA	hypothetical protein
TS28Clo06825|CDS|CDS	5.5	2.0	12.5	NA	NA	hypothetical protein
TS29Ali379|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
BDI1553|CDS|1,4-dihydroxy-2-naphthoate	11.0	4.0	12.5	NA	NA	hypothetical protein
TS29Fae01564|CDS|CDS	11.0	4.0	12.5	NA	NA	hypothetical protein
BDI0799|CDS|DNA	11.0	4.0	12.5	NA	NA	hypothetical protein
BDI2862|CDS|hypothetical	11.0	4.0	12.5	NA	NA	hypothetical protein
Aput0608|CDS|CDS	16.5	6.0	12.5	NA	NA	hypothetical protein
Aput1285|CDS|CDS	27.5	10.0	12.5	NA	NA	hypothetical protein
TS29Bac03217|CDS|CDS	7.3	2.7	12.5	NA	NA	hypothetical protein
TS29Bac02111|CDS|CDS	24.7	9.0	12.4	NA	NA	hypothetical protein
BFych464446|CDS|phosphoenolpyruvate	12.3	4.5	12.4	NA	NA	hypothetical protein
Begg0961|CDS|CDS	6.8	2.5	12.4	NA	NA	hypothetical protein
TS28Rum13483|CDS|CDS	49.0	18.0	12.4	NA	NA	hypothetical protein
BFych463332|CDS|pyruvate-flavodoxin	8.6	3.2	12.4	NA	NA	hypothetical protein
BFych463370|CDS|hypothetical	9.5	3.5	12.3	NA	NA	hypothetical protein
Cbol1701|CDS|CDS	19.0	7.0	12.3	NA	NA	hypothetical protein
Buni3051|CDS|CDS	9.5	3.5	12.3	NA	NA	hypothetical protein
TS29Fae02498|CDS|CDS	9.5	3.5	12.3	NA	NA	hypothetical protein
BFnctc3200|CDS|putative	9.5	3.5	12.3	NA	NA	hypothetical protein
RintL13322|CDS|CDS	0.5	0.2	12.3	NA	NA	hypothetical protein
Bxyl4310|CDS|CDS	4.5	1.7	12.3	NA	NA	hypothetical protein
TS29Bac07429|CDS|CDS	4.5	1.7	12.3	NA	NA	hypothetical protein
Bova1547|CDS|CDS	1.4	0.5	12.3	NA	NA	hypothetical protein
Msm0795|CDS|heterodisulfide	7.0	2.6	12.2	NA	NA	hypothetical protein
TS29Met0829|CDS|CDS	86.0	32.0	12.2	NA	NA	hypothetical protein
Begg0964|CDS|CDS	2.7	1.0	12.1	NA	NA	hypothetical protein
b3966|CDS|vitamin	2.7	1.0	12.1	NA	NA	hypothetical protein
TS28Bac3208|CDS|CDS	2.7	1.0	12.1	NA	NA	hypothetical protein
Dfor1980|CDS|CDS	1.3	0.5	12.1	NA	NA	hypothetical protein
Msm0242|CDS|exosome	0.7	0.3	12.1	NA	NA	hypothetical protein
Robe2314|CDS|CDS	1.3	0.5	12.1	NA	NA	hypothetical protein
Rgna2949|CDS|CDS	1.3	0.5	12.1	NA	NA	hypothetical protein
Msm1137|CDS|DNA	1.2	0.5	12.1	NA	NA	hypothetical protein
FpraM2120965|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
BFych462411|CDS|DNA	12.0	4.5	12.1	NA	NA	hypothetical protein
FpraM2121503|CDS|CDS	16.0	6.0	12.1	NA	NA	hypothetical protein
TS28Fae03741|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
TS28Fae12539|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
Aput1677|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
b3940|CDS|fused	1.3	0.5	12.1	NA	NA	hypothetical protein
TS29Clo3970|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
TS28Clo02770|CDS|CDS	16.0	6.0	12.1	NA	NA	hypothetical protein
BDI0091|CDS|hypothetical	8.0	3.0	12.1	NA	NA	hypothetical protein
TS28Bif0100|CDS|CDS	4.0	1.5	12.1	NA	NA	hypothetical protein

BFych464492|CDS|putative	4.0	1.5	12.1	NA	NA	hypothetical protein
TS29Fae03298|CDS|CDS	16.0	6.0	12.1	NA	NA	hypothetical protein
BFnctc3543|CDS|aconitate	4.0	1.5	12.1	NA	NA	hypothetical protein
TS28Met0007|CDS|CDS	4.0	1.5	12.1	NA	NA	hypothetical protein
BDI1693|CDS|conserved	8.0	3.0	12.1	NA	NA	hypothetical protein
TS29Rum00813|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
BFnctc2947|CDS|putative	4.0	1.5	12.1	NA	NA	hypothetical protein
EUBREC0425|CDS|50S	5.3	2.0	12.1	NA	NA	hypothetical protein
FpraM2120242|CDS|CDS	4.0	1.5	12.1	NA	NA	hypothetical protein
TS28RumUnc1587|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
Aput1878|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
TS29Bac11403|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
BDI1035|CDS|hypothetical	8.0	3.0	12.1	NA	NA	hypothetical protein
TS28Clo02623|CDS|CDS	8.0	3.0	12.1	NA	NA	hypothetical protein
TS28Rum16259|CDS|CDS	4.0	1.5	12.1	NA	NA	hypothetical protein
TS28Clo04812|CDS|CDS	2.0	0.8	12.1	NA	NA	hypothetical protein
BFnctc1021|CDS|putative	4.0	1.5	12.1	NA	NA	hypothetical protein
TS28Ali1989|CDS|CDS	5.3	2.0	12.1	NA	NA	hypothetical protein
TS29Fae08739|CDS|CDS	5.3	2.0	12.1	NA	NA	hypothetical protein
Msm0759|CDS|50S	0.5	0.2	12.1	NA	NA	hypothetical protein
BFnctc3785|CDS|30S	2.7	1.0	12.1	NA	NA	hypothetical protein
BFnctc0497|CDS|hypothetical	1.3	0.5	12.1	NA	NA	hypothetical protein
Msm1125|CDS|predicted	1.3	0.5	12.1	NA	NA	hypothetical protein
TS28Bac3016|CDS|CDS	1.3	0.5	12.1	NA	NA	hypothetical protein
Clep1567|CDS|CDS	1.3	0.5	12.1	NA	NA	hypothetical protein
BFnctc3817|CDS|hypothetical	1.3	0.5	12.1	NA	NA	hypothetical protein
BFych462852|CDS|putative	57.2	21.6	12.0	NA	NA	hypothetical protein
Msmi740853|CDS|CDS	3.1	1.2	12.0	NA	NA	hypothetical protein
Msmi750833|CDS|CDS	3.1	1.2	12.0	NA	NA	hypothetical protein
BFnctc2492|CDS|negative	11.8	4.5	11.9	NA	NA	hypothetical protein
Msm0436|CDS|V-type	1.8	0.7	11.9	NA	NA	hypothetical protein
TS28Fae01246|CDS|CDS	21.0	8.0	11.9	NA	NA	hypothetical protein
BDI1450|CDS|saccharopine	10.5	4.0	11.9	NA	NA	hypothetical protein
BFych460569|CDS|hypothetical	10.5	4.0	11.9	NA	NA	hypothetical protein
Msm0642|CDS|cell	1.8	0.7	11.9	NA	NA	hypothetical protein
Ccom1585|CDS|CDS	7.8	3.0	11.9	NA	NA	hypothetical protein
b0886|CDS|fused	13.0	5.0	11.8	NA	NA	hypothetical protein
TS29Bac07110|CDS|CDS	13.0	5.0	11.8	NA	NA	hypothetical protein
TS29Fae03871|CDS|CDS	13.0	5.0	11.8	NA	NA	hypothetical protein
BFych461018|CDS|putative	6.5	2.5	11.8	NA	NA	hypothetical protein
BFych464079|CDS|FKBP-type	5.2	2.0	11.8	NA	NA	hypothetical protein
BDI0970|CDS|putative	13.0	5.0	11.8	NA	NA	hypothetical protein
TS29Bac08197|CDS|CDS	13.0	5.0	11.8	NA	NA	hypothetical protein
Bste2291|CDS|CDS	2.6	1.0	11.8	NA	NA	hypothetical protein
Msm1616|CDS|hypothetical	0.7	0.3	11.8	NA	NA	hypothetical protein
TS29Dor1749|CDS|CDS	13.0	5.0	11.8	NA	NA	hypothetical protein
BDI1504|CDS|hypothetical	13.0	5.0	11.8	NA	NA	hypothetical protein
Aput0967|CDS|CDS	13.0	5.0	11.8	NA	NA	hypothetical protein
Aput0615|CDS|CDS	13.0	5.0	11.8	NA	NA	hypothetical protein
BFnctc3904|CDS|3-oxoacyl-(acyl	6.5	2.5	11.8	NA	NA	hypothetical protein
b0014|CDS|chaperone	5.2	2.0	11.7	NA	NA	hypothetical protein
BT1953|CDS|putative	5.1	2.0	11.7	NA	NA	hypothetical protein
BFych463029|CDS|putative	5.1	2.0	11.7	NA	NA	hypothetical protein
Bste0641|CDS|CDS	5.2	2.0	11.7	NA	NA	hypothetical protein
TS28Rum14941|CDS|CDS	24.5	9.5	11.7	NA	NA	hypothetical protein
TS29Rum04362|CDS|CDS	33.5	13.0	11.7	NA	NA	hypothetical protein
TS29Rum20570|CDS|CDS	18.0	7.0	11.7	NA	NA	hypothetical protein
TS29Rum16602|CDS|CDS	18.0	7.0	11.7	NA	NA	hypothetical protein
BFnctc0021|CDS|putative	9.0	3.5	11.7	NA	NA	hypothetical protein
FpraM2120937|CDS|CDS	2.6	1.0	11.7	NA	NA	hypothetical protein
Rtor0135|CDS|CDS	29.5	11.5	11.6	NA	NA	hypothetical protein
BDI0389|CDS|malate	10.3	4.0	11.6	NA	NA	hypothetical protein
TS28Fae17103|CDS|CDS	3.8	1.5	11.6	NA	NA	hypothetical protein
TS29Fae09430|CDS|CDS	3.8	1.5	11.6	NA	NA	hypothetical protein
BFnctc3769|CDS|hypothetical	3.8	1.5	11.6	NA	NA	hypothetical protein
BFych463994|CDS|Mrp/Nbp35	3.8	1.5	11.6	NA	NA	hypothetical protein
TS29Dor1444|CDS|CDS	25.5	10.0	11.6	NA	NA	hypothetical protein
BT2705|CDS|translation	0.6	0.3	11.5	NA	NA	hypothetical protein
RintL13425|CDS|CDS	52.0	20.5	11.5	NA	NA	hypothetical protein
BactD13738|CDS|CDS	1.3	0.5	11.5	NA	NA	hypothetical protein
Bxyl1523|CDS|CDS	2.5	1.0	11.5	NA	NA	hypothetical protein
Msm0435|CDS|V-type	3.5	1.4	11.5	NA	NA	hypothetical protein
Begg0849|CDS|CDS	5.2	2.1	11.4	NA	NA	hypothetical protein
BFnctc3472|CDS|hypothetical	1.7	0.7	11.3	NA	NA	hypothetical protein
TS28Bac4186|CDS|CDS	1.7	0.7	11.3	NA	NA	hypothetical protein
Buni2974|CDS|CDS	1.7	0.7	11.3	NA	NA	hypothetical protein
TS29Bac05921|CDS|CDS	1.7	0.7	11.3	NA	NA	hypothetical protein
BFych463675|CDS|hypothetical	1.7	0.7	11.3	NA	NA	hypothetical protein
Msmi751652|CDS|CDS	1.7	0.7	11.3	NA	NA	hypothetical protein
Msmi740158|CDS|CDS	1.7	0.7	11.3	NA	NA	hypothetical protein
TS28Met0053|CDS|CDS	1.7	0.7	11.3	NA	NA	hypothetical protein
Bpse1518|CDS|CDS	0.8	0.3	11.3	NA	NA	hypothetical protein
b0700|CDS|rhsC	5.0	2.0	11.3	NA	NA	hypothetical protein
Msm1223|CDS|carbonic	1.3	0.5	11.3	NA	NA	hypothetical protein
b2463|CDS|fused	2.5	1.0	11.3	NA	NA	hypothetical protein
BFnctc1713|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Rum04367|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS28RumUnc0349|CDS|CDS	10.0	4.0	11.3	NA	NA	hypothetical protein
b2933|CDS|predicted	2.5	1.0	11.3	NA	NA	hypothetical protein
Msm0708|CDS|hypothetical	1.3	0.5	11.3	NA	NA	hypothetical protein
ShigspD91786|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS28Clo06159|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
b1129|CDS|sensory	2.5	1.0	11.3	NA	NA	hypothetical protein
Aput0913|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Bac09447|CDS|CDS	20.0	8.0	11.3	NA	NA	hypothetical protein
TS28Rum03425|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein

TS28Fae21756|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BFnctc0185|CDS|putative	2.5	1.0	11.3	NA	NA	hypothetical protein
BFych463811|CDS|glycerol-3-phosphate	2.5	1.0	11.3	NA	NA	hypothetical protein
Bova3954|CDS|CDS	0.5	0.2	11.3	NA	NA	hypothetical protein
TS29Dor1757|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
Buni1747|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Clo0345|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
RintL10294|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BFnctc2072|CDS|phosphoserine	5.0	2.0	11.3	NA	NA	hypothetical protein
BFnctc2659|CDS|putative	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Bac07320|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
BFych461054|CDS|putative	2.5	1.0	11.3	NA	NA	hypothetical protein
BDI1653|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
Cbol4161|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
FpraM2120339|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
Cbol4423|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS28Rum15552|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
Bcap0852|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Rum05236|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
BFych461046|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
BDI3552|CDS|30S	5.0	2.0	11.3	NA	NA	hypothetical protein
Msm1471|CDS|acyl-CoA	1.3	0.5	11.3	NA	NA	hypothetical protein
b2942|CDS|methionine	2.5	1.0	11.3	NA	NA	hypothetical protein
BFnctc3257|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
Dfor2068|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
M23Apeg3632|CDS|Electron	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Rum04463|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI2172|CDS|putative	5.0	2.0	11.3	NA	NA	hypothetical protein
Pmer3505|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
TS28Clo05916|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI1480|CDS|fructose-bisphosphate	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI0668|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI1483|CDS|putative	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI2029|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
BFych460028|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
BFnctc0997|CDS|putative	2.5	1.0	11.3	NA	NA	hypothetical protein
BDI1304|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Fae09664|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
EUBREC2568|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
BactD24510|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BactD23564|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Fae02625|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
Cbol3708|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
b3243|CDS|predicted	2.5	1.0	11.3	NA	NA	hypothetical protein
Aput1852|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BFych461080|CDS|4-hydroxythreonine-4-phosphate	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Bac07334|CDS|CDS	10.0	4.0	11.3	NA	NA	hypothetical protein
Aput2068|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Fae06602|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI0918|CDS|putative	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Rum20257|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
RintL13873|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
b0146|CDS|predicted	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Rum14846|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BFych460660|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
TS28Dor1150|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BFnctc0962|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Fae01703|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
Buni3225|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
BL0852|CDS|branched-chain	0.5	0.2	11.3	NA	NA	hypothetical protein
M23Apeg2918|CDS|Chaperone	5.0	2.0	11.3	NA	NA	hypothetical protein
Rgna3674|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS28Rum00669|CDS|CDS	32.5	13.0	11.3	NA	NA	hypothetical protein
M23Apeg4097|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
BFnctc2006|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
BDI2997|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
Msm1609|CDS|molybdate	0.5	0.2	11.3	NA	NA	hypothetical protein
TS28Rum09491|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Clo2799|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS29Clo4086|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
Ccom0909|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
TS28Fae15346|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BDI2267|CDS|50S	10.0	4.0	11.3	NA	NA	hypothetical protein
Bbre0640|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BactD13192|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Rum19939|CDS|CDS	5.0	2.0	11.3	NA	NA	hypothetical protein
BFnctc3529|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
BFnctc2941|CDS|hypothetical	2.5	1.0	11.3	NA	NA	hypothetical protein
TS28Rum14406|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
BDI2560|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
BFych463369|CDS|hypothetical	10.0	4.0	11.3	NA	NA	hypothetical protein
BDI1233|CDS|hypothetical	5.0	2.0	11.3	NA	NA	hypothetical protein
TS28Rum04462|CDS|CDS	2.5	1.0	11.3	NA	NA	hypothetical protein
TS28Rum11941|CDS|CDS	10.0	4.0	11.3	NA	NA	hypothetical protein
b4382|CDS|thymidine	2.5	1.0	11.3	NA	NA	hypothetical protein
TS29Bac05568|CDS|CDS	15.0	6.0	11.3	NA	NA	hypothetical protein
BDI0796|CDS|sulfate	15.0	6.0	11.3	NA	NA	hypothetical protein
BL1344|CDS|N-acetylglucosamine-6-phosphate	3.8	1.5	11.3	NA	NA	hypothetical protein
TS28Fae08036|CDS|CDS	7.5	3.0	11.3	NA	NA	hypothetical protein
Buni0708|CDS|CDS	3.8	1.5	11.3	NA	NA	hypothetical protein
BFnctc4168|CDS|putative	7.5	3.0	11.3	NA	NA	hypothetical protein
Aput0431|CDS|CDS	15.0	6.0	11.3	NA	NA	hypothetical protein
BFnctc3207|CDS|putative	12.5	5.0	11.3	NA	NA	hypothetical protein

TS28Rum00558|CDS|CDS	7.5	3.0	11.3	NA	NA	hypothetical protein
BFych464037|CDS|major	1.7	0.7	11.3	NA	NA	hypothetical protein
BFnctc4014|CDS|DNA-directed	27.4	11.0	11.3	NA	NA	hypothetical protein
TS29Bac04457|CDS|CDS	19.8	8.0	11.3	NA	NA	hypothetical protein
Caer1086|CDS|CDS	8.7	3.5	11.2	NA	NA	hypothetical protein
Buni2580|CDS|CDS	11.1	4.5	11.2	NA	NA	hypothetical protein
TS29Bac02536|CDS|CDS	11.1	4.5	11.2	NA	NA	hypothetical protein
BFych462171|CDS|F0F1	11.1	4.5	11.2	NA	NA	hypothetical protein
BFych463800|CDS|methylmalonyl-CoA	6.2	2.5	11.2	NA	NA	hypothetical protein
BFych463812|CDS|glucose-6-phosphate	6.2	2.5	11.2	NA	NA	hypothetical protein
FpraM2121622|CDS|CDS	5.8	2.3	11.2	NA	NA	hypothetical protein
BFych463206|CDS|hypothetical	3.7	1.5	11.2	NA	NA	hypothetical protein
BFych460254|CDS|L-1,2-propanediol	4.5	1.8	11.1	NA	NA	hypothetical protein
Rbro0653|CDS|CDS	2.5	1.0	11.1	NA	NA	hypothetical protein
BFnctc3787|CDS|50S	3.7	1.5	11.1	NA	NA	hypothetical protein
TS28Fae02988|CDS|CDS	3.7	1.5	11.1	NA	NA	hypothetical protein
FpraM2120344|CDS|CDS	11.0	4.5	11.1	NA	NA	hypothetical protein
BDI1479|CDS|putative	7.3	3.0	11.1	NA	NA	hypothetical protein
BFych463164|CDS|hypothetical	7.3	3.0	11.1	NA	NA	hypothetical protein
BDI0236|CDS|N-acetylglucosamine-6-phosphate	19.5	8.0	11.1	NA	NA	hypothetical protein
TS29Bac04333|CDS|CDS	12.2	5.0	11.1	NA	NA	hypothetical protein
TS28Clo08175|CDS|CDS	5.7	2.3	11.0	NA	NA	hypothetical protein
FpraM2120328|CDS|CDS	17.0	7.0	11.0	NA	NA	hypothetical protein
BDI3591|CDS|TPR-domain	17.0	7.0	11.0	NA	NA	hypothetical protein
Aput0529|CDS|CDS	17.0	7.0	11.0	NA	NA	hypothetical protein
BL1640|CDS|permease	1.7	0.7	11.0	NA	NA	hypothetical protein
Bthe7332530|CDS|CDS	5.2	2.1	11.0	NA	NA	hypothetical protein
Bthe3733900|CDS|CDS	5.2	2.1	11.0	NA	NA	hypothetical protein
Bova1802|CDS|CDS	1.2	0.5	11.0	NA	NA	hypothetical protein
BL0279|CDS|glucose-6-phosphate	4.2	1.8	11.0	NA	NA	hypothetical protein
FpraM2122077|CDS|CDS	47.2	19.5	11.0	NA	NA	hypothetical protein
Bste2507|CDS|CDS	2.4	1.0	11.0	NA	NA	hypothetical protein
Msm0197|CDS|DNA-directed	0.8	0.3	10.9	NA	NA	hypothetical protein
Msm1233|CDS|glutamate-1-semialdehyde	0.8	0.3	10.9	NA	NA	hypothetical protein
BFnctc3560|CDS|hypothetical	2.0	0.8	10.9	NA	NA	hypothetical protein
BFych461690|CDS|50S	2.0	0.8	10.9	NA	NA	hypothetical protein
BLD0267|CDS|hypothetical	2.0	0.8	10.9	NA	NA	hypothetical protein
BFnctc1697|CDS|50S	2.0	0.8	10.9	NA	NA	hypothetical protein
TS28Fae18606|CDS|CDS	2.0	0.8	10.9	NA	NA	hypothetical protein
Msm0739|CDS|50S	1.2	0.5	10.9	NA	NA	hypothetical protein
BFych462731|CDS|V-type	1.2	0.5	10.9	NA	NA	hypothetical protein
Buni2753|CDS|CDS	6.0	2.5	10.9	NA	NA	hypothetical protein
BDI3208|CDS|succinate	12.0	5.0	10.9	NA	NA	hypothetical protein
BDI0474|CDS|glycoside	12.0	5.0	10.9	NA	NA	hypothetical protein
BDI3592|CDS|putative	12.0	5.0	10.9	NA	NA	hypothetical protein
BDI1729|CDS|ATP-dependent	12.0	5.0	10.9	NA	NA	hypothetical protein
TS28Col1508|CDS|CDS	12.0	5.0	10.9	NA	NA	hypothetical protein
Buni1594|CDS|CDS	12.0	5.0	10.9	NA	NA	hypothetical protein
BVU2185|CDS|hypothetical	12.0	5.0	10.9	NA	NA	hypothetical protein
TS29Rum14637|CDS|CDS	36.0	15.0	10.9	NA	NA	hypothetical protein
Msm0055|CDS|3-dehydroquinate	3.0	1.3	10.9	NA	NA	hypothetical protein
BFych463305|CDS|hypothetical	6.0	2.5	10.9	NA	NA	hypothetical protein
TS28Fae22715|CDS|CDS	45.5	19.0	10.9	NA	NA	hypothetical protein
b2557|CDS|phosphoribosylformyl-glycineamide	7.2	3.0	10.8	NA	NA	hypothetical protein
BDI3672|CDS|putative	43.0	18.0	10.8	NA	NA	hypothetical protein
BFych463421|CDS|adenylosuccinate	4.8	2.0	10.8	NA	NA	hypothetical protein
BL0415|CDS|single-strand	4.8	2.0	10.8	NA	NA	hypothetical protein
TS28Rum07936|CDS|CDS	9.5	4.0	10.8	NA	NA	hypothetical protein
TS29Fae07945|CDS|CDS	9.5	4.0	10.8	NA	NA	hypothetical protein
TS29Par768|CDS|CDS	19.0	8.0	10.8	NA	NA	hypothetical protein
BDI0232|CDS|putative	19.0	8.0	10.8	NA	NA	hypothetical protein
TS29Bac00414|CDS|CDS	28.5	12.0	10.8	NA	NA	hypothetical protein
BFnctc4003|CDS|50S	3.6	1.5	10.8	NA	NA	hypothetical protein
BFych464181|CDS|50S	3.6	1.5	10.8	NA	NA	hypothetical protein
FpraM2122376|CDS|CDS	2.4	1.0	10.7	NA	NA	hypothetical protein
TS28Rum13300|CDS|CDS	13.0	5.5	10.7	NA	NA	hypothetical protein
TS28Fae21067|CDS|CDS	17.7	7.5	10.7	NA	NA	hypothetical protein
Bova2001|CDS|CDS	1.2	0.5	10.7	NA	NA	hypothetical protein
FpraM2122078|CDS|CDS	35.2	15.0	10.6	NA	NA	hypothetical protein
BFych464205|CDS|3-deoxy-D-manno-octulosonic-acid	1.2	0.5	10.6	NA	NA	hypothetical protein
BFnctc0991|CDS|hypothetical	1.166666667	0.5	10.59281705	NA	NA	hypothetical protein
BactD21926|CDS|CDS	1.166666667	0.5	10.59281705	NA	NA	hypothetical protein
BFnctc3144|CDS|putative	3.5	1.5	10.59281705	NA	NA	hypothetical protein
BactD13946|CDS|CDS	9.333333333	4	10.59281705	NA	NA	hypothetical protein
TS29Bac07795|CDS|CDS	9.333333333	4	10.59281705	NA	NA	hypothetical protein
TS29Rum01606|CDS|CDS	21	9	10.59281705	NA	NA	hypothetical protein
BDI0181|CDS|TPR	21	9	10.59281705	NA	NA	hypothetical protein
TS28Bac4096|CDS|CDS	2.333333333	1	10.59281705	NA	NA	hypothetical protein
BFnctc3982|CDS|putative	7	3	10.59281705	NA	NA	hypothetical protein
BDI3169|CDS|RNA	7	3	10.59281705	NA	NA	hypothetical protein
Aput0925|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
BDI3578|CDS|phosphoribosylglycinamide	7	3	10.59281705	NA	NA	hypothetical protein
BFych462238|CDS|hypothetical	3.5	1.5	10.59281705	NA	NA	hypothetical protein
Aput0088|CDS|CDS	14	6	10.59281705	NA	NA	hypothetical protein
TS28Bif3516|CDS|CDS	35	15	10.59281705	NA	NA	hypothetical protein
Buni1445|CDS|CDS	3.5	1.5	10.59281705	NA	NA	hypothetical protein
Aput1290|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
BDI2911|CDS|putative	7	3	10.59281705	NA	NA	hypothetical protein
TS28Fae00786|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
BDI1014|CDS|formate-tetrahydrofolate	7	3	10.59281705	NA	NA	hypothetical protein
TS29Rum05023|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein

FpraM2122495|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
b3771|CDS|dihydroxyacid	2.333333333	1	10.59281705	NA	NA	hypothetical protein
BactD21067|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
BFnctc0723|CDS|AraC	3.5	1.5	10.59281705	NA	NA	hypothetical protein
BFych460222|CDS|erythronate-4-phosphate	3.5	1.5	10.59281705	NA	NA	hypothetical protein
BDI2110|CDS|hypothetical	7	3	10.59281705	NA	NA	hypothetical protein
BFych460236|CDS|hypothetical	3.5	1.5	10.59281705	NA	NA	hypothetical protein
TS28Bac3487|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
Buni1047|CDS|CDS	2.333333333	1	10.59281705	NA	NA	hypothetical protein
TS29Fae04137|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
Msmi740675|CDS|CDS	3.5	1.5	10.59281705	NA	NA	hypothetical protein
Aput0312|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
RintL10399|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
BFych464072|CDS|peptidyl-prolyl	3.5	1.5	10.59281705	NA	NA	hypothetical protein
TS28Fae21290|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
BDI1385|CDS|two-component	7	3	10.59281705	NA	NA	hypothetical protein
BDI0625|CDS|hypothetical	7	3	10.59281705	NA	NA	hypothetical protein
BDI2269|CDS|transcription	7	3	10.59281705	NA	NA	hypothetical protein
BFnctc3922|CDS|hypothetical	7	3	10.59281705	NA	NA	hypothetical protein
BDI1687|CDS|putative	3.5	1.5	10.59281705	NA	NA	hypothetical protein
BFych463593|CDS|putative	3.5	1.5	10.59281705	NA	NA	hypothetical protein
BDI0050|CDS|glycoside	7	3	10.59281705	NA	NA	hypothetical protein
BactD21950|CDS|CDS	7	3	10.59281705	NA	NA	hypothetical protein
TS29Rum19986|CDS|CDS	3.5	1.5	10.59281705	NA	NA	hypothetical protein
Msm1278|CDS|predicted	0.583333333	0.25	10.59281705	NA	NA	hypothetical protein
Bova0453|CDS|CDS	2.333333333	1	10.59281705	NA	NA	hypothetical protein
Cmet0498|CDS|CDS	2.333333333	1	10.59281705	NA	NA	hypothetical protein
BFych460662|CDS|hypothetical	2.333333333	1	10.59281705	NA	NA	hypothetical protein
BFnctc1290|CDS|glycine	2.333333333	1	10.59281705	NA	NA	hypothetical protein
FpraM2120335|CDS|CDS	2.333333333	1	10.59281705	NA	NA	hypothetical protein
TS28Fae17837|CDS|CDS	18.5	8	10.49823833	NA	NA	hypothetical protein
BFych463858|CDS|hypothetical	2.30952381	1	10.48472708	NA	NA	hypothetical protein
BFnctc3629|CDS|hypothetical	2.30952381	1	10.48472708	NA	NA	hypothetical protein
TS28Eub5026|CDS|CDS	1.533333333	0.666666667	10.44149109	NA	NA	hypothetical protein
BDI1878|CDS|hypothetical	11.5	5	10.44149109	NA	NA	hypothetical protein
Aput0473|CDS|CDS	11.5	5	10.44149109	NA	NA	hypothetical protein
Msm0743|CDS|50S	1.533333333	0.666666667	10.44149109	NA	NA	hypothetical protein
Bxyl1991|CDS|CDS	4.583333333	2	10.4036596	NA	NA	hypothetical protein
BFnctc2567|CDS|pyruvate	9.166666667	4	10.4036596	NA	NA	hypothetical protein
TS29Fae00069|CDS|CDS	4.583333333	2	10.4036596	NA	NA	hypothetical protein
BDI2724|CDS|hypothetical	16	7	10.37663711	NA	NA	hypothetical protein
BDI3765|CDS|elongation	16	7	10.37663711	NA	NA	hypothetical protein
Rtor1383|CDS|CDS	32	14	10.37663711	NA	NA	hypothetical protein
Buni1529|CDS|CDS	8	3.5	10.37663711	NA	NA	hypothetical protein
TS28Fae00290|CDS|CDS	52.5	23	10.36253842	NA	NA	hypothetical protein
TS29Fae00137|CDS|CDS	41	18	10.34060712	NA	NA	hypothetical protein
Ceut2209|CDS|CDS	16.28333333	7.166666667	10.31479959	NA	NA	hypothetical protein
TS29Fae04505|CDS|CDS	32.91666667	14.5	10.30581954	NA	NA	hypothetical protein
TS29Fae08626|CDS|CDS	45.33333333	20	10.29016514	NA	NA	hypothetical protein
TS29Fae09234|CDS|CDS	21.5	9.5	10.27423609	NA	NA	hypothetical protein
Msm0849|CDS|molybdenum	0.75	0.333333333	10.21450216	NA	NA	hypothetical protein
BLD1766|CDS|Putative	0.75	0.333333333	10.21450216	NA	NA	hypothetical protein
Msm0360|CDS|cell	0.75	0.333333333	10.21450216	NA	NA	hypothetical protein
BFych462859|CDS|hypothetical	3	1.333333333	10.21450216	NA	NA	hypothetical protein
Bthe3733501|CDS|CDS	3	1.333333333	10.21450216	NA	NA	hypothetical protein
EUBREC3260|CDS|DHH	9	4	10.21450216	NA	NA	hypothetical protein
TS29Bac11412|CDS|CDS	11.25	5	10.21450216	NA	NA	hypothetical protein
TS28Fae06816|CDS|CDS	9	4	10.21450216	NA	NA	hypothetical protein
BFnctc0246|CDS|DNA	2.25	1	10.21450216	NA	NA	hypothetical protein
BDI1509|CDS|hypothetical	9	4	10.21450216	NA	NA	hypothetical protein
BDI0585|CDS|putative	9	4	10.21450216	NA	NA	hypothetical protein
BDI0830|CDS|V-type	9	4	10.21450216	NA	NA	hypothetical protein
BDI2091|CDS|hypothetical	9	4	10.21450216	NA	NA	hypothetical protein
BFych461007|CDS|seryl-tRNA	4.5	2	10.21450216	NA	NA	hypothetical protein
Cbol1433|CDS|CDS	4.5	2	10.21450216	NA	NA	hypothetical protein
BactD23942|CDS|CDS	4.5	2	10.21450216	NA	NA	hypothetical protein
TS28Bac3060|CDS|CDS	2.25	1	10.21450216	NA	NA	hypothetical protein
BAD0326|CDS|50S	4.5	2	10.21450216	NA	NA	hypothetical protein
TS29Fae08824|CDS|CDS	4.5	2	10.21450216	NA	NA	hypothetical protein
BFnctc2230|CDS|putative	4.5	2	10.21450216	NA	NA	hypothetical protein
BFych462174|CDS|ATP	4.5	2	10.21450216	NA	NA	hypothetical protein
BFych461399|CDS|putative	4.5	2	10.21450216	NA	NA	hypothetical protein
BDI2769|CDS|GTP-binding	9	4	10.21450216	NA	NA	hypothetical protein
Aput0033|CDS|CDS	9	4	10.21450216	NA	NA	hypothetical protein
Aput2050|CDS|CDS	9	4	10.21450216	NA	NA	hypothetical protein
BDI1402|CDS|aspartyl-tRNA	9	4	10.21450216	NA	NA	hypothetical protein
TS29Rum18953|CDS|CDS	4.5	2	10.21450216	NA	NA	hypothetical protein
TS28Rum09431|CDS|CDS	4.5	2	10.21450216	NA	NA	hypothetical protein
Buni0326|CDS|CDS	6	2.666666667	10.21450216	NA	NA	hypothetical protein
TS28Bac6137|CDS|CDS	6	2.666666667	10.21450216	NA	NA	hypothetical protein
TS29Rum00504|CDS|CDS	177	79	10.17140299	NA	NA	hypothetical protein
FpraM2121115|CDS|CDS	6.333333333	2.833333333	10.1477407	NA	NA	hypothetical protein
FpraM2120861|CDS|CDS	11.16666667	5	10.13883918	NA	NA	hypothetical protein
Csci2183|CDS|CDS	6.7	3	10.13883918	NA	NA	hypothetical protein
BVU3585|CDS|glyceraldehyde	1.113636364	0.5	10.11132537	NA	NA	hypothetical protein
Caer1371|CDS|CDS	16.33333333	7.333333333	10.11132537	NA	NA	hypothetical protein
b3980|CDS|protein	2.592857143	1.166666667	10.08942662	NA	NA	hypothetical protein
Buni0387|CDS|CDS	1.666666667	0.75	10.08839719	NA	NA	hypothetical protein
b0042|CDS|predicted	3.333333333	1.5	10.08839719	NA	NA	hypothetical protein
Bxyl2956|CDS|CDS	22.16666667	10	10.0631762	NA	NA	hypothetical protein
TS29Bac02005|CDS|CDS	8.833333333	4	10.02534471	NA	NA	hypothetical protein
Msm1001|CDS|methyl	4.416666667	2	10.02534471	NA	NA	hypothetical protein
TS29Rum16049|CDS|CDS	43	19.5	10.01079414	NA	NA	hypothetical protein
BL0618|CDS|hypothetical	0.2	9.083333333	0.099958431	NA	NA	hypothetical protein
TS29Fae06689|CDS|CDS	2	91	0.099775357	NA	NA	hypothetical protein

BLD0522|CDS|Aspartate/tyrosine/aromatic	0.5	22.75	0.099775357	NA	NA	hypothetical protein
BL0783|CDS|aspartate	0.5	22.75	0.099775357	NA	NA	hypothetical protein
BLD0960|CDS|Transglutaminase-like	0.333333333	15.16666667	0.099775357	NA	NA	hypothetical protein
BL0942|CDS|sodium/proton	0.25	11.47619048	0.098895595	NA	NA	hypothetical protein
TS29Bif0139|CDS|CDS	0.833333333	38.33333333	0.098690842	NA	NA	hypothetical protein
TS29Fae09697|CDS|CDS	0.25	11.5	0.098690842	NA	NA	hypothetical protein
TS29Fae09128|CDS|CDS	1	46	0.098690842	NA	NA	hypothetical protein
TS28Bif1023|CDS|CDS	0.5	23	0.098690842	NA	NA	hypothetical protein
BL1045|CDS|hypothetical	0.5	23	0.098690842	NA	NA	hypothetical protein
BLD1209|CDS|hypothetical	0.5	23	0.098690842	NA	NA	hypothetical protein
BLD0795|CDS|Trk-type	0.5	23	0.098690842	NA	NA	hypothetical protein
TS29Fae07382|CDS|CDS	0.5	23	0.098690842	NA	NA	hypothetical protein
BL1662|CDS|hypothetical	0.5	23	0.098690842	NA	NA	hypothetical protein
TS28Rum14351|CDS|CDS	0.5	23	0.098690842	NA	NA	hypothetical protein
TS29Dor2213|CDS|CDS	0.5	23	0.098690842	NA	NA	hypothetical protein
Dlon1633|CDS|CDS	0.5	23	0.098690842	NA	NA	hypothetical protein
BL1746|CDS|hypothetical	0.5	23	0.098690842	NA	NA	hypothetical protein
TS29RumUnc0014|CDS|CDS	2	92	0.098690842	NA	NA	hypothetical protein
TS29Col0450|CDS|CDS	0.5	23	0.098690842	NA	NA	hypothetical protein
BactD14022|CDS|CDS	0.333333333	15.33333333	0.098690842	NA	NA	hypothetical protein
TS29Bac03731|CDS|CDS	0.333333333	15.33333333	0.098690842	NA	NA	hypothetical protein
Caer0792|CDS|CDS	2.142857143	99.11111111	0.098153448	NA	NA	hypothetical protein
TS29Bif3127|CDS|CDS	3	139	0.097980836	NA	NA	hypothetical protein
Bthe3733887|CDS|CDS	0.1	4.638095238	0.09788024	NA	NA	hypothetical protein
BL0445|CDS|hypothetical	0.833333333	38.66666667	0.097840059	NA	NA	hypothetical protein
TS28CloUnc037|CDS|CDS	0.5	23.25	0.09762965	NA	NA	hypothetical protein
TS29Fae04839|CDS|CDS	0.333333333	15.5	0.09762965	NA	NA	hypothetical protein
BactD12179|CDS|CDS	0.333333333	15.5	0.09762965	NA	NA	hypothetical protein
TS29Dor1689|CDS|CDS	0.428571429	20	0.097280973	NA	NA	hypothetical protein
TS29RumUnc1357|CDS|CDS	0.2	9.333333333	0.097280973	NA	NA	hypothetical protein
TS28Bif1170|CDS|CDS	0.75	35	0.097280973	NA	NA	hypothetical protein
BLD1307|CDS|Acyl-CoA	0.75	35	0.097280973	NA	NA	hypothetical protein
BL0513|CDS|acyl-CoA	0.75	35	0.097280973	NA	NA	hypothetical protein
Acol2744|CDS|CDS	1	47	0.096591037	NA	NA	hypothetical protein
TS28Fae22617|CDS|CDS	1	47	0.096591037	NA	NA	hypothetical protein
TS29Fae09590|CDS|CDS	0.5	23.5	0.096591037	NA	NA	hypothetical protein
Robe2597|CDS|CDS	1	47	0.096591037	NA	NA	hypothetical protein
TS28Rum01181|CDS|CDS	1	47	0.096591037	NA	NA	hypothetical protein
TS28Fae08665|CDS|CDS	0.5	23.5	0.096591037	NA	NA	hypothetical protein
TS28Bif0378|CDS|CDS	0.25	11.75	0.096591037	NA	NA	hypothetical protein
BLD1633|CDS|(acyl-carrier-protein)	1	47.13333333	0.096317795	NA	NA	hypothetical protein
TS29Col0448|CDS|CDS	2	94.5	0.096079973	NA	NA	hypothetical protein
TS29LacUnc129|CDS|CDS	0.805555556	38.11111111	0.095957422	NA	NA	hypothetical protein
TS29Bif4077|CDS|CDS	5.5	260.5833333	0.095818803	NA	NA	hypothetical protein
BLD0481|CDS|Prolipoprotein	0.2	9.5	0.095574289	NA	NA	hypothetical protein
Bbre0311|CDS|CDS	0.4	19	0.095574289	NA	NA	hypothetical protein
TS29Fae07296|CDS|CDS	1	47.5	0.095574289	NA	NA	hypothetical protein
BLD0801|CDS|hypothetical	0.5	23.75	0.095574289	NA	NA	hypothetical protein
TS29Bac03838|CDS|CDS	0.333333333	15.86666667	0.095373503	NA	NA	hypothetical protein
BLD1105|CDS|Aspartate	0.25	11.91666667	0.095240113	NA	NA	hypothetical protein
BLD0788|CDS|hypothetical	0.6	28.7	0.094908266	NA	NA	hypothetical protein
TS29Fae09519|CDS|CDS	0.5	24	0.094578724	NA	NA	hypothetical protein
BLD0057|CDS|Putative	0.25	12	0.094578724	NA	NA	hypothetical protein
TS29Rum17069|CDS|CDS	1	48	0.094578724	NA	NA	hypothetical protein
TS29Fae06309|CDS|CDS	0.5	24	0.094578724	NA	NA	hypothetical protein
Rumhyd3576|CDS|CDS	1.833333333	88	0.094578724	NA	NA	hypothetical protein
TS29Fae00811|CDS|CDS	2.5	120	0.094578724	NA	NA	hypothetical protein
Bbre0830|CDS|CDS	0.25	12	0.094578724	NA	NA	hypothetical protein
BL1029|CDS|hypothetical	0.75	36	0.094578724	NA	NA	hypothetical protein
TS29Bac02619|CDS|CDS	0.333333333	16	0.094578724	NA	NA	hypothetical protein
TS29Fae02094|CDS|CDS	0.333333333	16	0.094578724	NA	NA	hypothetical protein
BL1347|CDS|peptide	0.75	36.33333333	0.093711029	NA	NA	hypothetical protein
TS29Rum15689|CDS|CDS	2	97	0.093603685	NA	NA	hypothetical protein
TS29Bif4036|CDS|CDS	1.333333333	64.91666667	0.093243209	NA	NA	hypothetical protein
BLD0802|CDS|Tyrosyl-tRNA	0.75	36.58333333	0.093070635	NA	NA	hypothetical protein
BLD1693|CDS|Ribosomal	0.5	24.41666667	0.092964752	NA	NA	hypothetical protein
BLD1540|CDS|ABC-type	0.5	24.41666667	0.092964752	NA	NA	hypothetical protein
TS29Clo4937|CDS|CDS	1	49	0.092648546	NA	NA	hypothetical protein
TS29Bac10779|CDS|CDS	0.5	24.5	0.092648546	NA	NA	hypothetical protein
TS29Bac04738|CDS|CDS	0.5	24.5	0.092648546	NA	NA	hypothetical protein
TS28Fae17279|CDS|CDS	0.5	24.5	0.092648546	NA	NA	hypothetical protein
TS29Fae08040|CDS|CDS	0.5	24.5	0.092648546	NA	NA	hypothetical protein
TS29Fae00928|CDS|CDS	1	49	0.092648546	NA	NA	hypothetical protein
TS29Fae03769|CDS|CDS	1	49	0.092648546	NA	NA	hypothetical protein
TS29Bac05253|CDS|CDS	0.333333333	16.33333333	0.092648546	NA	NA	hypothetical protein
BLD0933|CDS|Glucosamine	0.5	24.66666667	0.092022542	NA	NA	hypothetical protein
TS29Bac10467|CDS|CDS	0.666666667	33	0.091712702	NA	NA	hypothetical protein
TS29Fae04964|CDS|CDS	1	49.5	0.091712702	NA	NA	hypothetical protein
TS29Fae05429|CDS|CDS	2	99	0.091712702	NA	NA	hypothetical protein
TS29Fae01416|CDS|CDS	1.666666667	82.5	0.091712702	NA	NA	hypothetical protein
Rumhyd3577|CDS|CDS	14	695	0.09144878	NA	NA	hypothetical protein
BAD0021|CDS|hypothetical	0.5	24.83333333	0.091404941	NA	NA	hypothetical protein
BLD0435|CDS|L-2-hydroxyisocaproate/malate/lactate	0.5	24.83333333	0.091404941	NA	NA	hypothetical protein
TS29Fae06745|CDS|CDS	1.5	75	0.090795575	NA	NA	hypothetical protein
TS29Rum20702|CDS|CDS	0.5	25	0.090795575	NA	NA	hypothetical protein
TS29Rum11725|CDS|CDS	1	50	0.090795575	NA	NA	hypothetical protein
TS28Fae14450|CDS|CDS	0.5	25	0.090795575	NA	NA	hypothetical protein
TS29Rum20767|CDS|CDS	2	100	0.090795575	NA	NA	hypothetical protein
TS29Fae05435|CDS|CDS	2	100	0.090795575	NA	NA	hypothetical protein
TS28Fae02073|CDS|CDS	0.5	25	0.090795575	NA	NA	hypothetical protein
FpraM2120695|CDS|CDS	0.25	12.5	0.090795575	NA	NA	hypothetical protein
CspM6212553|CDS|CDS	0.2	10	0.090795575	NA	NA	hypothetical protein
TS29Bac08381|CDS|CDS	0.666666667	33.5	0.090343855	NA	NA	hypothetical protein
TS29Bac08284|CDS|CDS	1	50.33333333	0.09019428	NA	NA	hypothetical protein

TS29Bac10345|CDS|CDS	0.333333333	16.83333333	0.089896609	NA	NA	hypothetical protein
BLD1931|CDS|Activator	0.75	38.16666667	0.089209626	NA	NA	hypothetical protein
TS29Bac08512|CDS|CDS	0.5	25.5	0.089015269	NA	NA	hypothetical protein
TS28Fae01204|CDS|CDS	0.5	25.5	0.089015269	NA	NA	hypothetical protein
TS29Rum11417|CDS|CDS	2	102	0.089015269	NA	NA	hypothetical protein
TS28Rum14113|CDS|CDS	0.5	25.5	0.089015269	NA	NA	hypothetical protein
FpraM2120615|CDS|CDS	0.833333333	42.5	0.089015269	NA	NA	hypothetical protein
TS29RumUnc1279|CDS|CDS	0.333333333	17	0.089015269	NA	NA	hypothetical protein
Rbro0060|CDS|CDS	0.333333333	17	0.089015269	NA	NA	hypothetical protein
TS28Clo10457|CDS|CDS	0.333333333	17	0.089015269	NA	NA	hypothetical protein
TS29Bif1246|CDS|CDS	0.333333333	17	0.089015269	NA	NA	hypothetical protein
TS29Fae01568|CDS|CDS	0.333333333	17	0.089015269	NA	NA	hypothetical protein
BL0294|CDS|50S	0.142857143	7.333333333	0.088437248	NA	NA	hypothetical protein
TS29Bif0861|CDS|CDS	0.142857143	7.333333333	0.088437248	NA	NA	hypothetical protein
BLD1040|CDS|Ribosomal	0.142857143	7.333333333	0.088437248	NA	NA	hypothetical protein
BLD1417|CDS|4-aminobutyrate	1.333333333	68.5	0.088365523	NA	NA	hypothetical protein
TS29Fae00298|CDS|CDS	2	103	0.088151043	NA	NA	hypothetical protein
TS29Fae08937|CDS|CDS	1	51.5	0.088151043	NA	NA	hypothetical protein
TS28Bif4733|CDS|CDS	0.5	25.75	0.088151043	NA	NA	hypothetical protein
FpraM2121349|CDS|CDS	0.333333333	17.16666667	0.088151043	NA	NA	hypothetical protein
TS28Bif1874|CDS|CDS	0.2	10.33333333	0.087866685	NA	NA	hypothetical protein
BL0982|CDS|glycogen	0.666666667	34.66666667	0.087303437	NA	NA	hypothetical protein
TS29Fae03505|CDS|CDS	0.25	13	0.087303437	NA	NA	hypothetical protein
TS29Fae08618|CDS|CDS	1.5	78	0.087303437	NA	NA	hypothetical protein
Cbol3893|CDS|CDS	1	52	0.087303437	NA	NA	hypothetical protein
TS28Bif0151|CDS|CDS	0.25	13	0.087303437	NA	NA	hypothetical protein
TS29Fae01454|CDS|CDS	1	52	0.087303437	NA	NA	hypothetical protein
TS29Fae10349|CDS|CDS	1	52	0.087303437	NA	NA	hypothetical protein
TS29Bac11777|CDS|CDS	0.333333333	17.33333333	0.087303437	NA	NA	hypothetical protein
Dfor3099|CDS|CDS	3.25	169.65	0.086968941	NA	NA	hypothetical protein
Svar1594|CDS|CDS	0.090909091	4.766666667	0.086581921	NA	NA	hypothetical protein
BLD1780|CDS|Phosphate	0.5	26.25	0.086471976	NA	NA	hypothetical protein
Bcat0442|CDS|CDS	0.1	5.25	0.086471976	NA	NA	hypothetical protein
TS29Bac12233|CDS|CDS	0.333333333	17.5	0.086471976	NA	NA	hypothetical protein
FpraM2120671|CDS|CDS	0.333333333	17.5	0.086471976	NA	NA	hypothetical protein
BLD0010|CDS|ATP-binding	1.125	59.08333333	0.086441485	NA	NA	hypothetical protein
TS29Fae03170|CDS|CDS	2.5	131.5	0.086307581	NA	NA	hypothetical protein
TS29Rum00537|CDS|CDS	1	53	0.085656203	NA	NA	hypothetical protein
TS28Fae16679|CDS|CDS	1	53	0.085656203	NA	NA	hypothetical protein
BLD0955|CDS|Superfamily	1.5	79.91666667	0.085209611	NA	NA	hypothetical protein
TS29Bac08380|CDS|CDS	0.25	13.33333333	0.085120851	NA	NA	hypothetical protein
BLD1306|CDS|3-oxoacyl-acyl	0.4	21.33333333	0.085120851	NA	NA	hypothetical protein
BLD0589|CDS|NAD/NADP	0.25	13.33333333	0.085120851	NA	NA	hypothetical protein
TS29Fae08344|CDS|CDS	2	107	0.084855677	NA	NA	hypothetical protein
TS29Fae08245|CDS|CDS	1	53.5	0.084855677	NA	NA	hypothetical protein
TS29Bif2313|CDS|CDS	0.666666667	35.83333333	0.084461	NA	NA	hypothetical protein
TS29Rum11864|CDS|CDS	0.342857143	18.5	0.084134895	NA	NA	hypothetical protein
BLD1881|CDS|hypothetical	1	54	0.084069977	NA	NA	hypothetical protein
TS29Col1621|CDS|CDS	1	54	0.084069977	NA	NA	hypothetical protein
TS29Rum11908|CDS|CDS	0.5	27	0.084069977	NA	NA	hypothetical protein
BLD1443|CDS|Putative	0.5	27	0.084069977	NA	NA	hypothetical protein
TS28Fae00367|CDS|CDS	1	54	0.084069977	NA	NA	hypothetical protein
BLD1382|CDS|Serine/threonine	0.25	13.5	0.084069977	NA	NA	hypothetical protein
Acol2769|CDS|CDS	0.333333333	18	0.084069977	NA	NA	hypothetical protein
TS28Rum14227|CDS|CDS	0.25	13.58333333	0.08355421	NA	NA	hypothetical protein
BLD1338|CDS|LacI-type	0.25	13.58333333	0.08355421	NA	NA	hypothetical protein
Bova0233|CDS|CDS	1.25	68	0.083451815	NA	NA	hypothetical protein
Bova2230|CDS|CDS	1.25	68	0.083451815	NA	NA	hypothetical protein
TS29Bac12110|CDS|CDS	0.25	13.66666667	0.083044733	NA	NA	hypothetical protein
Cbol3982|CDS|CDS	1.25	68.5	0.082842678	NA	NA	hypothetical protein
TS28Bif4641|CDS|CDS	0.5	27.5	0.082541432	NA	NA	hypothetical protein
TS29Fae08270|CDS|CDS	0.5	27.5	0.082541432	NA	NA	hypothetical protein
TS29Rum20753|CDS|CDS	1	55	0.082541432	NA	NA	hypothetical protein
TS29Bac00422|CDS|CDS	0.5	27.5	0.082541432	NA	NA	hypothetical protein
BLD0875|CDS|ABC-type	0.25	13.75	0.082541432	NA	NA	hypothetical protein
TS29Rum20483|CDS|CDS	1	55	0.082541432	NA	NA	hypothetical protein
TS29Par961|CDS|CDS	3	165	0.082541432	NA	NA	hypothetical protein
Bxyl2941|CDS|CDS	0.090909091	5	0.082541432	NA	NA	hypothetical protein
M23Apeg881|CDS|Translation	0.090909091	5	0.082541432	NA	NA	hypothetical protein
TS29Bac00834|CDS|CDS	0.333333333	18.33333333	0.082541432	NA	NA	hypothetical protein
TS29Bif3555|CDS|CDS	6.25	344.25	0.082421546	NA	NA	hypothetical protein
BactD10004|CDS|CDS	1.25	69	0.082242368	NA	NA	hypothetical protein
BLD1536|CDS|Putative	0.5	27.66666667	0.082044194	NA	NA	hypothetical protein
BL1124|CDS|fatty	0.666666667	37	0.081797815	NA	NA	hypothetical protein
TS29Bif1960|CDS|CDS	0.333333333	18.5	0.081797815	NA	NA	hypothetical protein
TS28CloUnc025|CDS|CDS	0.333333333	18.5	0.081797815	NA	NA	hypothetical protein
TS29Bif3844|CDS|CDS	1.5	83.5	0.081552911	NA	NA	hypothetical protein
TS28Fae12097|CDS|CDS	1.5	83.5	0.081552911	NA	NA	hypothetical protein
Dfor1849|CDS|CDS	0.25	13.91666667	0.081552911	NA	NA	hypothetical protein
BactD10025|CDS|CDS	2.388888889	133.0361111	0.081519423	NA	NA	hypothetical protein
Bthe3735756|CDS|CDS	2.388888889	133.0361111	0.081519423	NA	NA	hypothetical protein
TS29Col1603|CDS|CDS	2	111.5	0.081431009	NA	NA	hypothetical protein
TS29Bac10930|CDS|CDS	0.666666667	37.33333333	0.081067477	NA	NA	hypothetical protein
TS29Fae01272|CDS|CDS	1	56	0.081067477	NA	NA	hypothetical protein
TS29Fae06820|CDS|CDS	0.25	14	0.081067477	NA	NA	hypothetical protein
TS29Bac00506|CDS|CDS	0.2	11.2	0.081067477	NA	NA	hypothetical protein
TS29Fae03179|CDS|CDS	0.5	28	0.081067477	NA	NA	hypothetical protein
TS29Fae01278|CDS|CDS	1	56	0.081067477	NA	NA	hypothetical protein
Rtor0322|CDS|CDS	0.25	14	0.081067477	NA	NA	hypothetical protein
Bfra31120043|CDS|CDS	2.388888889	134.0361111	0.080911233	NA	NA	hypothetical protein
BLD1087|CDS|RecG-like	0.916666667	51.5	0.080805123	NA	NA	hypothetical protein
EUBREC3563|CDS|hypothetical	1.333333333	74.91666667	0.080796952	NA	NA	hypothetical protein
TS29Bif0717|CDS|CDS	1	56.41666667	0.080468752	NA	NA	hypothetical protein
TS29Fae08492|CDS|CDS	3	169.5	0.080350066	NA	NA	hypothetical protein
BL0138|CDS|hypothetical	1	56.58333333	0.08023173	NA	NA	hypothetical protein
Rlac0723|CDS|CDS	0.058823529	3.333333333	0.080113742	NA	NA	hypothetical protein

CspL22445|CDS|CDS	0.058823529	3.333333333	0.080113742	NA	NA	hypothetical protein
TS29Bif2565|CDS|CDS	1.25	70.91666667	0.080019602	NA	NA	hypothetical protein
TS29Bac01538|CDS|CDS	1	57	0.079645241	NA	NA	hypothetical protein
TS29Rum00194|CDS|CDS	1	57	0.079645241	NA	NA	hypothetical protein
TS29Fae06280|CDS|CDS	0.5	28.5	0.079645241	NA	NA	hypothetical protein
TS29Bac04296|CDS|CDS	0.333333333	19	0.079645241	NA	NA	hypothetical protein
Cnex1531|CDS|CDS	0.071428571	4.083333333	0.079413039	NA	NA	hypothetical protein
TS29Bif0556|CDS|CDS	2	114.5	0.079297445	NA	NA	hypothetical protein
TS29Rum17012|CDS|CDS	0.366666667	21	0.079265978	NA	NA	hypothetical protein
BL1317|CDS|peptidoglycan	0.25	14.33333333	0.079182187	NA	NA	hypothetical protein
BL1121|CDS|amidophosphoribosyltransferase	0.5	28.66666667	0.079182187	NA	NA	hypothetical protein
Dlon1659|CDS|CDS	0.166666667	9.583333333	0.078952674	NA	NA	hypothetical protein
BL1626|CDS|class	0.833333333	48.16666667	0.078542885	NA	NA	hypothetical protein
BL0329|CDS|ATP-dependent	0.916666667	53	0.078518186	NA	NA	hypothetical protein
TS29Fae08919|CDS|CDS	0.5	29	0.078272047	NA	NA	hypothetical protein
TS29Col0553|CDS|CDS	0.5	29	0.078272047	NA	NA	hypothetical protein
FpraM2121613|CDS|CDS	0.5	29	0.078272047	NA	NA	hypothetical protein
EUBREC3528|CDS|cassette	1	58	0.078272047	NA	NA	hypothetical protein
BL1319|CDS|UDP-N-acetylmuramoylalanyl-D-glutamyl-2,	0.25	14.5	0.078272047	NA	NA	hypothetical protein
TS28Fae14611|CDS|CDS	0.5	29	0.078272047	NA	NA	hypothetical protein
FpraM2120220|CDS|CDS	0.5	29	0.078272047	NA	NA	hypothetical protein
TS29Fae05201|CDS|CDS	0.5	29	0.078272047	NA	NA	hypothetical protein
BLD1639|CDS|hypothetical	0.5	29	0.078272047	NA	NA	hypothetical protein
TS29Bac00792|CDS|CDS	0.333333333	19.33333333	0.078272047	NA	NA	hypothetical protein
TS28Clo00166|CDS|CDS	3	175	0.077824778	NA	NA	hypothetical protein
TS29Bif3365|CDS|CDS	0.333333333	19.5	0.077603055	NA	NA	hypothetical protein
TS28Bif4782|CDS|CDS	0.333333333	19.5	0.077603055	NA	NA	hypothetical protein
TS29Bac11486|CDS|CDS	0.4	23.5	0.07727283	NA	NA	hypothetical protein
TS29Fae05612|CDS|CDS	2	117.5	0.07727283	NA	NA	hypothetical protein
BLD1653|CDS|Lantibiotic	1.666666667	98.16666667	0.07707604	NA	NA	hypothetical protein
Bfra31120044|CDS|CDS	1.5	88.5	0.076945402	NA	NA	hypothetical protein
TS29Fae07235|CDS|CDS	3	177	0.076945402	NA	NA	hypothetical protein
TS29Bac03997|CDS|CDS	1	59	0.076945402	NA	NA	hypothetical protein
TS29Rum19818|CDS|CDS	0.5	29.5	0.076945402	NA	NA	hypothetical protein
TS29Rum16725|CDS|CDS	1	59	0.076945402	NA	NA	hypothetical protein
BL0586|CDS|protein	0.25	14.75	0.076945402	NA	NA	hypothetical protein
BLD1752|CDS|acetoin/pyruvate	0.5	29.5	0.076945402	NA	NA	hypothetical protein
TS28Fae19435|CDS|CDS	1	59	0.076945402	NA	NA	hypothetical protein
TS29Bac02268|CDS|CDS	0.333333333	19.66666667	0.076945402	NA	NA	hypothetical protein
BLD0978|CDS|Membrane	0.5	29.58333333	0.076728655	NA	NA	hypothetical protein
TS29Fae04150|CDS|CDS	0.25	14.83333333	0.076513125	NA	NA	hypothetical protein
TS29Fae00877|CDS|CDS	2	119	0.076298802	NA	NA	hypothetical protein
TS29Fae08322|CDS|CDS	1	59.5	0.076298802	NA	NA	hypothetical protein
TS29Fae05960|CDS|CDS	2	119	0.076298802	NA	NA	hypothetical protein
Bbre0196|CDS|CDS	1.6	95.3	0.076218741	NA	NA	hypothetical protein
TS28Bac5945|CDS|CDS	1	59.66666667	0.076085677	NA	NA	hypothetical protein
TS29Fae00842|CDS|CDS	0.5	30	0.075662979	NA	NA	hypothetical protein
BLD0460|CDS|hypothetical	0.2	12	0.075662979	NA	NA	hypothetical protein
BL0288|CDS|hypothetical	0.25	15	0.075662979	NA	NA	hypothetical protein
TS29Bac02801|CDS|CDS	0.4	24	0.075662979	NA	NA	hypothetical protein
BLD0455|CDS|Adenine/guanine	0.25	15	0.075662979	NA	NA	hypothetical protein
FpraM2121654|CDS|CDS	0.333333333	20	0.075662979	NA	NA	hypothetical protein
FpraM2122510|CDS|CDS	0.333333333	20	0.075662979	NA	NA	hypothetical protein
TS29Bac02308|CDS|CDS	0.333333333	20	0.075662979	NA	NA	hypothetical protein
TS29Bif0699|CDS|CDS	1.366666667	82.33333333	0.075356651	NA	NA	hypothetical protein
EUBREC3557|CDS|hypothetical	0.5	30.25	0.075037665	NA	NA	hypothetical protein
BL1139|CDS|hypothetical	0.583333333	35.33333333	0.074949177	NA	NA	hypothetical protein
TS29Bif1051|CDS|CDS	0.583333333	35.33333333	0.074949177	NA	NA	hypothetical protein
Bpse1643|CDS|CDS	0.583333333	35.33333333	0.074949177	NA	NA	hypothetical protein
TS29Rum19434|CDS|CDS	0.25	15.25	0.074422602	NA	NA	hypothetical protein
TS29Bac10133|CDS|CDS	0.5	30.5	0.074422602	NA	NA	hypothetical protein
TS29Fae01383|CDS|CDS	1.666666667	102	0.074179391	NA	NA	hypothetical protein
BLD1593|CDS|Polyphosphate	0.833333333	51.08333333	0.074058381	NA	NA	hypothetical protein
TS29Bif3390|CDS|CDS	0.5	30.66666667	0.074018132	NA	NA	hypothetical protein
TS28Bif4812|CDS|CDS	0.5	30.66666667	0.074018132	NA	NA	hypothetical protein
TS29Bac04093|CDS|CDS	0.5	30.66666667	0.074018132	NA	NA	hypothetical protein
BLD1261|CDS|Glutamyl-tRNA	0.5	30.75	0.07381754	NA	NA	hypothetical protein
BL0469|CDS|glutamyl-tRNA	0.5	30.75	0.07381754	NA	NA	hypothetical protein
TS29Clo4343|CDS|CDS	0.333333333	20.5	0.07381754	NA	NA	hypothetical protein
Ccom2073|CDS|CDS	0.333333333	20.5	0.07381754	NA	NA	hypothetical protein
TS29Rum19575|CDS|CDS	0.333333333	20.5	0.07381754	NA	NA	hypothetical protein
TS29Fae06707|CDS|CDS	1.25	77	0.073697707	NA	NA	hypothetical protein
TS28Bif1978|CDS|CDS	0.25	15.41666667	0.073618034	NA	NA	hypothetical protein
BL1068|CDS|rRNA	0.75	46.33333333	0.073485627	NA	NA	hypothetical protein
TS28Eub6361|CDS|CDS	1.333333333	82.41666667	0.073444348	NA	NA	hypothetical protein
TS29Rum21229|CDS|CDS	1.333333333	82.41666667	0.073444348	NA	NA	hypothetical protein
Rgna1418|CDS|CDS	0.142857143	8.833333333	0.073419602	NA	NA	hypothetical protein
BL1074|CDS|dihydrolipoamide	0.25	15.5	0.073222238	NA	NA	hypothetical protein
TS29Fae09554|CDS|CDS	0.5	31	0.073222238	NA	NA	hypothetical protein
TS29Fae07134|CDS|CDS	0.5	31	0.073222238	NA	NA	hypothetical protein
TS29Bac08007|CDS|CDS	0.5	31	0.073222238	NA	NA	hypothetical protein
TS29Fae02381|CDS|CDS	0.5	31	0.073222238	NA	NA	hypothetical protein
Cnex2741|CDS|CDS	1	62.5	0.07263646	NA	NA	hypothetical protein
FpraM2120534|CDS|CDS	1	62.5	0.07263646	NA	NA	hypothetical protein
TS29Bac08026|CDS|CDS	0.333333333	20.83333333	0.07263646	NA	NA	hypothetical protein
TS28Bac5957|CDS|CDS	0.333333333	20.83333333	0.07263646	NA	NA	hypothetical protein
BLD0667|CDS|Putative	0.25	15.66666667	0.072443278	NA	NA	hypothetical protein
BLD1559|CDS|hypothetical	0.5	31.41666667	0.07225112	NA	NA	hypothetical protein
Acol0868|CDS|CDS	0.5	31.5	0.07205998	NA	NA	hypothetical protein
FpraM2121552|CDS|CDS	0.5	31.5	0.07205998	NA	NA	hypothetical protein
TS29Clo4971|CDS|CDS	0.4	25.2	0.07205998	NA	NA	hypothetical protein
TS28Fae08468|CDS|CDS	1	63	0.07205998	NA	NA	hypothetical protein
TS28Rum13642|CDS|CDS	0.5	31.5	0.07205998	NA	NA	hypothetical protein
EUBREC3540|CDS|hypothetical	1	63	0.07205998	NA	NA	hypothetical protein

BLD1899|CDS|IMP	0.5	31.5	0.07205998	NA	NA	hypothetical protein
TS29Fae01532|CDS|CDS	0.333333333	21	0.07205998	NA	NA	hypothetical protein
BL1369|CDS|large	0.75	47.33333333	0.071933114	NA	NA	hypothetical protein
TS29Fae10167|CDS|CDS	2.5	158.5	0.071605343	NA	NA	hypothetical protein
TS29Bac09009|CDS|CDS	0.333333333	21.16666667	0.071492579	NA	NA	hypothetical protein
BLD0650|CDS|Xanthine/uracil	0.4	25.41666667	0.071445698	NA	NA	hypothetical protein
BL0670|CDS|ribonucleotide-diphosphate	0.5	31.83333333	0.071305425	NA	NA	hypothetical protein
BLD1462|CDS|Ribonucleotide	0.5	31.83333333	0.071305425	NA	NA	hypothetical protein
TS28Bif1961|CDS|CDS	5.25	335.75	0.07098686	NA	NA	hypothetical protein
TS29Fae01205|CDS|CDS	0.5	32	0.070934043	NA	NA	hypothetical protein
Robe0058|CDS|CDS	0.5	32	0.070934043	NA	NA	hypothetical protein
TS29Fae08605|CDS|CDS	1	64	0.070934043	NA	NA	hypothetical protein
TS29Col1803|CDS|CDS	0.5	32	0.070934043	NA	NA	hypothetical protein
TS29Rum15254|CDS|CDS	0.5	32	0.070934043	NA	NA	hypothetical protein
BLD0738|CDS|DNA	0.75	48.33333333	0.070444842	NA	NA	hypothetical protein
TS28Fae21994|CDS|CDS	1	64.5	0.070384166	NA	NA	hypothetical protein
TS29Fae08707|CDS|CDS	2	129	0.070384166	NA	NA	hypothetical protein
TS29Fae07415|CDS|CDS	0.333333333	21.5	0.070384166	NA	NA	hypothetical protein
TS29Fae01394|CDS|CDS	0.583333333	37.83333333	0.069996588	NA	NA	hypothetical protein
TS29Bif0741|CDS|CDS	0.666666667	43.33333333	0.06984275	NA	NA	hypothetical protein
TS28Bif0969|CDS|CDS	0.666666667	43.33333333	0.06984275	NA	NA	hypothetical protein
TS29Fae03136|CDS|CDS	0.2	13	0.06984275	NA	NA	hypothetical protein
TS29Fae09995|CDS|CDS	1	65	0.06984275	NA	NA	hypothetical protein
TS29Clo4940|CDS|CDS	1	65	0.06984275	NA	NA	hypothetical protein
TS29Bif0850|CDS|CDS	0.25	16.33333333	0.069486409	NA	NA	hypothetical protein
TS29Bac07411|CDS|CDS	0.25	16.33333333	0.069486409	NA	NA	hypothetical protein
Rbro0068|CDS|CDS	1.25	81.66666667	0.069486409	NA	NA	hypothetical protein
TS29Fae06060|CDS|CDS	1	65.5	0.069309599	NA	NA	hypothetical protein
TS29Dor1484|CDS|CDS	0.333333333	21.83333333	0.069309599	NA	NA	hypothetical protein
TS29Fae01396|CDS|CDS	0.333333333	21.83333333	0.069309599	NA	NA	hypothetical protein
Hfil2884|CDS|CDS	1.5	98.83333333	0.06890052	NA	NA	hypothetical protein
BLD0891|CDS|S-layer	0.666666667	44	0.068784526	NA	NA	hypothetical protein
TS29Rum11717|CDS|CDS	1	66	0.068784526	NA	NA	hypothetical protein
TS29RumUnc0206|CDS|CDS	1	66	0.068784526	NA	NA	hypothetical protein
Hfil2897|CDS|CDS	0.571428571	37.75	0.068719451	NA	NA	hypothetical protein
Cnex1080|CDS|CDS	0.166666667	11.01666667	0.068680465	NA	NA	hypothetical protein
EUBREC2709|CDS|cassette	0.311361738	20.5952381	0.06863302	NA	NA	hypothetical protein
EUBREC0786|CDS|cassette	0.311361738	20.5952381	0.06863302	NA	NA	hypothetical protein
BL0327|CDS|tRNA	0.25	16.625	0.068267349	NA	NA	hypothetical protein
TS29Fae08726|CDS|CDS	1	66.5	0.068267349	NA	NA	hypothetical protein
BL0926|CDS|translation-associated	0.25	16.66666667	0.068096681	NA	NA	hypothetical protein
BLD0125|CDS|LacI-type	0.25	16.66666667	0.068096681	NA	NA	hypothetical protein
TS29RumUnc0542|CDS|CDS	1	67	0.067757892	NA	NA	hypothetical protein
TS29Fae06317|CDS|CDS	0.5	33.5	0.067757892	NA	NA	hypothetical protein
TS29Rum19920|CDS|CDS	2.5	167.5	0.067757892	NA	NA	hypothetical protein
TS28Bif5344|CDS|CDS	1	67	0.067757892	NA	NA	hypothetical protein
TS29RumUnc0730|CDS|CDS	1	67	0.067757892	NA	NA	hypothetical protein
TS29Fae01375|CDS|CDS	0.5	33.5	0.067757892	NA	NA	hypothetical protein
TS29Fae06692|CDS|CDS	1	67	0.067757892	NA	NA	hypothetical protein
Rgna1425|CDS|CDS	0.333333333	22.33333333	0.067757892	NA	NA	hypothetical protein
TS29Bac10245|CDS|CDS	1	67.21666667	0.06753948	NA	NA	hypothetical protein
Bthe3735772|CDS|CDS	1	67.21666667	0.06753948	NA	NA	hypothetical protein
TS28Bac5424|CDS|CDS	1	67.21666667	0.06753948	NA	NA	hypothetical protein
BWH25668|CDS|CDS	1	67.21666667	0.06753948	NA	NA	hypothetical protein
BLD0916|CDS|ABC-type	0.5	33.66666667	0.067422456	NA	NA	hypothetical protein
TS28Bif0994|CDS|CDS	1	67.33333333	0.067422456	NA	NA	hypothetical protein
TS29Fae00140|CDS|CDS	2.5	169.5	0.066958388	NA	NA	hypothetical protein
TS29Bif3433|CDS|CDS	0.5	34	0.066761452	NA	NA	hypothetical protein
Ehal0369|CDS|CDS	1	68	0.066761452	NA	NA	hypothetical protein
BLD0733|CDS|Hypothetical	0.25	17	0.066761452	NA	NA	hypothetical protein
TS29Bac08000|CDS|CDS	0.5	34	0.066761452	NA	NA	hypothetical protein
TS28Bif4860|CDS|CDS	0.5	34	0.066761452	NA	NA	hypothetical protein
TS29Fae10019|CDS|CDS	0.5	34	0.066761452	NA	NA	hypothetical protein
TS29Fae09865|CDS|CDS	0.5	34	0.066761452	NA	NA	hypothetical protein
EUBREC3556|CDS|ABC-type	0.25	17	0.066761452	NA	NA	hypothetical protein
TS28Fae07682|CDS|CDS	0.25	17	0.066761452	NA	NA	hypothetical protein
TS29Bac00907|CDS|CDS	0.333333333	22.66666667	0.066761452	NA	NA	hypothetical protein
TS29Rum11994|CDS|CDS	0.25	17.08333333	0.066435786	NA	NA	hypothetical protein
BL1034|CDS|gamma-glutamyl	1	68.5	0.066274142	NA	NA	hypothetical protein
TS29Fae00218|CDS|CDS	1	68.5	0.066274142	NA	NA	hypothetical protein
TS29Rum17186|CDS|CDS	1	68.5	0.066274142	NA	NA	hypothetical protein
BL1286|CDS|aspartate	0.25	17.16666667	0.066113283	NA	NA	hypothetical protein
Acac2259|CDS|CDS	0.666666667	46	0.065793895	NA	NA	hypothetical protein
BL1003|CDS|hypothetical	1	69	0.065793895	NA	NA	hypothetical protein
TS29Rum19532|CDS|CDS	1	69	0.065793895	NA	NA	hypothetical protein
Rtor0858|CDS|CDS	0.5	34.5	0.065793895	NA	NA	hypothetical protein
TS29RumUnc1092|CDS|CDS	1	69	0.065793895	NA	NA	hypothetical protein
TS29Fae03736|CDS|CDS	1	69	0.065793895	NA	NA	hypothetical protein
Bste1760|CDS|CDS	0.333333333	23	0.065793895	NA	NA	hypothetical protein
TS29Bac08047|CDS|CDS	0.333333333	23	0.065793895	NA	NA	hypothetical protein
TS29Rum01257|CDS|CDS	0.333333333	23	0.065793895	NA	NA	hypothetical protein
TS28Bac5948|CDS|CDS	0.333333333	23	0.065793895	NA	NA	hypothetical protein
TS29Fae03046|CDS|CDS	0.5	34.83333333	0.065164288	NA	NA	hypothetical protein
Bbre0193|CDS|CDS	0.643589744	45	0.06492789	NA	NA	hypothetical protein
TS28Fae01855|CDS|CDS	0.5	35	0.064853982	NA	NA	hypothetical protein
TS29Bif2775|CDS|CDS	1	70	0.064853982	NA	NA	hypothetical protein
BL1623|CDS|ribose-5-phosphate	0.333333333	23.41666667	0.064623185	NA	NA	hypothetical protein
BLD0748|CDS|ABC-type	0.25	17.58333333	0.064546617	NA	NA	hypothetical protein
TS28Eub0311|CDS|CDS	0.333333333	23.5	0.064394025	NA	NA	hypothetical protein
BLD0878|CDS|Glutamine	0.5	35.33333333	0.064242152	NA	NA	hypothetical protein
TS29Fae02374|CDS|CDS	0.333333333	23.66666667	0.063940546	NA	NA	hypothetical protein
TS29Fae03345|CDS|CDS	1	71	0.063940546	NA	NA	hypothetical protein
BL1504|CDS|elongation	0.25	17.75	0.063940546	NA	NA	hypothetical protein
BLD0404|CDS|Translation	0.25	17.75	0.063940546	NA	NA	hypothetical protein
BL0658|CDS|hypothetical	0.666666667	47.5	0.063716193	NA	NA	hypothetical protein

BL0017|CDS|histidyl-tRNA	0.5	35.66666667	0.063641758	NA	NA	hypothetical protein
TS29Bif3310|CDS|CDS	0.333333333	23.83333333	0.063493409	NA	NA	hypothetical protein
FpraM2120898|CDS|CDS	3.5	251.3333333	0.06321973	NA	NA	hypothetical protein
EUBREC3581|CDS|hypothetical	0.333333333	24	0.063052482	NA	NA	hypothetical protein
FpraM2120112|CDS|CDS	0.166666667	12	0.063052482	NA	NA	hypothetical protein
TS29Bac01930|CDS|CDS	0.333333333	24	0.063052482	NA	NA	hypothetical protein
TS29RumUnc0144|CDS|CDS	1	72	0.063052482	NA	NA	hypothetical protein
TS29Fae00065|CDS|CDS	0.25	18	0.063052482	NA	NA	hypothetical protein
TS29Fae07117|CDS|CDS	0.5	36	0.063052482	NA	NA	hypothetical protein
Bhan2439|CDS|CDS	0.5	36	0.063052482	NA	NA	hypothetical protein
TS28Fae21490|CDS|CDS	0.25	18	0.063052482	NA	NA	hypothetical protein
TS28Bac6168|CDS|CDS	0.5	36	0.063052482	NA	NA	hypothetical protein
Bcoprop2863|CDS|CDS	0.333333333	24	0.063052482	NA	NA	hypothetical protein
BL0905|CDS|hypothetical	0.6	43.25	0.062979589	NA	NA	hypothetical protein
Rgna2844|CDS|CDS	0.142857143	10.33333333	0.062761918	NA	NA	hypothetical protein
Rgna1324|CDS|CDS	0.142857143	10.33333333	0.062761918	NA	NA	hypothetical protein
Bste1754|CDS|CDS	1	72.33333333	0.062761918	NA	NA	hypothetical protein
TS28Bif4916|CDS|CDS	0.333333333	24.16666667	0.062617638	NA	NA	hypothetical protein
BL1428|CDS|RNA	0.666666667	48.41666667	0.062509862	NA	NA	hypothetical protein
Acol2742|CDS|CDS	0.5	36.33333333	0.062474019	NA	NA	hypothetical protein
TS29Fae00935|CDS|CDS	0.4	29.08333333	0.062438218	NA	NA	hypothetical protein
TS29RumUnc1290|CDS|CDS	1.25	91.16666667	0.062245595	NA	NA	hypothetical protein
TS28Fae13657|CDS|CDS	0.5	36.5	0.06218875	NA	NA	hypothetical protein
TS29Fae01401|CDS|CDS	1.866666667	136.3333333	0.06215834	NA	NA	hypothetical protein
TS28Clo10839|CDS|CDS	0.25	18.33333333	0.061906074	NA	NA	hypothetical protein
TS29Rum20629|CDS|CDS	1	73.5	0.061765697	NA	NA	hypothetical protein
BLD0147|CDS|Putative	0.25	18.41666667	0.061625956	NA	NA	hypothetical protein
TS29Fae05540|CDS|CDS	1	74	0.061348361	NA	NA	hypothetical protein
TS28Fae18152|CDS|CDS	0.5	37	0.061348361	NA	NA	hypothetical protein
BLD1037|CDS|Phosphopantetheine	0.25	18.5	0.061348361	NA	NA	hypothetical protein
TS28Bif2180|CDS|CDS	0.25	18.5	0.061348361	NA	NA	hypothetical protein
BL0291|CDS|phosphopantetheine	0.25	18.5	0.061348361	NA	NA	hypothetical protein
TS29Fae10363|CDS|CDS	1	74.08333333	0.061279353	NA	NA	hypothetical protein
TS29Bif2369|CDS|CDS	1.5	111.3333333	0.061164684	NA	NA	hypothetical protein
BL1016|CDS|Fk506-binding	0.5	37.16666667	0.061073257	NA	NA	hypothetical protein
BL0487|CDS|penicillin-binding	1	74.5	0.060936627	NA	NA	hypothetical protein
BL1200|CDS|hypothetical	0.75	56.08333333	0.060710265	NA	NA	hypothetical protein
Rgna2922|CDS|CDS	0.142857143	10.7	0.060611198	NA	NA	hypothetical protein
Rgna1168|CDS|CDS	0.142857143	10.7	0.060611198	NA	NA	hypothetical protein
TS29Rum12392|CDS|CDS	0.5	37.5	0.060530383	NA	NA	hypothetical protein
Bcap1463|CDS|CDS	0.2	15	0.060530383	NA	NA	hypothetical protein
BLD0754|CDS|Signal	0.25	18.75	0.060530383	NA	NA	hypothetical protein
TS29Rum15297|CDS|CDS	1	75	0.060530383	NA	NA	hypothetical protein
EUBREC2687|CDS|TraG	0.2	15	0.060530383	NA	NA	hypothetical protein
EUBREC0808|CDS|TraG	0.2	15	0.060530383	NA	NA	hypothetical protein
BLD1051|CDS|Metal-dependent	0.25	18.83333333	0.06026255	NA	NA	hypothetical protein
TS28Bif0642|CDS|CDS	0.75	57	0.059733931	NA	NA	hypothetical protein
TS29Bif3941|CDS|CDS	0.75	57	0.059733931	NA	NA	hypothetical protein
Dlon2151|CDS|CDS	0.25	19	0.059733931	NA	NA	hypothetical protein
TS29Fae03477|CDS|CDS	1	76	0.059733931	NA	NA	hypothetical protein
TS29Fae08157|CDS|CDS	0.5	38	0.059733931	NA	NA	hypothetical protein
TS29Rum20834|CDS|CDS	0.5	38	0.059733931	NA	NA	hypothetical protein
BL1679|CDS|hypothetical	0.333333333	25.33333333	0.059733931	NA	NA	hypothetical protein
TS28Bif1904|CDS|CDS	0.5	38.16666667	0.059473084	NA	NA	hypothetical protein
TS29Fae00818|CDS|CDS	1.5	115	0.059214505	NA	NA	hypothetical protein
TS29Col0158|CDS|CDS	0.5	38.5	0.058958165	NA	NA	hypothetical protein
TS29Fae00683|CDS|CDS	1	77	0.058958165	NA	NA	hypothetical protein
TS29Bac10023|CDS|CDS	0.5	38.5	0.058958165	NA	NA	hypothetical protein
TS29Fae02951|CDS|CDS	0.5	38.5	0.058958165	NA	NA	hypothetical protein
BLD0753|CDS|Putative	0.25	19.5	0.058202291	NA	NA	hypothetical protein
TS29Bac03715|CDS|CDS	0.5	39	0.058202291	NA	NA	hypothetical protein
TS29LacUnc132|CDS|CDS	0.25	19.5	0.058202291	NA	NA	hypothetical protein
TS28Fae07424|CDS|CDS	1	78	0.058202291	NA	NA	hypothetical protein
BL1259|CDS|polyphosphate	0.833333333	65.08333333	0.058127769	NA	NA	hypothetical protein
TS29Fae08113|CDS|CDS	0.333333333	26.16666667	0.057831576	NA	NA	hypothetical protein
TS29Bac00504|CDS|CDS	0.2	15.75	0.057647984	NA	NA	hypothetical protein
BLD1349|CDS|Zn-dependent	0.25	19.75	0.057465554	NA	NA	hypothetical protein
BL0564|CDS|modification	0.25	19.75	0.057465554	NA	NA	hypothetical protein
TS29Fae08221|CDS|CDS	0.5	39.5	0.057465554	NA	NA	hypothetical protein
BLD1359|CDS|Site-specific	0.25	19.75	0.057465554	NA	NA	hypothetical protein
TS28Bac5958|CDS|CDS	0.5	39.83333333	0.05698467	NA	NA	hypothetical protein
TS29Bac09054|CDS|CDS	0.2	16	0.056747234	NA	NA	hypothetical protein
TS29Fae08956|CDS|CDS	1	80	0.056747234	NA	NA	hypothetical protein
TS29Rum20489|CDS|CDS	1	80	0.056747234	NA	NA	hypothetical protein
TS29Col1681|CDS|CDS	0.5	40	0.056747234	NA	NA	hypothetical protein
TS29Col0294|CDS|CDS	1	80	0.056747234	NA	NA	hypothetical protein
TS28Bif3723|CDS|CDS	0.916666667	73.33333333	0.056747234	NA	NA	hypothetical protein
TS29Rum21223|CDS|CDS	0.5	40.25	0.056394767	NA	NA	hypothetical protein
TS29Bac02161|CDS|CDS	0.333333333	26.91666667	0.05622017	NA	NA	hypothetical protein
TS29Fae01468|CDS|CDS	0.5	40.5	0.056046651	NA	NA	hypothetical protein
BL1412|CDS|CDP-diacylglycerol--glycerol-3-phosphate	0.25	20.25	0.056046651	NA	NA	hypothetical protein
Rgna2112|CDS|CDS	0.5	40.5	0.056046651	NA	NA	hypothetical protein
TS29Col1975|CDS|CDS	1	81	0.056046651	NA	NA	hypothetical protein
TS29Fae08172|CDS|CDS	0.5	40.5	0.056046651	NA	NA	hypothetical protein
TS29Rum19890|CDS|CDS	0.5	40.5	0.056046651	NA	NA	hypothetical protein
TS28LacUnc478|CDS|CDS	0.333333333	27	0.056046651	NA	NA	hypothetical protein
BLD1608|CDS|Homoserine	0.25	20.5	0.055363155	NA	NA	hypothetical protein
TS29Bif0458|CDS|CDS	0.333333333	27.33333333	0.055363155	NA	NA	hypothetical protein
BL0655|CDS|hypothetical	0.333333333	27.33333333	0.055363155	NA	NA	hypothetical protein
BLD1450|CDS|hypothetical	0.333333333	27.33333333	0.055363155	NA	NA	hypothetical protein
BL1274|CDS|homoserine	0.375	30.91666667	0.055064702	NA	NA	hypothetical protein
TS29Fae08271|CDS|CDS	1	82.5	0.055027621	NA	NA	hypothetical protein
RintL13977|CDS|CDS	0.666666667	55.33333333	0.054696129	NA	NA	hypothetical protein
TS29Fae06508|CDS|CDS	0.5	41.5	0.054696129	NA	NA	hypothetical protein
TS29Fae03209|CDS|CDS	1	83	0.054696129	NA	NA	hypothetical protein

TS29Rum00494|CDS|CDS	1	83	0.054696129	NA	NA	hypothetical protein
BL0338|CDS|aspartate	0.583333333	48.41666667	0.054696129	NA	NA	hypothetical protein
BL1675|CDS|hypothetical	0.333333333	27.91666667	0.054206313	NA	NA	hypothetical protein
TS29Fae04140|CDS|CDS	0.25	21	0.054044985	NA	NA	hypothetical protein
TS28Bif0747|CDS|CDS	0.5	42	0.054044985	NA	NA	hypothetical protein
EUBREC3538|CDS|hypothetical	0.5	42	0.054044985	NA	NA	hypothetical protein
TS29Eub2197|CDS|CDS	0.5	42	0.054044985	NA	NA	hypothetical protein
TS28Bif0925|CDS|CDS	0.5	42.33333333	0.053619434	NA	NA	hypothetical protein
BLD0830|CDS|Hypothetical	0.25	21.16666667	0.053619434	NA	NA	hypothetical protein
TS29Bif0857|CDS|CDS	0.333333333	28.33333333	0.053409162	NA	NA	hypothetical protein
BL1498|CDS|hypothetical	0.25	21.25	0.053409162	NA	NA	hypothetical protein
TS29Fae04618|CDS|CDS	1	85	0.053409162	NA	NA	hypothetical protein
Rtor1330|CDS|CDS	1	85	0.053409162	NA	NA	hypothetical protein
TS29Rum16956|CDS|CDS	0.2	17	0.053409162	NA	NA	hypothetical protein
EUBREC3533|CDS|hypothetical	0.5	42.5	0.053409162	NA	NA	hypothetical protein
BL0175|CDS|AraC/XylS-type	0.5	42.66666667	0.053200532	NA	NA	hypothetical protein
BL1434|CDS|DNA	0.25	21.41666667	0.052993526	NA	NA	hypothetical protein
BL0394|CDS|ABC	0.25	21.41666667	0.052993526	NA	NA	hypothetical protein
BLD1358|CDS|DNA	0.25	21.5	0.052788125	NA	NA	hypothetical protein
BL0563|CDS|type	0.25	21.5	0.052788125	NA	NA	hypothetical protein
TS28Fae00285|CDS|CDS	0.5	43	0.052788125	NA	NA	hypothetical protein
BL1246|CDS|hypothetical	1	86.25	0.052635116	NA	NA	hypothetical protein
TS28Bif4971|CDS|CDS	0.8	69.31666667	0.052394657	NA	NA	hypothetical protein
TS29Fae05591|CDS|CDS	1	87	0.052181365	NA	NA	hypothetical protein
TS29Bif3315|CDS|CDS	0.6	52.2	0.052181365	NA	NA	hypothetical protein
TS29Bac10481|CDS|CDS	0.333333333	29	0.052181365	NA	NA	hypothetical protein
TS29Rum01103|CDS|CDS	0.25	21.91666667	0.051784548	NA	NA	hypothetical protein
BLD1858|CDS|NagC-type	0.5	43.91666667	0.051686285	NA	NA	hypothetical protein
TS29Rum00197|CDS|CDS	1	88	0.051588395	NA	NA	hypothetical protein
TS29Fae05346|CDS|CDS	1	88	0.051588395	NA	NA	hypothetical protein
BL0630|CDS|glutamate	0.25	22	0.051588395	NA	NA	hypothetical protein
TS29Bac00304|CDS|CDS	0.5	44	0.051588395	NA	NA	hypothetical protein
BL0682|CDS|xylan	0.5	44.08333333	0.051490874	NA	NA	hypothetical protein
BLD0016|CDS|Hypothetical	0.333333333	29.41666667	0.051442252	NA	NA	hypothetical protein
BL0428|CDS|hypothetical	0.5	44.33333333	0.051200512	NA	NA	hypothetical protein
BLD0158|CDS|hypothetical	0.25	22.25	0.05100875	NA	NA	hypothetical protein
TS28Fae11427|CDS|CDS	1	89	0.05100875	NA	NA	hypothetical protein
TS29Fae04718|CDS|CDS	1	89	0.05100875	NA	NA	hypothetical protein
TS29RumUnc0142|CDS|CDS	1	89	0.05100875	NA	NA	hypothetical protein
TS29Bif1452|CDS|CDS	0.333333333	29.66666667	0.05100875	NA	NA	hypothetical protein
BLD0456|CDS|Succinyl-CoA	0.333333333	29.66666667	0.05100875	NA	NA	hypothetical protein
TS29Bac11149|CDS|CDS	0.333333333	29.66666667	0.05100875	NA	NA	hypothetical protein
BL0099|CDS|hypothetical	0.25	22.41666667	0.050629503	NA	NA	hypothetical protein
TS29Bac08057|CDS|CDS	1	89.66666667	0.050629503	NA	NA	hypothetical protein
TS29Rum00211|CDS|CDS	1	90	0.050441986	NA	NA	hypothetical protein
FpraM2122462|CDS|CDS	0.5	45	0.050441986	NA	NA	hypothetical protein
Bxyl2752|CDS|CDS	0.25	22.5	0.050441986	NA	NA	hypothetical protein
TS29Bif1709|CDS|CDS	0.25	22.5	0.050441986	NA	NA	hypothetical protein
TS28Bif1445|CDS|CDS	0.5	45.5	0.049887678	NA	NA	hypothetical protein
TS28Bif0760|CDS|CDS	1.5	136.5	0.049887678	NA	NA	hypothetical protein
TS29Bif3148|CDS|CDS	0.5	45.5	0.049887678	NA	NA	hypothetical protein
BL1032|CDS|nicotinic	0.25	22.83333333	0.049705607	NA	NA	hypothetical protein
BLD0782|CDS|Nicotinic	0.25	22.83333333	0.049705607	NA	NA	hypothetical protein
TS29Rum19365|CDS|CDS	0.5	45.66666667	0.049705607	NA	NA	hypothetical protein
TS29Rum16631|CDS|CDS	1	91.5	0.049615068	NA	NA	hypothetical protein
TS29Fae09145|CDS|CDS	1	91.5	0.049615068	NA	NA	hypothetical protein
TS28Bif5151|CDS|CDS	0.25	22.95	0.049452927	NA	NA	hypothetical protein
TS28Bif0173|CDS|CDS	0.5	46	0.049345421	NA	NA	hypothetical protein
TS29Bif2628|CDS|CDS	0.5	46	0.049345421	NA	NA	hypothetical protein
TS28Fae02049|CDS|CDS	0.5	46	0.049345421	NA	NA	hypothetical protein
TS29Fae00179|CDS|CDS	0.5	46	0.049345421	NA	NA	hypothetical protein
BLD0263|CDS|Cation	0.333333333	30.91666667	0.048946401	NA	NA	hypothetical protein
TS29Bif2629|CDS|CDS	0.5	46.5	0.048814825	NA	NA	hypothetical protein
TS28Bif0172|CDS|CDS	0.5	46.5	0.048814825	NA	NA	hypothetical protein
BLD1660|CDS|Carbohydrate	0.5	46.75	0.048553783	NA	NA	hypothetical protein
TS29Par966|CDS|CDS	0.5	47	0.048295518	NA	NA	hypothetical protein
BL1273|CDS|diaminopimelate	0.75	70.5	0.048295518	NA	NA	hypothetical protein
BLD0935|CDS|ABC-type	0.333333333	31.33333333	0.048295518	NA	NA	hypothetical protein
TS29Fae01270|CDS|CDS	3	283	0.048124863	NA	NA	hypothetical protein
EUBREC2716|CDS|hypothetical	0.4	37.86666667	0.047955409	NA	NA	hypothetical protein
EUBREC0779|CDS|hypothetical	0.4	37.86666667	0.047955409	NA	NA	hypothetical protein
TS29Fae08727|CDS|CDS	0.833333333	79	0.047887961	NA	NA	hypothetical protein
TS28Bif0548|CDS|CDS	0.5	47.41666667	0.047871129	NA	NA	hypothetical protein
TS29Bac02112|CDS|CDS	0.333333333	31.66666667	0.047787145	NA	NA	hypothetical protein
BLD1239|CDS|Glycosyltransferase	0.25	23.83333333	0.047620057	NA	NA	hypothetical protein
BL0619|CDS|hypothetical	0.4	38.2	0.04753695	NA	NA	hypothetical protein
BLD1411|CDS|Putative	0.4	38.2	0.04753695	NA	NA	hypothetical protein
TS29Bif3418|CDS|CDS	0.666666667	64	0.047289362	NA	NA	hypothetical protein
TS29Rum11478|CDS|CDS	0.5	48	0.047289362	NA	NA	hypothetical protein
TS29Bac04880|CDS|CDS	0.25	24	0.047289362	NA	NA	hypothetical protein
TS29Bac08705|CDS|CDS	0.333333333	32.25	0.046922778	NA	NA	hypothetical protein
TS29Rum19891|CDS|CDS	0.5	48.5	0.046801843	NA	NA	hypothetical protein
BL0995|CDS|ATP	0.25	24.25	0.046801843	NA	NA	hypothetical protein
BL1102|CDS|Na+	0.5	48.83333333	0.046482376	NA	NA	hypothetical protein
BLD0131|CDS|Hydroxymethylpyrimidine/phosphomethylpyrimidine	0.2	19.56666667	0.04640319	NA	NA	hypothetical protein
Bpse1636|CDS|CDS	0.25	24.5	0.046324273	NA	NA	hypothetical protein
TS29Fae06734|CDS|CDS	0.5	49	0.046324273	NA	NA	hypothetical protein
TS29Fae05465|CDS|CDS	1	98	0.046324273	NA	NA	hypothetical protein
Rbro1710|CDS|CDS	0.071428571	7	0.046324273	NA	NA	hypothetical protein
TS29Rum15965|CDS|CDS	2	196.5	0.046206399	NA	NA	hypothetical protein
BLD0646|CDS|Carbon	0.25	24.58333333	0.046167241	NA	NA	hypothetical protein
BL0440|CDS|glucose-6-phosphate	0.75	74.16666667	0.045907875	NA	NA	hypothetical protein
BLD1046|CDS|ABC	0.5	49.45833333	0.045894983	NA	NA	hypothetical protein
TS29Fae00444|CDS|CDS	0.5	49.5	0.045856351	NA	NA	hypothetical protein
TS28Clo02252|CDS|CDS	0.5	49.5	0.045856351	NA	NA	hypothetical protein

TS29Fae08173|CDS|CDS	1	99	0.045856351	NA	NA	hypothetical protein
TS29Rum21253|CDS|CDS	0.25	25	0.045397787	NA	NA	hypothetical protein
TS29Bac04682|CDS|CDS	0.333333333	33.33333333	0.045397787	NA	NA	hypothetical protein
TS29Fae00159|CDS|CDS	0.5	50	0.045397787	NA	NA	hypothetical protein
BLD1777|CDS|Lysyl-tRNA	0.25	25.08333333	0.045246964	NA	NA	hypothetical protein
TS29Fae05598|CDS|CDS	1	100.5	0.045171928	NA	NA	hypothetical protein
TS28Bif2124|CDS|CDS	0.5	50.41666667	0.045022599	NA	NA	hypothetical protein
TS28Fae22362|CDS|CDS	0.5	50.5	0.044948304	NA	NA	hypothetical protein
BLD1196|CDS|ABC-type	0.25	25.41666667	0.044653561	NA	NA	hypothetical protein
BLD0942|CDS|Protein	0.25	25.41666667	0.044653561	NA	NA	hypothetical protein
TS29Fae06392|CDS|CDS	0.5	51	0.044507635	NA	NA	hypothetical protein
TS29Fae00727|CDS|CDS	0.5	51	0.044507635	NA	NA	hypothetical protein
TS29Fae06040|CDS|CDS	0.5	51	0.044507635	NA	NA	hypothetical protein
TS29Bac10515|CDS|CDS	0.333333333	34	0.044507635	NA	NA	hypothetical protein
EUBREC3552|CDS|transcriptional	0.333333333	34	0.044507635	NA	NA	hypothetical protein
EUBREC3564|CDS|possible	3.75	384.3333333	0.044295326	NA	NA	hypothetical protein
Even0940|CDS|CDS	0.2	20.5	0.044290524	NA	NA	hypothetical protein
TS29Bif1225|CDS|CDS	0.5	51.33333333	0.044218624	NA	NA	hypothetical protein
BL0798|CDS|5-methyltetrahydropteroyltriglutamate--homocysteine	0.25	25.7	0.044161272	NA	NA	hypothetical protein
BLD0538|CDS|Cobalamin-independent	0.25	25.7	0.044161272	NA	NA	hypothetical protein
TS29Fae08699|CDS|CDS	2	206	0.044075522	NA	NA	hypothetical protein
BL1659|CDS|hypothetical	0.333333333	34.33333333	0.044075522	NA	NA	hypothetical protein
TS29Fae03387|CDS|CDS	0.5	51.5	0.044075522	NA	NA	hypothetical protein
BLD0787|CDS|Cation	0.25	26	0.043651719	NA	NA	hypothetical protein
TS29Bif3092|CDS|CDS	0.25	26	0.043651719	NA	NA	hypothetical protein
TS29Bac08083|CDS|CDS	0.5	52	0.043651719	NA	NA	hypothetical protein
Robe0032|CDS|CDS	0.125	13	0.043651719	NA	NA	hypothetical protein
TS28Bac5956|CDS|CDS	0.333333333	34.66666667	0.043651719	NA	NA	hypothetical protein
Bste1777|CDS|CDS	0.333333333	34.66666667	0.043651719	NA	NA	hypothetical protein
TS29Bac08028|CDS|CDS	0.333333333	34.66666667	0.043651719	NA	NA	hypothetical protein
TS29Rum19863|CDS|CDS	0.388888889	40.5	0.04359184	NA	NA	hypothetical protein
BL0512|CDS|3-oxoacyl-[acyl-carrier	0.4	41.66666667	0.043581876	NA	NA	hypothetical protein
BL0299|CDS|ATP	0.5	52.125	0.043547038	NA	NA	hypothetical protein
BL0987|CDS|MutT	0.25	26.16666667	0.043373682	NA	NA	hypothetical protein
BLD0873|CDS|Cytosine	0.25	26.20833333	0.043304726	NA	NA	hypothetical protein
TS29Fae05338|CDS|CDS	0.5	52.5	0.043235988	NA	NA	hypothetical protein
BLD0465|CDS|Hypothetical	0.5	52.5	0.043235988	NA	NA	hypothetical protein
BLD0397|CDS|hypothetical	0.25	26.41666667	0.042963206	NA	NA	hypothetical protein
TS29Eub2196|CDS|CDS	0.25	26.5	0.042828101	NA	NA	hypothetical protein
TS29Bac03249|CDS|CDS	0.1	10.63809524	0.042674733	NA	NA	hypothetical protein
TS29Bif0599|CDS|CDS	0.75	80	0.042560426	NA	NA	hypothetical protein
BLD1694|CDS|Ribosomal	0.142857143	15.25	0.042527201	NA	NA	hypothetical protein
BL1572|CDS|30S	0.142857143	15.25	0.042527201	NA	NA	hypothetical protein
TS29Fae00234|CDS|CDS	0.5	53.5	0.042427839	NA	NA	hypothetical protein
BL1118|CDS|amino-acid	0.25	26.75	0.042427839	NA	NA	hypothetical protein
BL1109|CDS|carboxylesterase	0.25	26.83333333	0.042296075	NA	NA	hypothetical protein
TS29Bif0870|CDS|CDS	0.25	27	0.042034988	NA	NA	hypothetical protein
TS28Bif0415|CDS|CDS	0.25	27	0.042034988	NA	NA	hypothetical protein
BLD1033|CDS|hypothetical	0.25	27	0.042034988	NA	NA	hypothetical protein
BL0199|CDS|hypothetical	0.5	54.25	0.041841279	NA	NA	hypothetical protein
BLD1447|CDS|hypothetical	0.5	54.33333333	0.041777105	NA	NA	hypothetical protein
TS29Rum15380|CDS|CDS	1	109	0.041649346	NA	NA	hypothetical protein
TS29Bif3143|CDS|CDS	0.5	54.5	0.041649346	NA	NA	hypothetical protein
BL1001|CDS|histidine	0.25	27.25	0.041649346	NA	NA	hypothetical protein
TS29Col0132|CDS|CDS	1	110	0.041270716	NA	NA	hypothetical protein
BLD0826|CDS|acetoin/pyruvate	0.25	27.5	0.041270716	NA	NA	hypothetical protein
BLD1962|CDS|Type	1	110.4166667	0.041114977	NA	NA	hypothetical protein
BL1322|CDS|FtsW-like	0.25	27.75	0.040898908	NA	NA	hypothetical protein
BLD0780|CDS|Na+-driven	0.75	83.33333333	0.040858009	NA	NA	hypothetical protein
TS28Bif4382|CDS|CDS	0.25	28	0.040533739	NA	NA	hypothetical protein
EUBREC3553|CDS|serine-type	0.333333333	37.66666667	0.040175033	NA	NA	hypothetical protein
BL1543|CDS|endo-1,4-beta-xylanase	0.5	56.75	0.039998051	NA	NA	hypothetical protein
EUBREC3578|CDS|site-specific	0.678571429	77.34285714	0.039829976	NA	NA	hypothetical protein
TS29Rum19867|CDS|CDS	0.271428571	31	0.039749215	NA	NA	hypothetical protein
TS28Bif0736|CDS|CDS	0.5	57.25	0.039648723	NA	NA	hypothetical protein
EUBREC3542|CDS|DNA-directed	0.5	57.33333333	0.039591094	NA	NA	hypothetical protein
TS29Fae03388|CDS|CDS	0.5	57.5	0.039476337	NA	NA	hypothetical protein
BL1023|CDS|aldo/keto	0.25	28.75	0.039476337	NA	NA	hypothetical protein
BL1722|CDS|inosine-5'-monophosphate	0.5	57.5	0.039476337	NA	NA	hypothetical protein
EUBREC3586|CDS|hypothetical	0.5	57.5	0.039476337	NA	NA	hypothetical protein
TS29Fae08953|CDS|CDS	0.25	29	0.039136024	NA	NA	hypothetical protein
TS28Fae11189|CDS|CDS	0.25	29	0.039136024	NA	NA	hypothetical protein
BL1654|CDS|lysyl-tRNA	0.25	29.41666667	0.038581689	NA	NA	hypothetical protein
TS28Fae19298|CDS|CDS	0.25	29.5	0.038472701	NA	NA	hypothetical protein
BLD0035|CDS|truncated	0.2	23.75396825	0.038223329	NA	NA	hypothetical protein
Ceut1808|CDS|CDS	1	119	0.038149401	NA	NA	hypothetical protein
TS29Eub0075|CDS|CDS	0.166666667	20	0.037831489	NA	NA	hypothetical protein
Bcap2331|CDS|CDS	0.5	60	0.037831489	NA	NA	hypothetical protein
BLD0253|CDS|ABC-type	0.25	30	0.037831489	NA	NA	hypothetical protein
TS29Rum15610|CDS|CDS	0.2	24	0.037831489	NA	NA	hypothetical protein
TS29Fae00852|CDS|CDS	0.333333333	40	0.037831489	NA	NA	hypothetical protein
TS29Bif2807|CDS|CDS	0.5	60.16666667	0.037726693	NA	NA	hypothetical protein
BLD1221|CDS|Phosphoribosylpyrophosphate	0.25	30.16666667	0.037622476	NA	NA	hypothetical protein
TS29Fae09152|CDS|CDS	0.666666667	81	0.037364434	NA	NA	hypothetical protein
CspSS21646|CDS|CDS	0.058823529	7.166666667	0.037262206	NA	NA	hypothetical protein
BLD0177|CDS|UDP-N-acetylmuramyl	0.25	30.5	0.037211301	NA	NA	hypothetical protein
BLD0759|CDS|hypothetical	0.25	30.75	0.03690877	NA	NA	hypothetical protein
EUBREC3561|CDS|hypothetical	0.333333333	41	0.03690877	NA	NA	hypothetical protein
BLD1493|CDS|MalF-type	0.333333333	41	0.03690877	NA	NA	hypothetical protein
TS29Rum14526|CDS|CDS	1	123.5	0.036759342	NA	NA	hypothetical protein
TS28Fae00197|CDS|CDS	0.5	62	0.036611119	NA	NA	hypothetical protein
TS29Fae03177|CDS|CDS	0.5	62	0.036611119	NA	NA	hypothetical protein
TS29Fae00317|CDS|CDS	0.333333333	41.5	0.036464086	NA	NA	hypothetical protein

BL0269|CDS|ABC	0.4	50	0.03631823	NA	NA	hypothetical protein
BLD1978|CDS|Adenylosuccinate	0.333333333	41.83333333	0.036173536	NA	NA	hypothetical protein
TS29Fae06811|CDS|CDS	0.5	63	0.03602999	NA	NA	hypothetical protein
TS29Bif0906|CDS|CDS	0.25	31.75	0.035746289	NA	NA	hypothetical protein
BL1203|CDS|hypothetical	0.45	57.5	0.035528703	NA	NA	hypothetical protein
Hfil2148|CDS|CDS	0.25	32	0.035467021	NA	NA	hypothetical protein
TS29Dor2244|CDS|CDS	0.166666667	21.58333333	0.035056206	NA	NA	hypothetical protein
Cnex3096|CDS|CDS	0.166666667	21.58333333	0.035056206	NA	NA	hypothetical protein
TS29Fae05588|CDS|CDS	0.5	65	0.034921375	NA	NA	hypothetical protein
TS29Bif3530|CDS|CDS	0.8	104.3166667	0.034815367	NA	NA	hypothetical protein
TS29Fae03223|CDS|CDS	0.5	65.5	0.0346548	NA	NA	hypothetical protein
BLD0683|CDS|Kef-type	0.25	32.80952381	0.034591928	NA	NA	hypothetical protein
TS28Fae01850|CDS|CDS	0.5	66	0.034392263	NA	NA	hypothetical protein
TS29Bac03035|CDS|CDS	0.090909091	12	0.034392263	NA	NA	hypothetical protein
BL0519|CDS|GrpE	0.25	33.08333333	0.034305633	NA	NA	hypothetical protein
BL1009|CDS|hypothetical	0.25	33.16666667	0.034219438	NA	NA	hypothetical protein
BL0651|CDS|hypothetical	0.25	33.33333333	0.034048341	NA	NA	hypothetical protein
BL0964|CDS|UDP-N-acetylglucosamine	0.25	33.58333333	0.033794879	NA	NA	hypothetical protein
BL0113|CDS|phosphomethylpyrimidine	0.2	26.9	0.033753002	NA	NA	hypothetical protein
TS29Fae01196|CDS|CDS	1	137	0.033137071	NA	NA	hypothetical protein
TS29Bif0503|CDS|CDS	1	137.5	0.033016573	NA	NA	hypothetical protein
TS29Dor2238|CDS|CDS	0.2	27.83333333	0.032621165	NA	NA	hypothetical protein
Acol2763|CDS|CDS	0.071428571	10	0.032426991	NA	NA	hypothetical protein
TS29Fae08942|CDS|CDS	0.5	71	0.031970273	NA	NA	hypothetical protein
Rbro1699|CDS|CDS	0.333333333	47.5	0.031858096	NA	NA	hypothetical protein
TS29Bif0843|CDS|CDS	1	142.8333333	0.031783748	NA	NA	hypothetical protein
TS29Fae05216|CDS|CDS	0.5	72	0.031526241	NA	NA	hypothetical protein
TS28Bif4624|CDS|CDS	0.25	36	0.031526241	NA	NA	hypothetical protein
TS29Fae06041|CDS|CDS	0.5	72	0.031526241	NA	NA	hypothetical protein
FpraM2120366|CDS|CDS	0.333333333	48	0.031526241	NA	NA	hypothetical protein
RintL10348|CDS|CDS	0.058823529	8.5	0.031417154	NA	NA	hypothetical protein
BL0543|CDS|LacI-type	0.25	36.25	0.031308819	NA	NA	hypothetical protein
TS28Bif0171|CDS|CDS	0.5	72.5	0.031308819	NA	NA	hypothetical protein
TS29Bif2630|CDS|CDS	0.5	72.5	0.031308819	NA	NA	hypothetical protein
BL0652|CDS|hypothetical	0.5	73	0.031094375	NA	NA	hypothetical protein
BL1215|CDS|penicillin-binding	0.5	73.25	0.030988251	NA	NA	hypothetical protein
TS28Bif0921|CDS|CDS	0.333333333	48.83333333	0.030988251	NA	NA	hypothetical protein
TS29Col0428|CDS|CDS	1	147.5	0.030778161	NA	NA	hypothetical protein
BL1293|CDS|xylulose	0.25	37.33333333	0.030400304	NA	NA	hypothetical protein
TS28Bif4619|CDS|CDS	0.25	37.41666667	0.030332597	NA	NA	hypothetical protein
TS29Bif3217|CDS|CDS	0.25	37.41666667	0.030332597	NA	NA	hypothetical protein
BL1006|CDS|hypothetical	0.25	37.41666667	0.030332597	NA	NA	hypothetical protein
TS28Bif4620|CDS|CDS	0.25	37.5	0.030265192	NA	NA	hypothetical protein
BL0953|CDS|glutamine-dependent	0.25	37.75	0.03006476	NA	NA	hypothetical protein
BL1301|CDS|hypothetical	0.25	38.75	0.029288895	NA	NA	hypothetical protein
BL1179|CDS|ABC	0.25	40	0.028373617	NA	NA	hypothetical protein
TS29Fae00493|CDS|CDS	0.5	80	0.028373617	NA	NA	hypothetical protein
Clep1852|CDS|CDS	0.590909091	96.5	0.027798928	NA	NA	hypothetical protein
BL0906|CDS|carbon	0.25	40.91666667	0.027737956	NA	NA	hypothetical protein
CspM6211849|CDS|CDS	0.215909091	35.74801587	0.02741913	NA	NA	hypothetical protein
Rbro1723|CDS|CDS	0.215909091	35.74801587	0.02741913	NA	NA	hypothetical protein
Acol2781|CDS|CDS	0.215909091	35.74801587	0.02741913	NA	NA	hypothetical protein
Dfor2033|CDS|CDS	0.215909091	35.74801587	0.02741913	NA	NA	hypothetical protein
Acac2252|CDS|CDS	0.215909091	35.74801587	0.02741913	NA	NA	hypothetical protein
Cnex2286|CDS|CDS	0.215909091	35.74801587	0.02741913	NA	NA	hypothetical protein
TS29Fae01446|CDS|CDS	0.333333333	55.5	0.027265938	NA	NA	hypothetical protein
Even0583|CDS|CDS	0.6	100.5833333	0.027080702	NA	NA	hypothetical protein
TS28Clo00184|CDS|CDS	0.215909091	36.24801587	0.027040915	NA	NA	hypothetical protein
TS29Fae06294|CDS|CDS	0.5	85	0.026704581	NA	NA	hypothetical protein
TS29Bif4076|CDS|CDS	1	170.8333333	0.026574315	NA	NA	hypothetical protein
BL0598|CDS|hypothetical	0.25	42.75	0.026548414	NA	NA	hypothetical protein
Robe2653|CDS|CDS	0.090909091	15.58333333	0.026483882	NA	NA	hypothetical protein
TS29Bac08382|CDS|CDS	0.25	43	0.026394062	NA	NA	hypothetical protein
Cnex2742|CDS|CDS	0.4	70.25	0.025849274	NA	NA	hypothetical protein
TS28Bif4393|CDS|CDS	0.5	87.83333333	0.025843143	NA	NA	hypothetical protein
TS29Bif0461|CDS|CDS	0.5	87.83333333	0.025843143	NA	NA	hypothetical protein
TS29Fae05506|CDS|CDS	1	176	0.025794197	NA	NA	hypothetical protein
BL1116|CDS|chlorohydrolase-like	0.25	44.20833333	0.025672641	NA	NA	hypothetical protein
BL1452|CDS|putative	0.333333333	59.25	0.025540246	NA	NA	hypothetical protein
TS29Bif2813|CDS|CDS	0.5	89.5	0.025361892	NA	NA	hypothetical protein
BLD0303|CDS|DNA	0.25	45.25	0.02508165	NA	NA	hypothetical protein
TS29Rum17139|CDS|CDS	0.5	90.5	0.02508165	NA	NA	hypothetical protein
TS29Fae05552|CDS|CDS	0.5	90.5	0.02508165	NA	NA	hypothetical protein
EUBREC0803|CDS|hypothetical	0.267857143	49	0.024816575	NA	NA	hypothetical protein
EUBREC2692|CDS|hypothetical	0.267857143	49	0.024816575	NA	NA	hypothetical protein
TS29Rum16533|CDS|CDS	0.333333333	61	0.024807534	NA	NA	hypothetical protein
BL0400a|CDS|hypothetical	0.2	36.75	0.024706279	NA	NA	hypothetical protein
TS29Fae01195|CDS|CDS	0.5	92	0.024672711	NA	NA	hypothetical protein
TS29Bif3606|CDS|CDS	0.5	93.25	0.024341977	NA	NA	hypothetical protein
BLD0728|CDS|Na+/xyloside	0.25	47.08333333	0.02410502	NA	NA	hypothetical protein
TS28Bif5373|CDS|CDS	0.25	47.75	0.023768475	NA	NA	hypothetical protein
TS29Bif2384|CDS|CDS	0.333333333	63.83333333	0.023706416	NA	NA	hypothetical protein
TS28Bif5122|CDS|CDS	0.333333333	63.91666667	0.023675508	NA	NA	hypothetical protein
TS29Bif3999|CDS|CDS	0.333333333	63.91666667	0.023675508	NA	NA	hypothetical protein
BLD1380|CDS|Bacterial	0.25	48.41666667	0.023441198	NA	NA	hypothetical protein
TS29Bac10729|CDS|CDS	0.2	39	0.023280917	NA	NA	hypothetical protein
BL0634|CDS|DNA	0.30952381	61.58333333	0.022817368	NA	NA	hypothetical protein
TS29Bac10503|CDS|CDS	0.4	81	0.02241866	NA	NA	hypothetical protein
TS29Fae10181|CDS|CDS	0.5	101.5	0.022363442	NA	NA	hypothetical protein
RintL10504|CDS|CDS	0.058823529	12	0.022253817	NA	NA	hypothetical protein
BL0143|CDS|ABC	0.25	51.25	0.022145262	NA	NA	hypothetical protein
TS29Fae08536|CDS|CDS	0.5	103.5	0.021931298	NA	NA	hypothetical protein
TS29RumUnc0603|CDS|CDS	1	210	0.021617994	NA	NA	hypothetical protein
TS29Bif0960|CDS|CDS	0.333333333	70.83333333	0.021363665	NA	NA	hypothetical protein
BLD0815|CDS|N-acetylglutamate	0.25	53.5	0.021213919	NA	NA	hypothetical protein

Edol0301|CDS|CDS	0.2	43.08333333	0.021074408	NA	NA	hypothetical protein
BL0163|CDS|ABC	0.25	54.08333333	0.02098511	NA	NA	hypothetical protein
TS29Fae03171|CDS|CDS	0.5	108.5	0.020920639	NA	NA	hypothetical protein
Dfor3073|CDS|CDS	0.2	44.08333333	0.02059635	NA	NA	hypothetical protein
TS29Par963|CDS|CDS	1	220.5	0.020588566	NA	NA	hypothetical protein
TS28Dor3153|CDS|CDS	0.2	44.58333333	0.020365363	NA	NA	hypothetical protein
BLD0760|CDS|Putative	0.25	55.83333333	0.020327367	NA	NA	hypothetical protein
TS29Fae03346|CDS|CDS	0.5	112	0.020266869	NA	NA	hypothetical protein
TS29Bif0441|CDS|CDS	0.5	113.9166667	0.019925876	NA	NA	hypothetical protein
BL0976|CDS|galactoside	0.25	57.08333333	0.019882243	NA	NA	hypothetical protein
BL1669|CDS|hypothetical	0.25	57.55952381	0.019717757	NA	NA	hypothetical protein
Even0581|CDS|CDS	1	231.0833333	0.019645635	NA	NA	hypothetical protein
BLD1431|CDS|Type	0.30952381	72.08333333	0.019493682	NA	NA	hypothetical protein
Ccom1197|CDS|CDS	0.058823529	14	0.019074701	NA	NA	hypothetical protein
TS29Fae10352|CDS|CDS	0.25	61	0.018605651	NA	NA	hypothetical protein
TS29Fae10062|CDS|CDS	0.333333333	81.5	0.018567602	NA	NA	hypothetical protein
BLD0219|CDS|Chromosome	0.25	61.16666667	0.018554954	NA	NA	hypothetical protein
TS29Bif0550|CDS|CDS	0.25	62.5	0.018159115	NA	NA	hypothetical protein
TS28Bif5319|CDS|CDS	0.25	62.5	0.018159115	NA	NA	hypothetical protein
TS29Fae00843|CDS|CDS	0.5	126.5	0.017943789	NA	NA	hypothetical protein
BLD1383|CDS|Serine/threonine	0.333333333	84.33333333	0.017943789	NA	NA	hypothetical protein
BL1275|CDS|homoserine	0.25	63.5	0.017873145	NA	NA	hypothetical protein
TS29Fae06362|CDS|CDS	0.5	127	0.017873145	NA	NA	hypothetical protein
TS29Bif3585|CDS|CDS	0.5	129.9166667	0.017471887	NA	NA	hypothetical protein
BL1007|CDS|hypothetical	0.25	65.66666667	0.017283422	NA	NA	hypothetical protein
TS29Bif0578|CDS|CDS	0.5	131.6666667	0.017239666	NA	NA	hypothetical protein
TS29Bif0927|CDS|CDS	0.25	66.5	0.017066837	NA	NA	hypothetical protein
TS29Bif2378|CDS|CDS	0.75	205.5	0.016568536	NA	NA	hypothetical protein
BLD1427|CDS|Glutamate	0.25	69.33333333	0.016369394	NA	NA	hypothetical protein
BL0157|CDS|hypothetical	0.25	69.41666667	0.016349743	NA	NA	hypothetical protein
TS28Bif2174|CDS|CDS	0.25	70.08333333	0.016194217	NA	NA	hypothetical protein
TS29Bif3481|CDS|CDS	0.333333333	95.16666667	0.015901151	NA	NA	hypothetical protein
Dfor3101|CDS|CDS	0.5	143.3333333	0.015836437	NA	NA	hypothetical protein
TS28Bif1972|CDS|CDS	0.333333333	95.66666667	0.015818044	NA	NA	hypothetical protein
BLD0762|CDS|Transcriptional	0.25	72.66666667	0.015618505	NA	NA	hypothetical protein
TS29Bif2503|CDS|CDS	0.25	74	0.01533709	NA	NA	hypothetical protein
BL1544|CDS|extracellular	0.25	76.16666667	0.014900805	NA	NA	hypothetical protein
TS29Bif2691|CDS|CDS	0.25	76.91666667	0.014755511	NA	NA	hypothetical protein
BLD1934|CDS|Beta-glucosidase-related	0.25	77.08333333	0.014723607	NA	NA	hypothetical protein
Bbre0542|CDS|CDS	0.1	31	0.014644448	NA	NA	hypothetical protein
TS29Rum20468|CDS|CDS	0.5	156	0.014550573	NA	NA	hypothetical protein
BL0304|CDS|hypothetical	0.25	82.33333333	0.013784753	NA	NA	hypothetical protein
Rgna2449|CDS|CDS	0.058823529	19.83333333	0.013464495	NA	NA	hypothetical protein
Cbar1018|CDS|CDS	0.25	87.41666667	0.012983161	NA	NA	hypothetical protein
BAD0020|CDS|hypothetical	0.333333333	117	0.012933843	NA	NA	hypothetical protein
BL0627|CDS|hypothetical	0.25	91.33333333	0.012426402	NA	NA	hypothetical protein
TS29Fae07202|CDS|CDS	0.5	198.5	0.011435211	NA	NA	hypothetical protein
BLD1519|CDS|hypothetical	0.25	108.25	0.010484477	NA	NA	hypothetical protein
Even0582|CDS|CDS	0.25	110.5	0.010270993	NA	NA	hypothetical protein
TS28Bif5288|CDS|CDS	0.25	116.5	0.009742014	NA	NA	hypothetical protein
TS29Bif4127|CDS|CDS	0.25	120.4166667	0.009425146	NA	NA	hypothetical protein
Ceut2216|CDS|CDS	0.090909091	43.97777778	0.009384448	NA	NA	hypothetical protein
TS29Bif3218|CDS|CDS	0.25	131.5	0.008630758	NA	NA	hypothetical protein
TS29Bif3556|CDS|CDS	0.333333333	209.0833333	0.007237591	NA	NA	hypothetical protein
TS28Bif2171|CDS|CDS	0.333333333	228.5833333	0.006620166	NA	NA	hypothetical protein
Robe2666|CDS|CDS	0.25	180.3166667	0.006294175	NA	NA	hypothetical protein
Rtor1333|CDS|CDS	0.25	180.3166667	0.006294175	NA	NA	hypothetical protein
EUBREC3583|CDS|hypothetical	0.1	98.41666667	0.004612815	NA	NA	hypothetical protein
TS29Bif0022|CDS|CDS	0.25	299.0833333	0.003794744	NA	NA	hypothetical protein

Table S13: Assembly statistics for unmapped DNA sequences.

Reads assembled	563,275
Reads partially assembled	212,836
Singleton reads	508,756
Repeat reads	35,962
Outlier reads	6,429
Short reads	16,063
%Reads assembled	41.93
Total number reads	1,343,321
Number large contigs[a]	38,748
Bases in large contigs	35,063,243
Average large contig size	904
N50 large contig size	924
Largest contig size	95,032
Total number of contigs	106,978
Total bases in contigs	57,485,012

[a] Large contigs were defined as >500bp.

Table S14: Summary of 16S rRNA gene sequence datasets.

Name	Number of reads	Number of clean reads
Artificial	46,249	31,937
Even1	64,373	54,227
Even2	54,344	45,579
Even3	68,446	54,729
Uneven1	54,762	45,440
Uneven2	52,004	44,597
Uneven3	61,901	51,451
TS28	1,500,681	951,289
TS29	1,186,582	603,274

Legend - The initial read number and the number of reads remaining after filtering for low quality reads ('clean reads') are shown.

Table S15: PCR per base error probabilities derived from the three evenly distributed mock community datasets.

Real/ Observed	A	C	T	G
A	0.9995	7.2e-6	7.7e-6	5.1e-4
C	1.1e-05	0.9996	4.1e-4	2.1e-6
T	9.0e-6	5.7e-4	0.9994	1.4e-5
G	3.5e-4	3.2e-6	2.1e-5	0.9996

Table S16: Number of de-noised sequences and proportion classified 'good', bimeric', ‘trimeric’, 'quadrameric', and 'unclassified' for the seven test community datasets.

Category	Total	Good	Bimeric	Trimeric	Quadrameric	Unclassified
Artificial	116	91(78.4%)	21(18.1%)	0(0%)	0(0%)	4(3.4%)
Even1	1785	81(4.5%)	1386(77.6%)	200(11.2%)	4(0.2%)	114(6.4%)
Even2	1562	83(5.3%)	1216(77.8%)	187(2.0%)	4(0.3%)	72(4.6%)
Even3	1679	84(5.0%)	1331(79.3%)	147(8.8%)	2(0.1%)	115(6.8%)
Uneven1	813	74(9.1%)	582(71.6%)	61(7.5%)	1(0.1%)	95(11.7%)
Uneven2	641	64(10.0%)	487(76.0%)	57(8.9%)	2(0.3%)	31(4.8%)
Uneven3	804	69(8.6%)	620(77.1%)	64(8.0%)	0(0%)	51(6.3%)

Table S17: Frequencies of sequence co-occurrence over the three ‘Uneven’ datasets by category.

Category	Total	Once	Twice	Thrice
Good	97	34(35.1%)	31(32.0%)	32(33.0%)
Bimeric	1524	1450(95.1%)	69(4.5%)	5(0.3%)
Trimeric	177	176(99.4%)	1(0.6%)	0(0.0%)
Quadrameric	3	3(100.0%)	0(0.0%)	0(0.0%)
Unclassified	169	165(97.6%)	2(1.2%)	2(1.2%)
All	1970	1828(92.8%)	103(5.2%)	39(2.0%)

Table S18: Validation of chimera classification on datasets not used in training (50% probability cutoff for chimera definition).

Dataset	**Artificial**		**Uneven1**		**Uneven2**		**Uneven3**	
Classification	**Good**	**Chimeric**	**Good**	**Chimeric**	**Good**	**Chimeric**	**Good**	**Chimeric**
Good	89(97.8%)	2(2.2%)	68(91.9%)	6(8.1%)	57(89.1%)	7(10.9%)	59(85.5%)	10(14.5%)
Bimeric	0(0.0%)	21(100.0%)	6(1.0%)	576(99.0%)	8(1.6%)	479(98.4%)	6(1.0%)	614(99.0%)
Trimeric	**-**[a]	-	3(4.9%)	58(95.1%)	1(1.8%)	56(98.2%)	0(0.0%)	64(100.0%)
Quadrameric	**-**	**-**	0(0.0%)	1(100%)	1(50%)	1(50%)	-	**-**
Unclassified	4(100.0%)	0(0%)	24(25.3%)	71(74.7%)	6(19.4%)	25(80.6%)	13(25.5%)	38(74.5%)

[a] Dashes indicate categories in a given dataset with no observed chimeras.

Table S19: Validation of chimera classification using sequence abundance information on datasets not used in training (50% probability cutoff for chimera definition).

Dataset	**Artificial**		**Uneven1**		**Uneven2**		**Uneven3**	
Classification	**Good**	**Chimeric**	**Good**	**Chimeric**	**Good**	**Chimeric**	**Good**	**Chimeric**
Good	90(98.9%)	1(1.1%)	69(93.2%)	5(6.8%)	59(92.2%)	5(7.8%)	62(89.9%)	7(10.1%)
Bimeric	0(0.0%)	21(100.0%)	3(0.5%)	579(99.5%)	5(1.0%)	482(99.0%)	4(0.6%)	616(99.4%)
Trimeric	**-**[a]	-	1(1.6%)	60(98.4%)	1(1.8%)	56(98.2%)	0(0.0%)	64(100.0%)
Quadrameric	**-**	**-**	0(0.0%)	1(100.0%)	1(50.0%)	1(50.0%)	-	**-**
Unclassified	3(75.0%)	1(25.0%)	19(20.0%)	76(80.0%)	6(19.4%)	25(80.6%)	12(23.5%)	38(76.5%)

[a] Dashes indicate categories in a given dataset with no observed chimeras.

Table S20: Observed and total diversity estimates of 97%ID phylotypes for the three 'Uneven' mock communities.

Dataset	Sample Size	Diversity	Chao	Log-normal	Sichel
Uneven1	43,190	75	156	94;**146**;338	81;**96**;141
Uneven2	42,575	58	94	71;**112**;312	61;**73**;103
Uneven3	49,789	63	73	77;**119**;289	68;**80**;108

Legend - The results from fitting the log-normal and Sichel distributions are **medians** with 95% confidence intervals from the posterior distribution (11).

Table S21: Chimera removal from the de-noised deeply sequenced TS28 and TS29 16S rRNA datasets.

Dataset	No. reads	No. chimeric reads	No. de-noised sequences	No. chimeric sequences
TS28-Deep	951,274	102,762(10.8%)	9,251	8,722(94.3%)
TS29-Deep	603,263	49,847(8.2%)	4,012	3,629(90.5%)
TS28-Shallow	3,733	445(11.9%)	536	384(71.6%)
TS29-Shallow	1,401	223(15.9%)	254	163(64.2%)

Legend - Number (No.) of reads before and after chimera removal (50% classification cut-off with abundance information) and the same for de-noised sequences. The slight reduction in read number over "clean reads" in **Table S14** is due to removal of any reads with a homopolymer of length ≥10nt.

Table S22: Percentage 97%ID phylotype overlaps between fecal 16S rRNA datasets from MZ co-twins.

Dataset	TS28	TS28-Shallow	TS29	TS29-Shallow
TS28-Deep	100%	25.3%	35.9%	10.4%
TS28-Shallow	88.4%	100%	50.7%	23.2%
TS29-Deep	49.1%	19.9%	100%	20.2%
TS29-Shallow	62.5%	40.0%	88.7%	100%

Legend - The percentage of 97%ID phylotypes from each dataset (rows) found in each other dataset (columns).

Table S23: Percentage 95%ID phylotype overlaps between fecal 16S rRNA datasets from co-twins.

Dataset	TS28	TS28-Shallow	TS29	TS29-Shallow
TS28-Deep	100%	27.1%	39.0%	11.6%
TS28-Shallow	95.1%	100%	59.3%	26.8%
TS29-Deep	52.8%	23.0%	100%	21.1%
TS29-Shallow	68.5%	45.2%	91.8%	100%

Legend - The percentage of 95%ID phylotypes from each dataset (rows) found in each other dataset (columns).

Table S24: Deviance Information Criterion (DIC) values for Bayesian fits of the log-normal, inverse-Gaussian, log-Student's t and Sichel distributions to the 97%ID phylotype abundance distributions of the MZ co-twin's 16S rRNA datasets.

Dataset	Log-normal	Inverse-Gaussian	Log-Student's t	Sichel
TS28-Deep	836.4	910.5	837.6	829.4
TS29-Deep	621.7	675.8	623.2	617.1
TS28-Shallow	127.6	n.c.	128.9	127.25
TS29-Shallow	59.6	n.c.	60.6	60.0

Legend - Some fits labeled n.c. failed to converge.

Table S25: Deviance Information Criterion (DIC) values for Bayesian fits of the log-normal, inverse-Gaussian, log-Student's t and Sichel distributions to the 95%ID phylotype abundance distributions of the MZ co-twin's 16S rRNA datasets.

Dataset	Log-normal	Inverse-Gaussian	Log-Student's t	Sichel
TS28-Deep	754.9	817.9	755.8	749.4
TS29-Deep	560.8	606.5	561.7	557.3
TS28-Shallow	116.5	117.9	117.5	117.0
TS29-Shallow	61.8	62.1	62.8	62.8

Table S26: Total diversity estimates for Bayesian fits of the log-normal, inverse-Gaussian, log-Student's t and Sichel distributions to the 97%ID phylotype abundance distributions of the MZ co-twin's 16S rRNA datasets.

Dataset	Log-normal	Inverse-Gaussian	Log-Student's t	Sichel
TS28-Deep	919;**1373**;2926	516;**541**;576	960;**1568**;3237	724;**878**;1686
TS29-Deep	874;**1787**;7015	394;**426**;476	1002;**3270**;10045	577;**768**;1812
TS28-Shallow	537;**2119**;8803	n.c.	703;**5204**;16901	242;**386**;830
TS29-Shallow	364;**1920**;9664	n.c.	28;**162**;432	134;**209**;457

Legend - Results are given as lower 2.5% quantile, 50% quantile (**median**), 97.5% quantile of the posterior distribution. Some fits labeled n.c. failed to converge.

Table S27: Total diversity estimates for Bayesian fits of the log-normal, inverse-Gaussian, log-Student's t and Sichel distributions to the 95%ID phylotype abundance distributions of the Twins datasets.

Dataset	Log-normal	Inverse-Gaussian	Log-Student's t	Sichel
TS28-Deep	926;**1673**;9864	456;**482**;521	1002;**1940**;5729	598;**752**;1223
TS29-Deep	1174;**4647**;19411	362;**402**;463	1036;**4928**;14281	546;**791**;1741
TS28-Shallow	719;**5503**;31790	226;**505**;4693	503;**5880**;19905	455;**975**;4108
TS29-Shallow	347;**2196**;10204	133;**442**;3162	174;**444**;1357	96;**137**;296

Legend - Results are given as lower 2.5% quantile, 50% quantile (**median**), 97.5% quantile of the posterior distribution.

SUPPORTING FIGURES

Fig. S1. Frequency-abundance distributions for the 97%ID phylotypes in the 'Deep Twins' 16S rRNA gene sequence datasets. (**A,B**) Values from TS28 (panel A) and TS29 (panel B) are shown after noise and chimera removal. The number of phylotypes observed at a given abundance versus abundance is shown. For phylotypes at high abundance, where the data becomes sparser, we aggregated observed abundance bins to achieve a count of at least 20 and then divided by the number of bins aggregated. We subsequently plotted this value against the mean abundance of the aggregated bins. The expected curves from log-normal and Sichel fits are also shown.

Turnbaugh *et al.*, Fig. S1

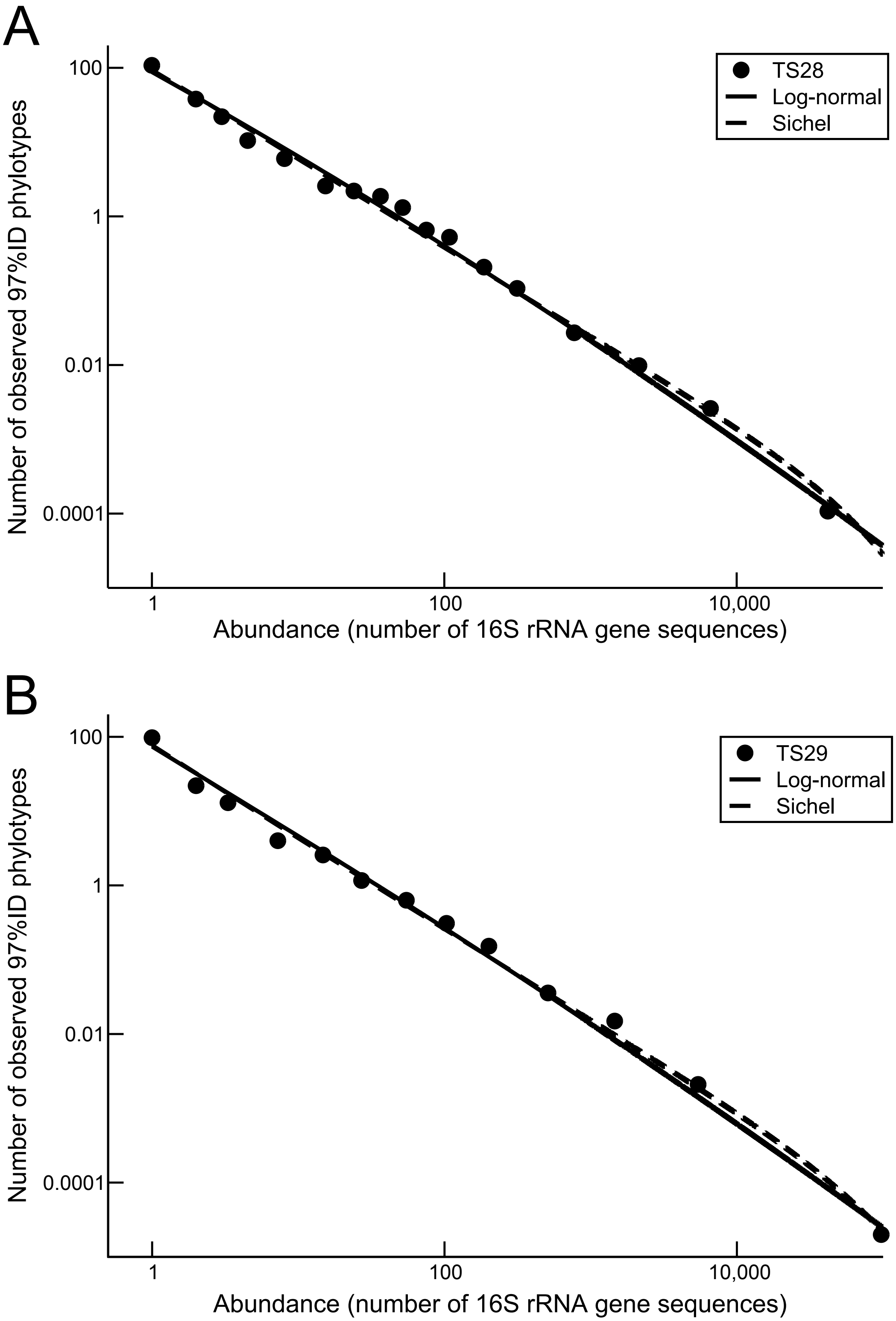


Fig. S2. Genetic diversity of the fecal microbiome. (A) Distribution of gene clusters across gut microbial genomes and microbiome bins. All protein sequences from 122 gut genomes and the microbiome bins were clustered using cd-hit at 40%ID, 60%ID, and 80%ID. **(B)** The consistency of taxonomic assignment within gene clusters grouped at 40%ID, 60%ID, and 80%ID. Comparisons between gut genome sequences (red), TS28 and TS29 bin sequences (blue), TS28 and gut genome sequences (purple), and TS29 and gut genome sequences (green) are shown.

Turnbaugh *et al.*, Fig. S2

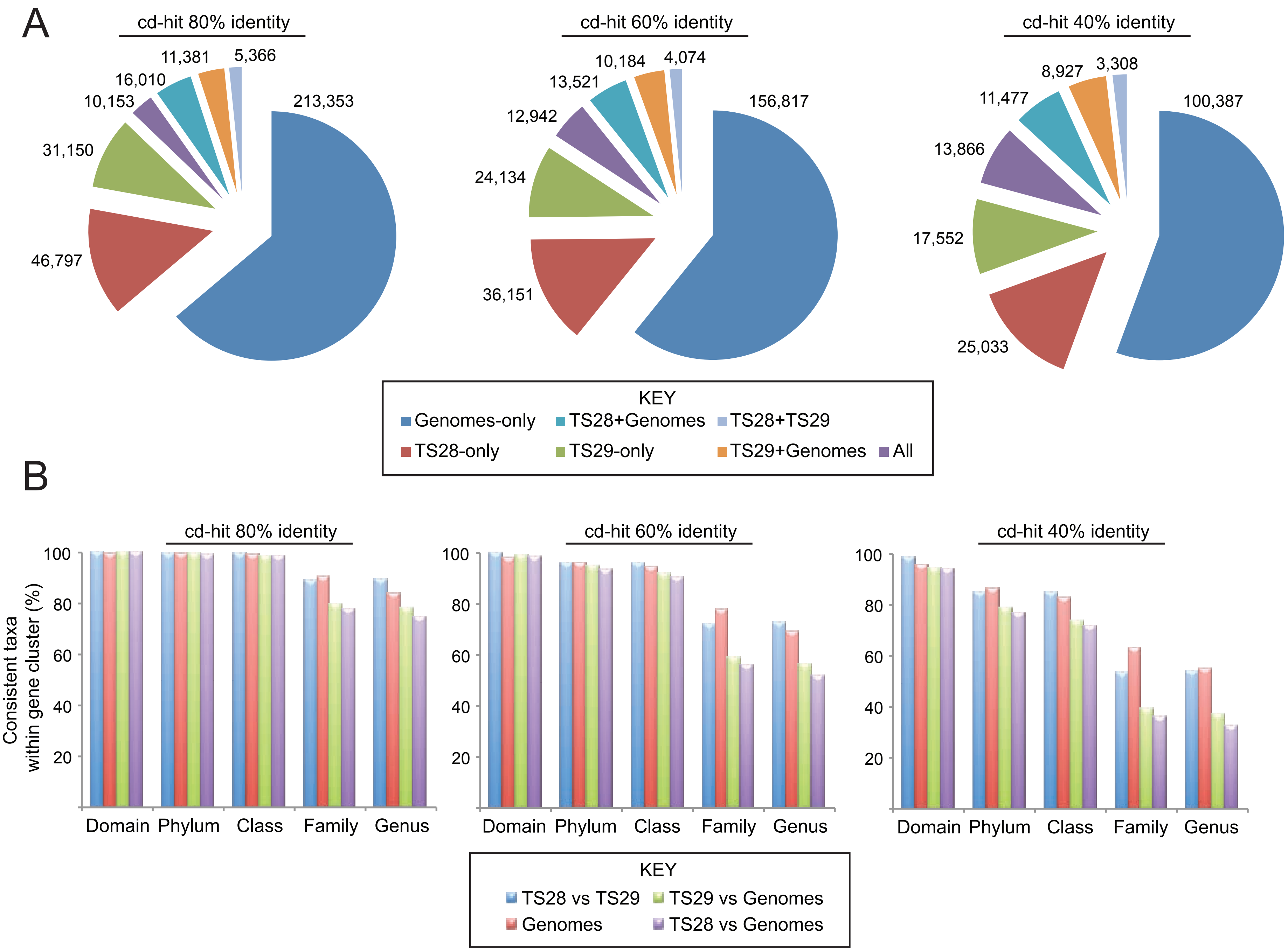


Fig. S3. Validation of PhyloPythia bins of microbiome scaffolds. Each copy of 30 different marker genes from each set of scaffolds (blue for TS28, red for TS29) and from the gut microbial genomes (green) was evaluated for consistent taxonomic assignment. Briefly, each set of marker genes were translated into amino acid sequences, aligned using clustalw, and added to a neighbor-joining tree. Individual sequences were assigned to taxa based on the consensus taxonomy of all sequences found at the first node.

Turnbaugh *et al.*, Fig. S3

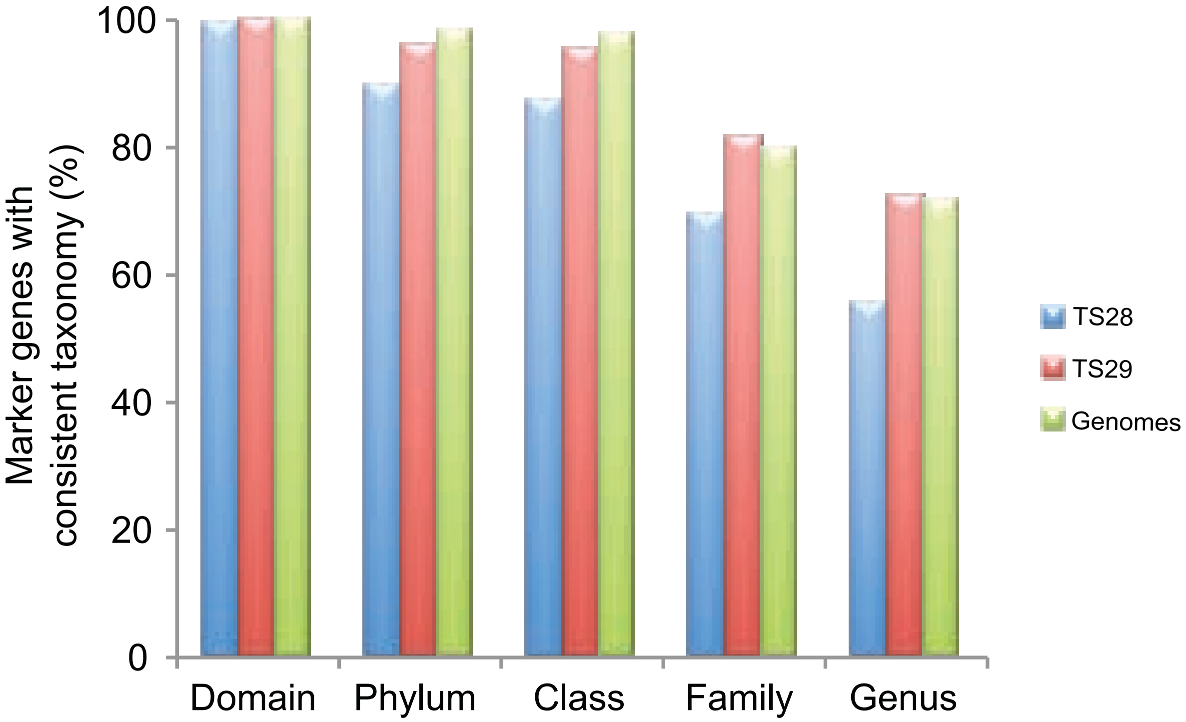


Fig. S4. Distribution of phylotypes in the mock community datasets and taxonomic profiles from PCR and shotgun sequencing. (A) Ratio of observed and expected 16S rRNA gene sequences mapped to each species-level phylotype in the three evenly mixed mock communities (Even1, Even2, and Even3). Sequencing reads were aligned globally to reference 16S rRNA gene sequences using the Needleman-Wunsch algorithm (≥98%ID required for assignment). Two DNA preparations were from genomes from the same phylotype: (i) *Bifidobacterium catenulatum* and *Bifidobacterium pseudocatenulatum*, and (ii) *Providencia rettgeri* and *Providencia alcalifaciens*. Sequences with mismatches in the 8F primer region are indicated with a red bar (single mismatches) or a black bar (multiple mismatches). **(B)** The observed relative abundance of each phylotype in the unevenly mixed datasets (Uneven1, Uneven2, and Uneven3) as a function of the predicted relative abundance of each phylotype. Predicted relative abundance were calculated based on the average observed relative abundance in the evenly mixed datasets (ObsEven), the expected relative abundance in the evenly mixed datasets (ExpEven), and the expected relative abundance in each unevenly mixed dataset [ExpUneven; i.e. Predicted(ObsUneven) = (ObsEven*ExpUneven)/ExpEven]. **(C)** Relative abundance of bacterial classes represented in 16S rRNA gene amplicons (PCR), 16S rRNA gene fragments from shotgun sequenced fecal microbiomes, and the gene content of the fecal microbiomes. 16S rRNA profiles were determined using the RDPClassifier (cutoff=0.8) (15), while gene content profiles were determined by mapping them to a database containing all genes from 122 gut microbial genomes and microbiome bins.

Turnbaugh *et al.*, Fig. S4

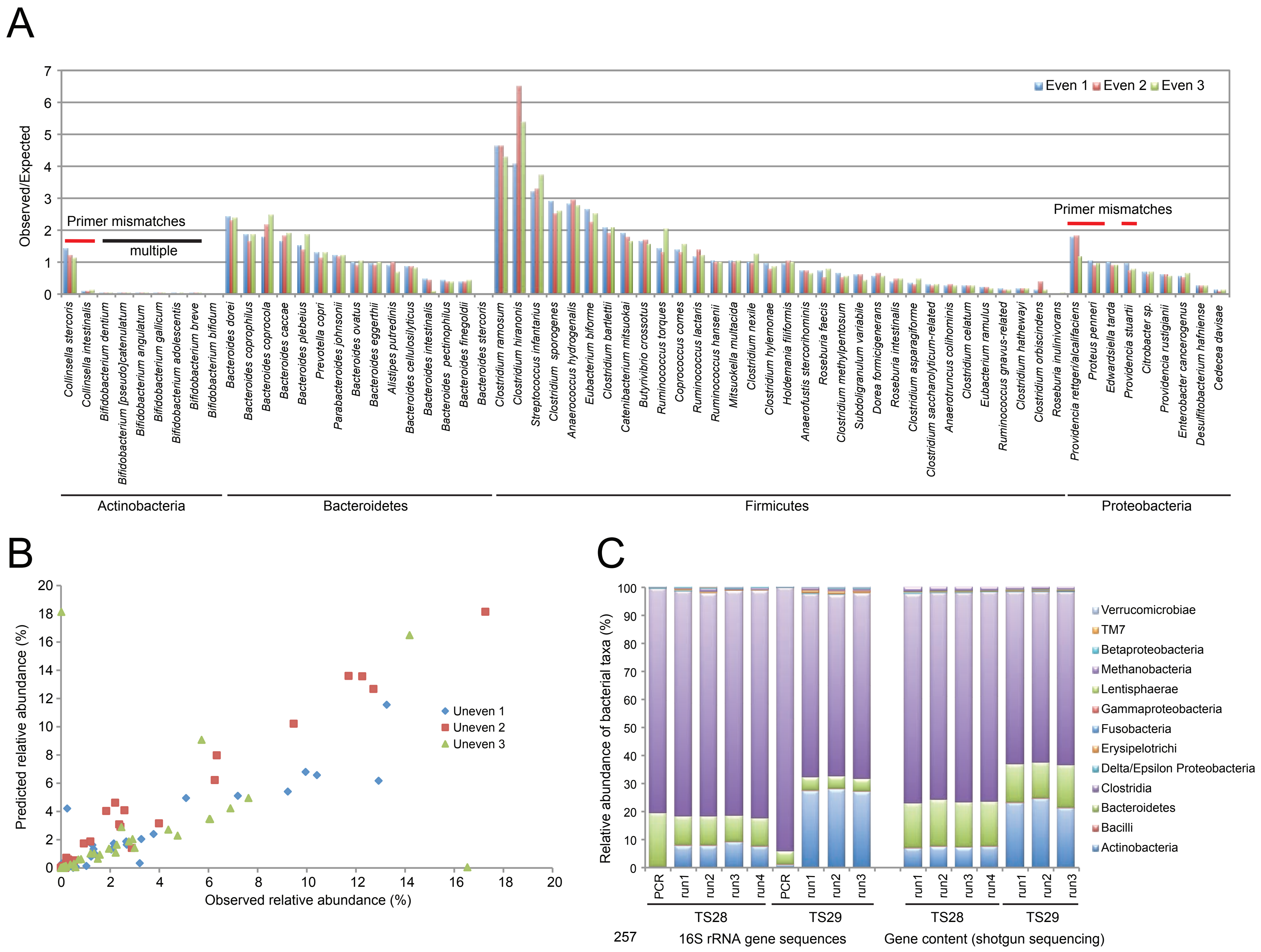


Fig. S5. Rarefaction analysis of the number of genes assigned to Carbohydrate Active Enzymes (CAZymes) and CAZy families based on DNA and cDNA datasets generated from the fecal microbiomes and metatranscriptomes of TS28 and TS29. The number of (**A**) CAZymes and (**B**) CAZy families was tallied as a function of sequencing depth after mapping each dataset to the CAZy annotated microbiome bins.

Turnbaugh *et al.*, Fig. S5

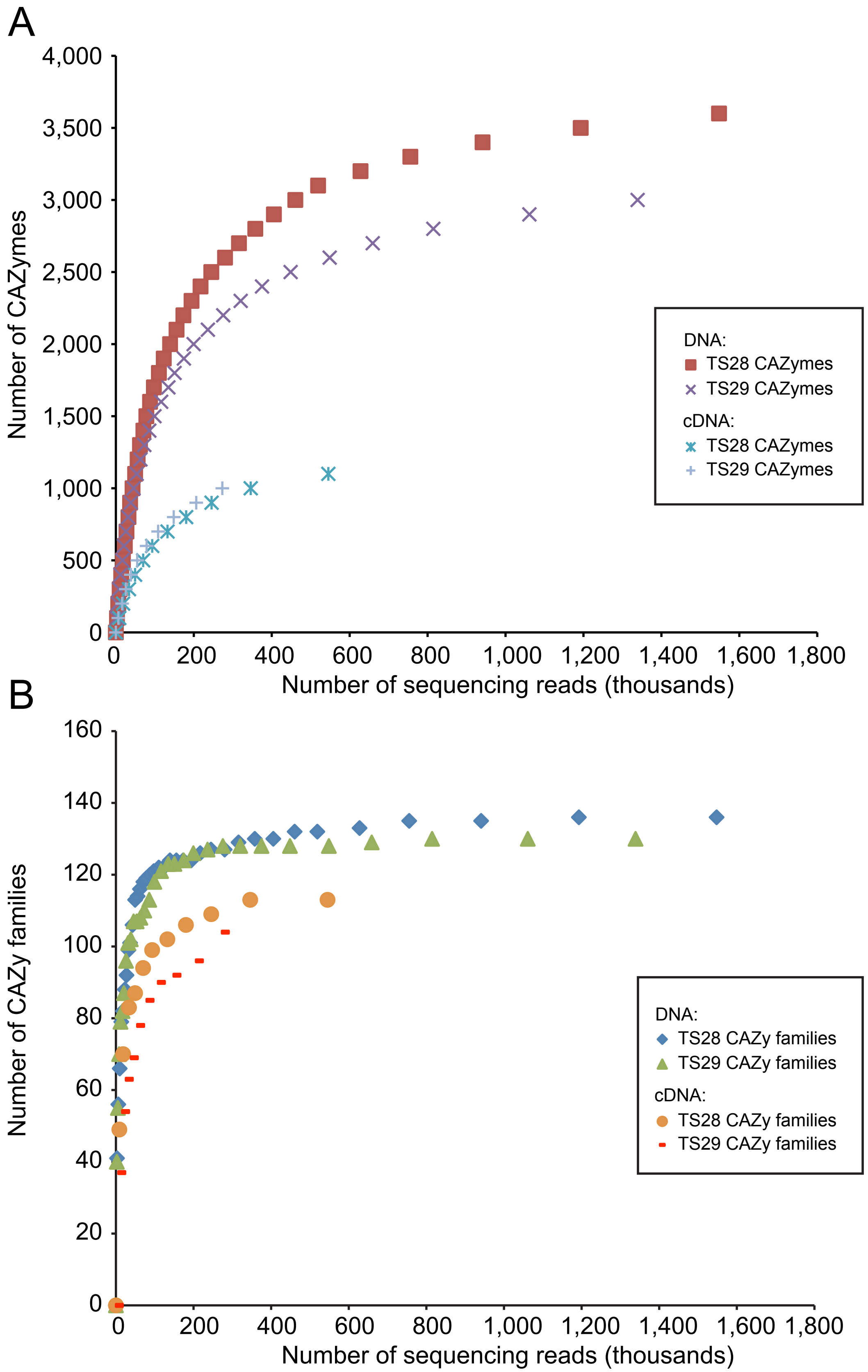
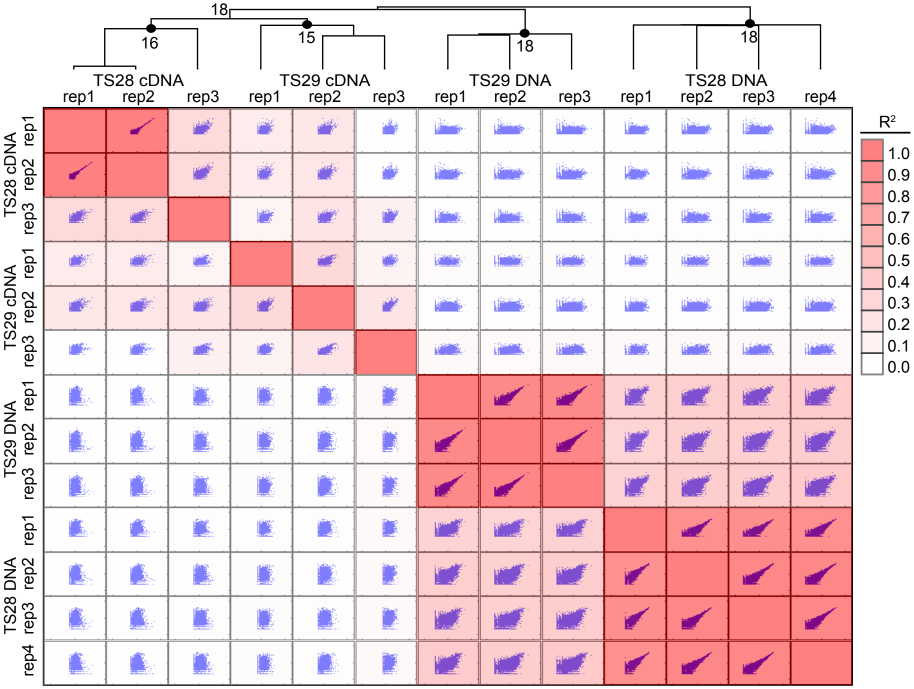


Fig. S6. UPGMA clustering based on the abudance of gene clusters (DNA) and expressed transcripts (cDNA). Datasets were clustered and compared with scatterplots according to the relative abundance of gene clusters. Values are shown on a log-scale, with x-axis labels are on the top of the matrix, and y-axis labels are on the left (rep=replicate datasets). 50,000 randomly selected sequences per dataset were used for z-score normalization and UPGMA clustering. Black circles represent clustered nodes (inconsistency threshold=0.75, 'cluster' function in Matlab v7.7.0). Correlations are shown as a heatmap from white (R^2=0) to dark red (R^2=1). We subsampled each dataset to only include gene clusters from each of 18 different COG functional categories (see **Fig. 3B** for category names). The pattern of clustering of microbiomes and meta-transcriptomes for each individual was detectable across each of the 18 functional categories, and not restricted to housekeeping genes. The number at each node indicates the number of COG categories with consistent clustering compared to that observed with the entire dataset.

Turnbaugh *et al.*, Fig. S6



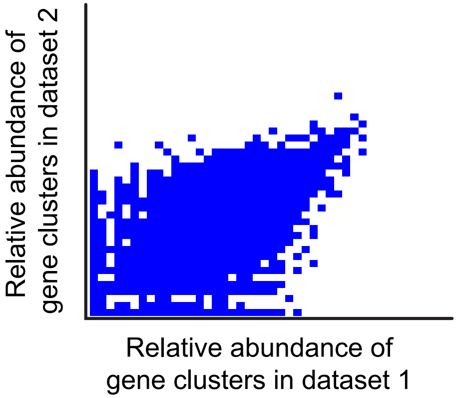


Fig. S7. Comparison of gene abundance and gene expression in the fecal microbiomes of TS28 and TS29. (A) The percentage of DNA sequences matching CDS (coding sequences) from genus-level taxa in 122 gut microbial genomes and microbiome bins. **(B)** The percentage of cDNA sequences matching CDS from each taxa. Columns labeled 'Reads' are weighted based on the number of sequencing reads mapped to each gene. Columns labeled 'Genes' indicate the distribution of genes observed in each fecal microbiome dataset without abundance weighting.

Turnbaugh *et al.*, Fig. S7

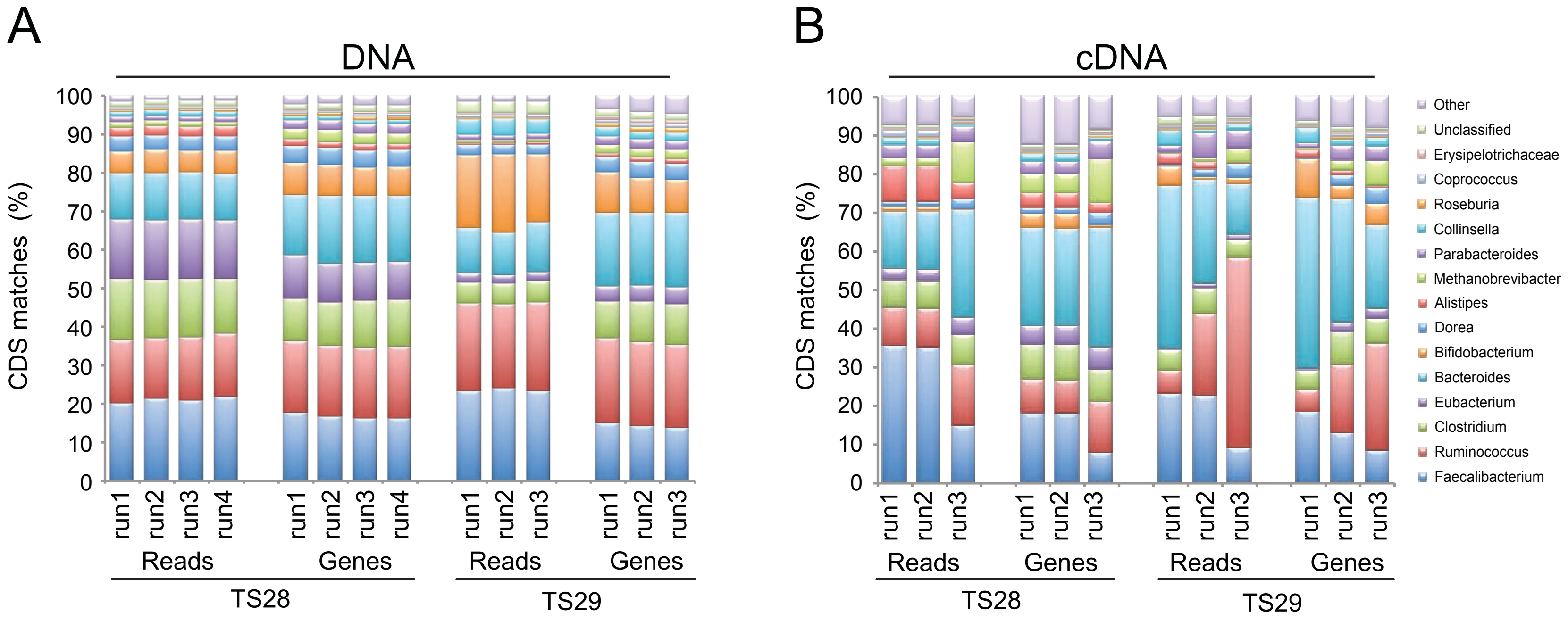


Fig. S8. Analysis of variation between technical replicates in DNA and cDNA datasets plus KEGG annotation of genes with high or low relative expression. (A) The relative abundance of each gene observed in each DNA or cDNA dataset was compared against the relative abundance in each technical replicate (all pairwise comparisons; n=3-4 replicates per sample). A histogram depicting the fraction of shared genes at each ratio is shown for each pairwise comparison. Ratios were defined as the natural log ratio of the relative abundance in replicate 1 versus the relative abundance in replicate 2. The fold-change cutoff used for biological comparisons is indicated by a black box (log ratio=2.3 corresponding to 10-fold difference in relative abundance). (**B**) Clustering of KEGG pathway representation among genes with high relative expression (High-Expr) or low relative expression (Low-Expr) , and genes unique to cDNA or DNA datasets. The relative abundance of KEGG pathway assignments was normalized by z-score across all datasets, clustered with the UPGMA method (average linkage) using Cluster 3.0 (16), and visualized with TreeView (17).

Turnbaugh *et al.*, Fig. S8

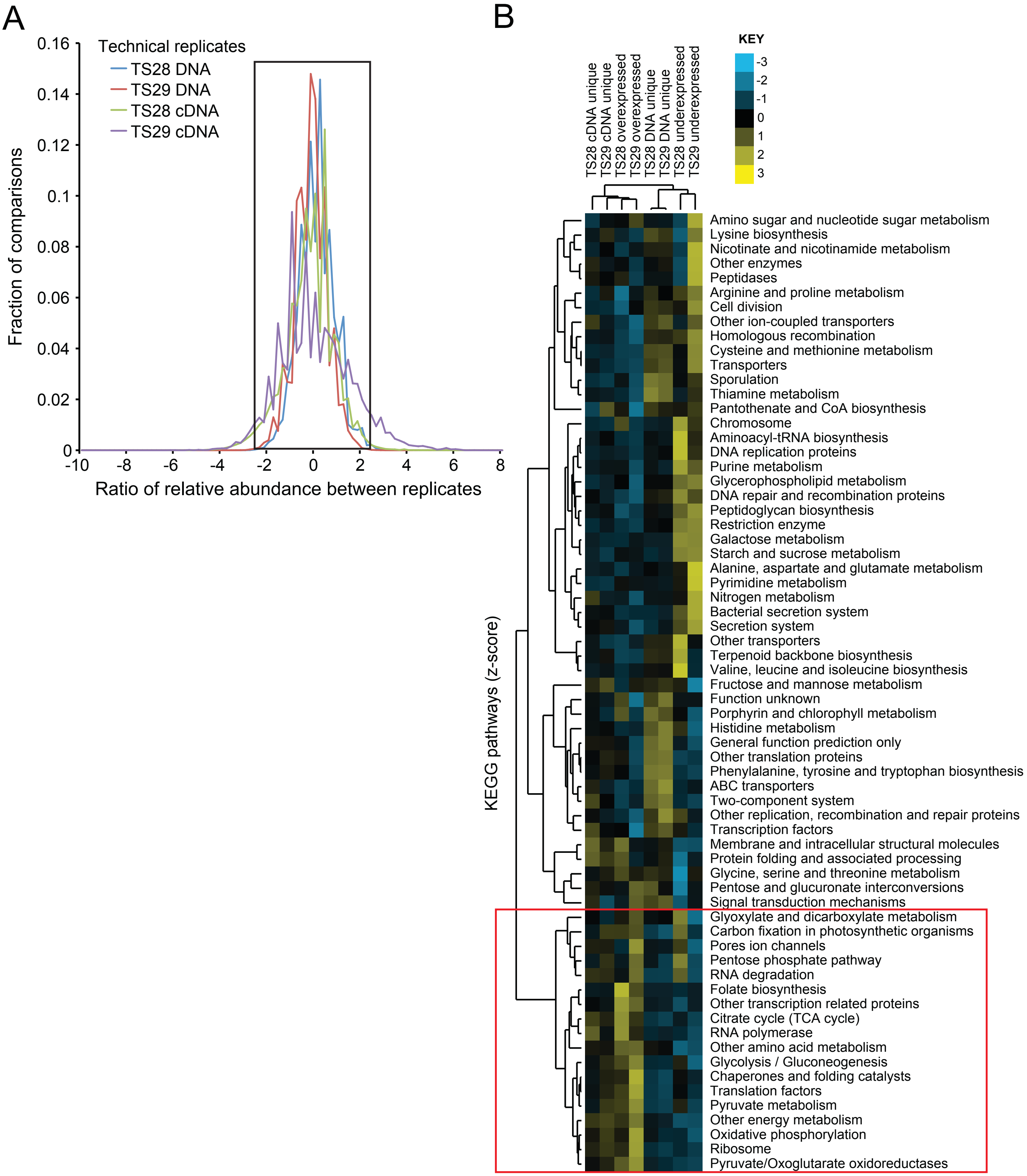


Fig. S9. Comparison of gene expression and abundance in seven fecal microbiomes representing three MZ twin pairs and an unrelated individual. (A) Percentage of genes unique to cDNA or DNA datasets assigned to each COG category. Percentages are represented by the area of each colored circle (the black circle labeled 5% provides a reference). The mean of all ‘TSDA’ samples (n=5 representing two MZ twin pairs, other than TS28 and TS29, and an unrelated individual) is shown. Asterisks indicate significant differences between genes unique to the cDNA or DNA datasets from the ‘TSDA’ samples (Student’s t-test; $P<0.05$). (**B**) Clustering of KEGG pathways in genes unique to cDNA or DNA datasets from TS28, TS29, and the five TSDA datasets. The relative abundance of KEGG pathway assignments was normalized by z-score across all datasets, clustered with the UPGMA method (average linkage) using Cluster 3.0 (16), and visualized with TreeView (17).

Turnbaugh *et al.*, Fig. S9

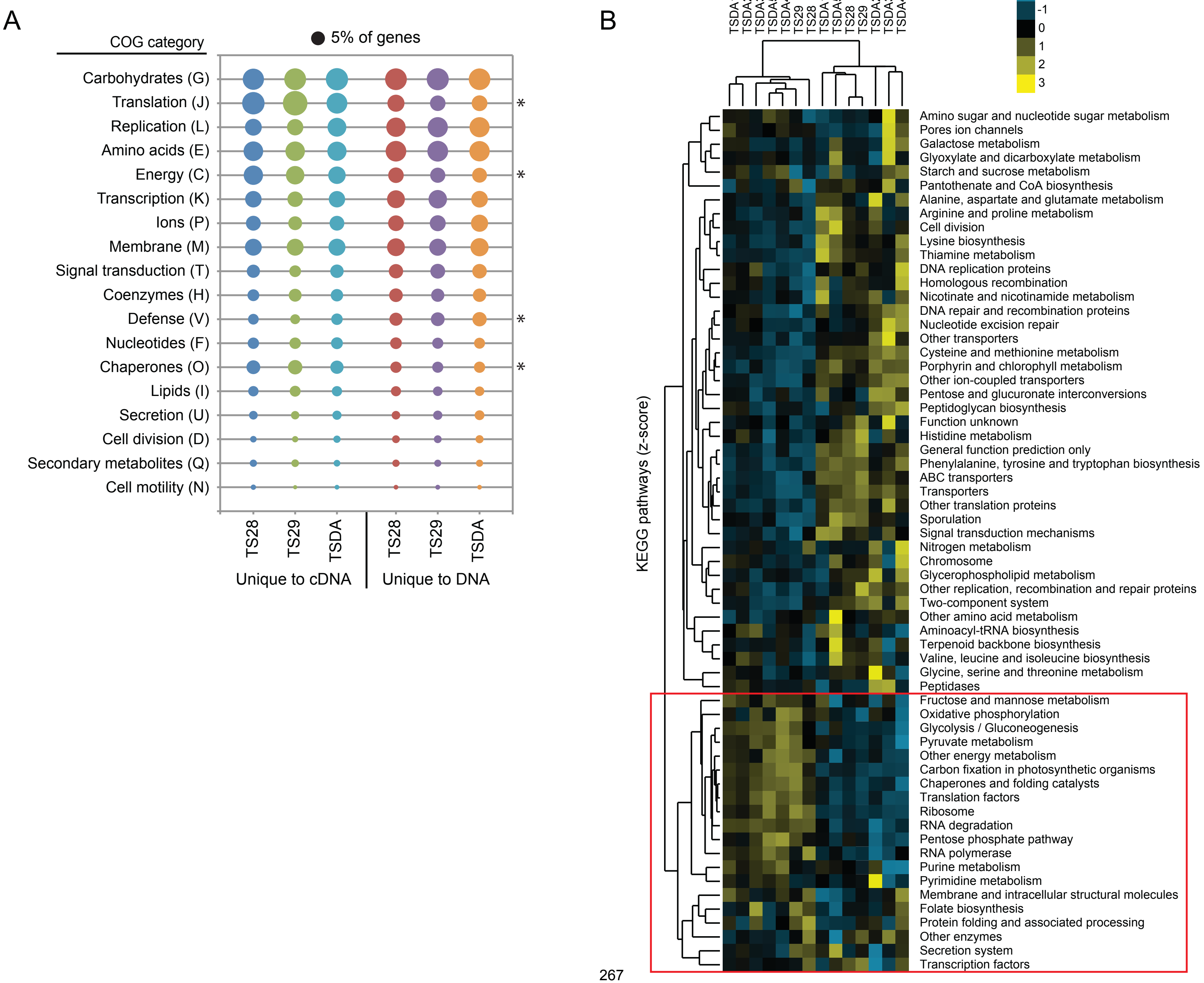


Fig. S10. Comparison of gene content and transcriptional activity. Results of mapping **(A**) DNA and **(B)** cDNA sequences to 122 gut microbial genomes and microbiome bins. The number of sequences assigned to 16S rRNA, 23S rRNA, 5S rRNA, CDS (coding sequences), tRNA, and ‘intergenic regions’ (includes mislabeled CDS and miscellaneous noncoding RNAs) was tallied. The combined percentage of assignments is shown as a pie chart above each graph. **(C)** The percentage of DNA sequencing reads that were mapped to CDS or were unmapped is plotted as a function of read length.

Turnbaugh *et al.*, Fig. S10

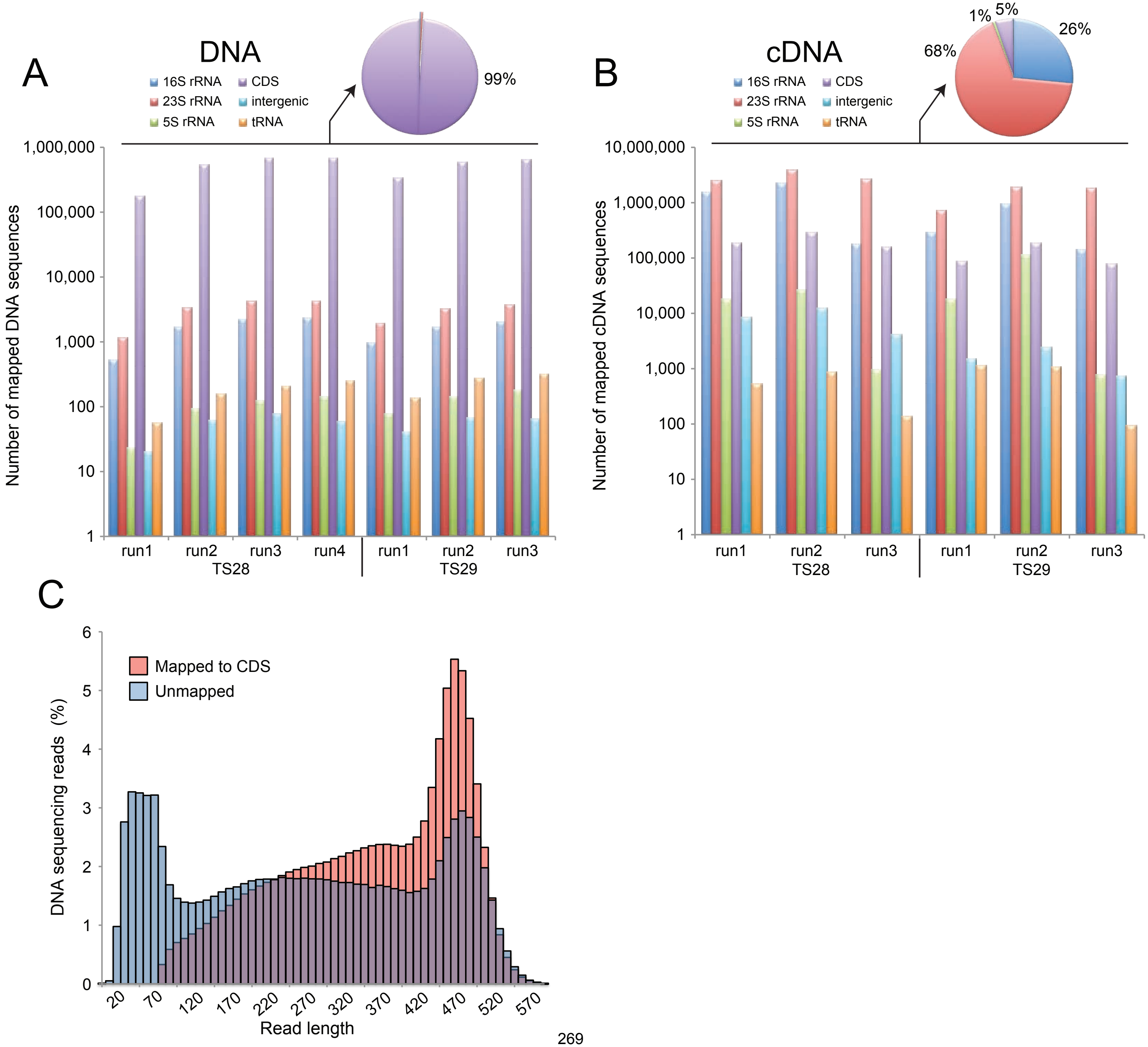


Fig. S11. The percentage of DNA and cDNA sequences mapped to 122 gut microbial genomes and microbiome bins. The percentage of (**A**) DNA or (**B**) cDNA sequences mapped to microbiome bins (blue), reference genomes (red), or equally well to both (green) is shown. The percentage of (**C**) DNA or (**D**) cDNA sequences mapped to TS28 bins (blue), TS29 bins (red), or equally well to both (green) is plotted. **(E)** The percentage of sequencing reads mapped to a database containing 122 gut genomes with (red) or without (blue) the microbiome bins is noted. Microbiome datasets from the fecal sampling of six adult female MZ twin-pairs and their mothers were analyzed (5).

Turnbaugh *et al.*, Fig. S11

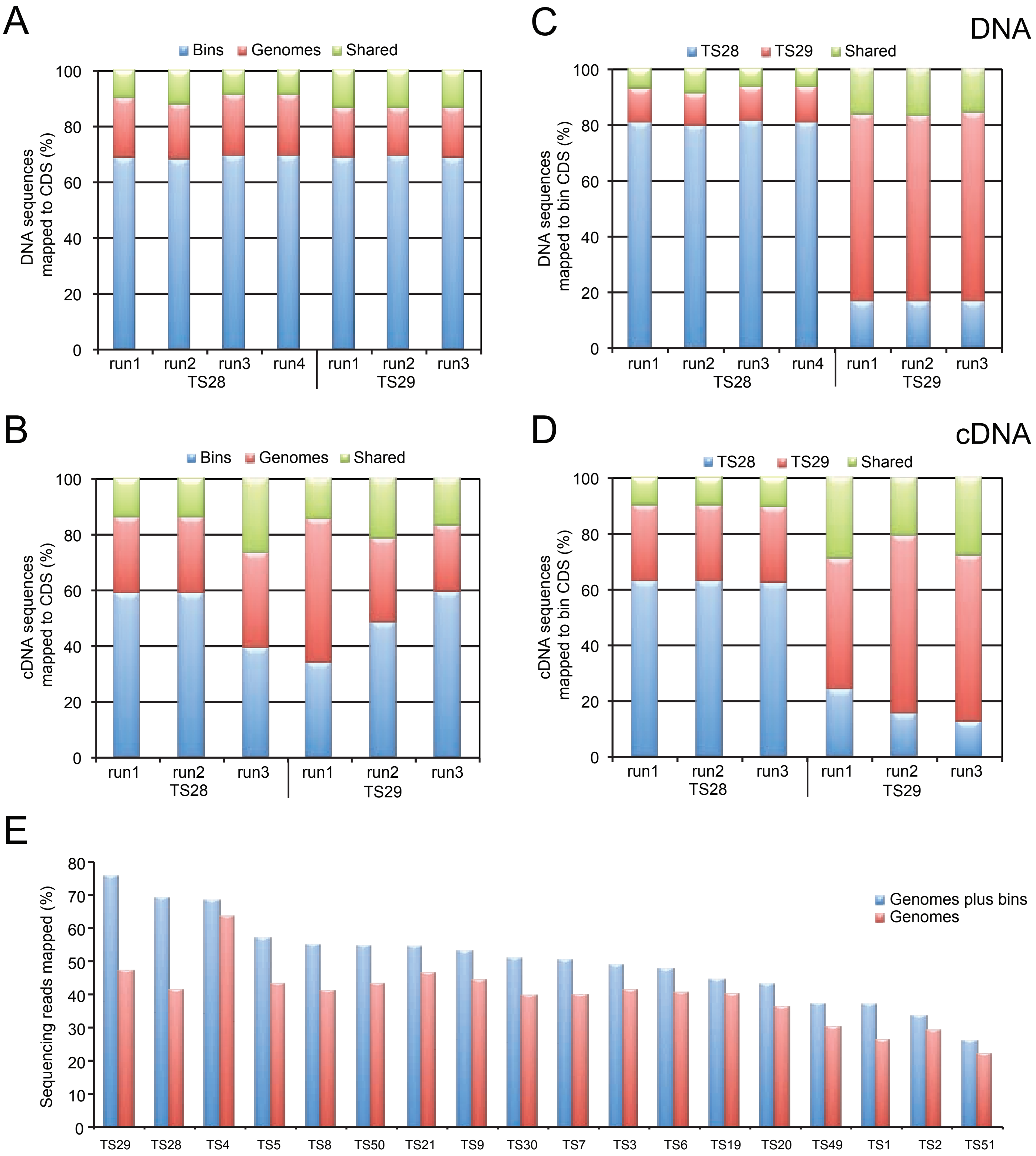


Fig. S12. Probability distribution of signal intensities for different lengths of homopolymer for the GS FLX implementation (homopolymer length marked on figure).

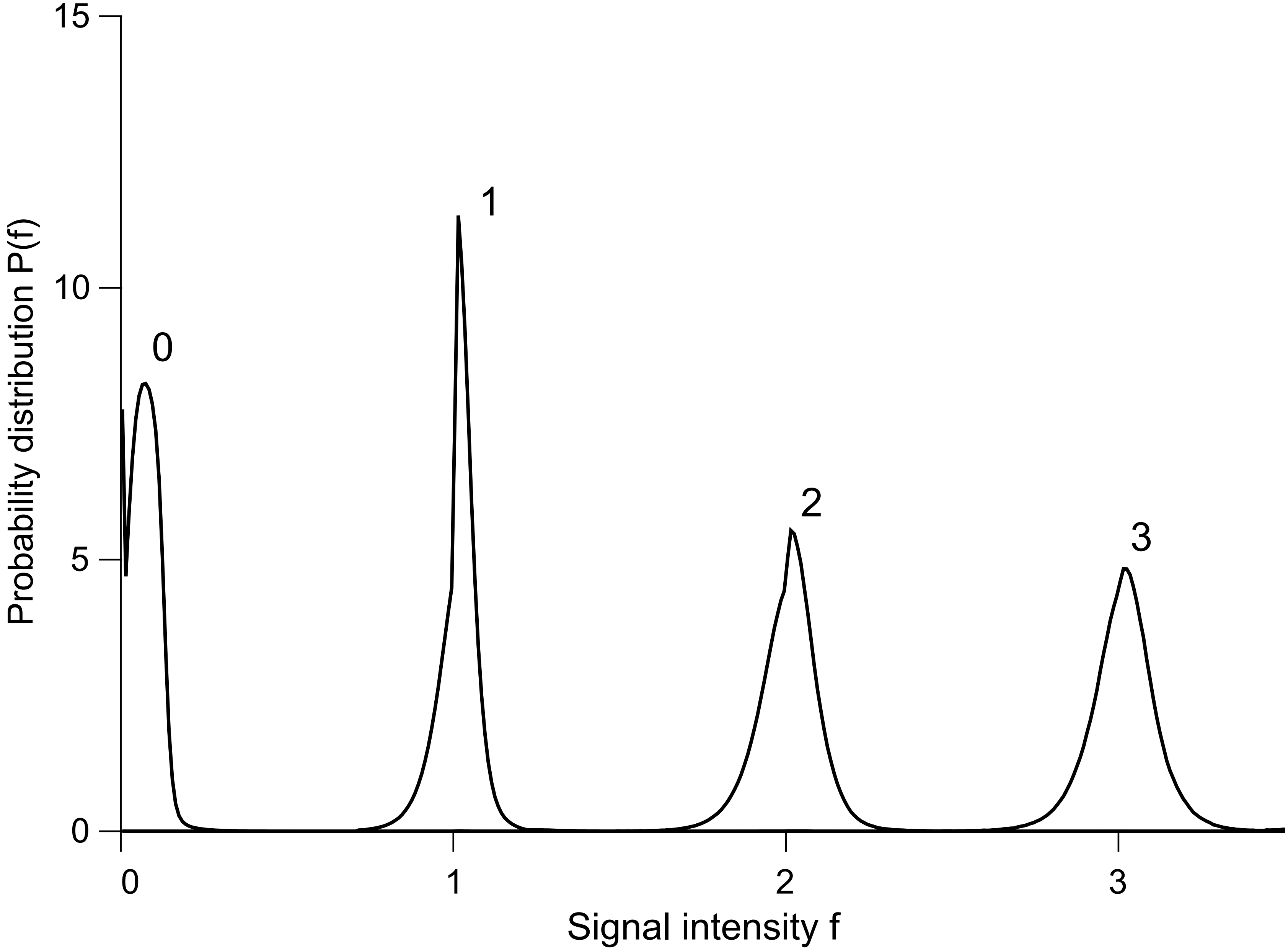

15
10
5
0
Probability distribution P(f)
0
1
2
3
0
1
2
3
Signal intensity f

Fig. S13. Number of phylotypes as a function of sequence difference for complete linkage clustering of the 'Artificial Community'. Distances were calculated using exact Needleman-Wunsch pairwise alignments. Results are shown for the filtered sequences and following removal of pyrosequencing and PCR noise.

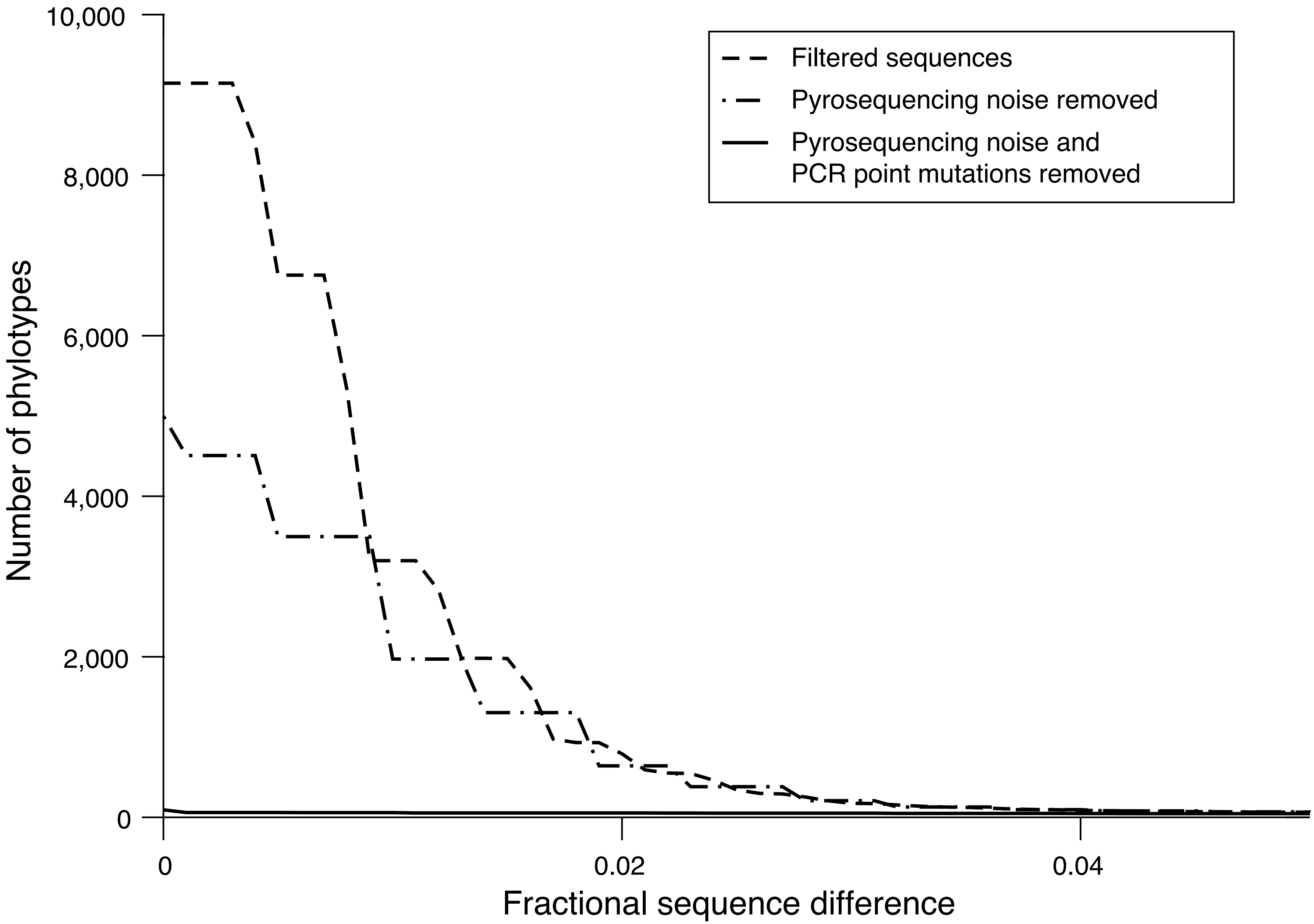

10,000
8,000
6,000
4,000
2,000
0
Number of phylotypes
0
0.02
0.04
Fractional sequence difference
Filtered sequences
Pyrosequencing noise removed
Pyrosequencing noise and
PCR point mutations removed

Fig. S14. The frequency-abundance distributions for sequences classified as ‘chimeric’ (open symbols) or ‘good’ (filled symbols) by logistic regression for the Uneven1 dataset. Values are prior to (circles) and after (squares) incorporating abundance information. The final maximum likelihood abundance distribution fits are also shown.

Turnbaugh *et al.*, Fig. S14

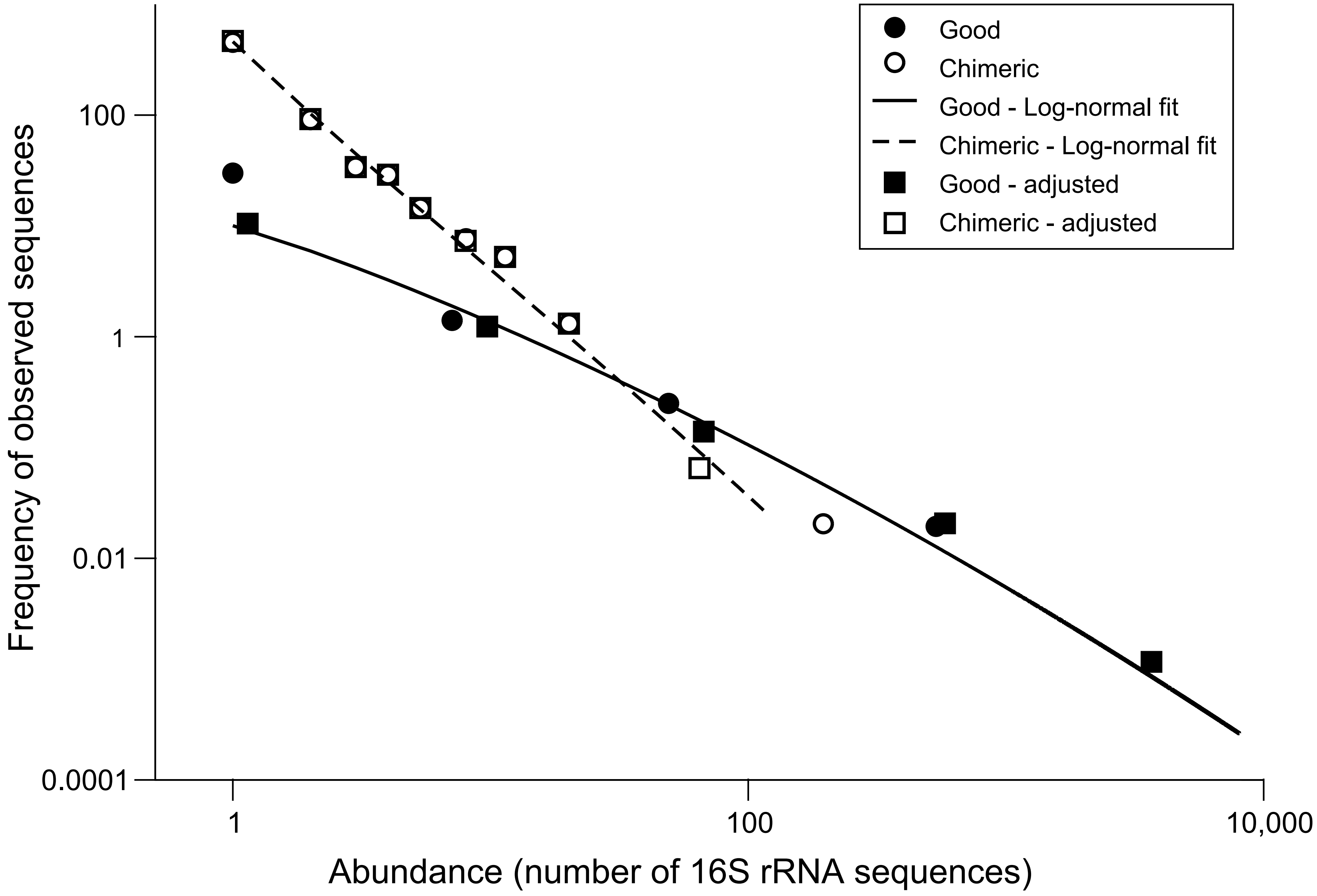


Fig. S15. Rarefaction curves for all three unevenly mixed mock communities. The 50% probability cut-off was used to classify sequences as chimeric. For comparison the total 97%ID phylotype richness in the control sequences is also shown (grey line).

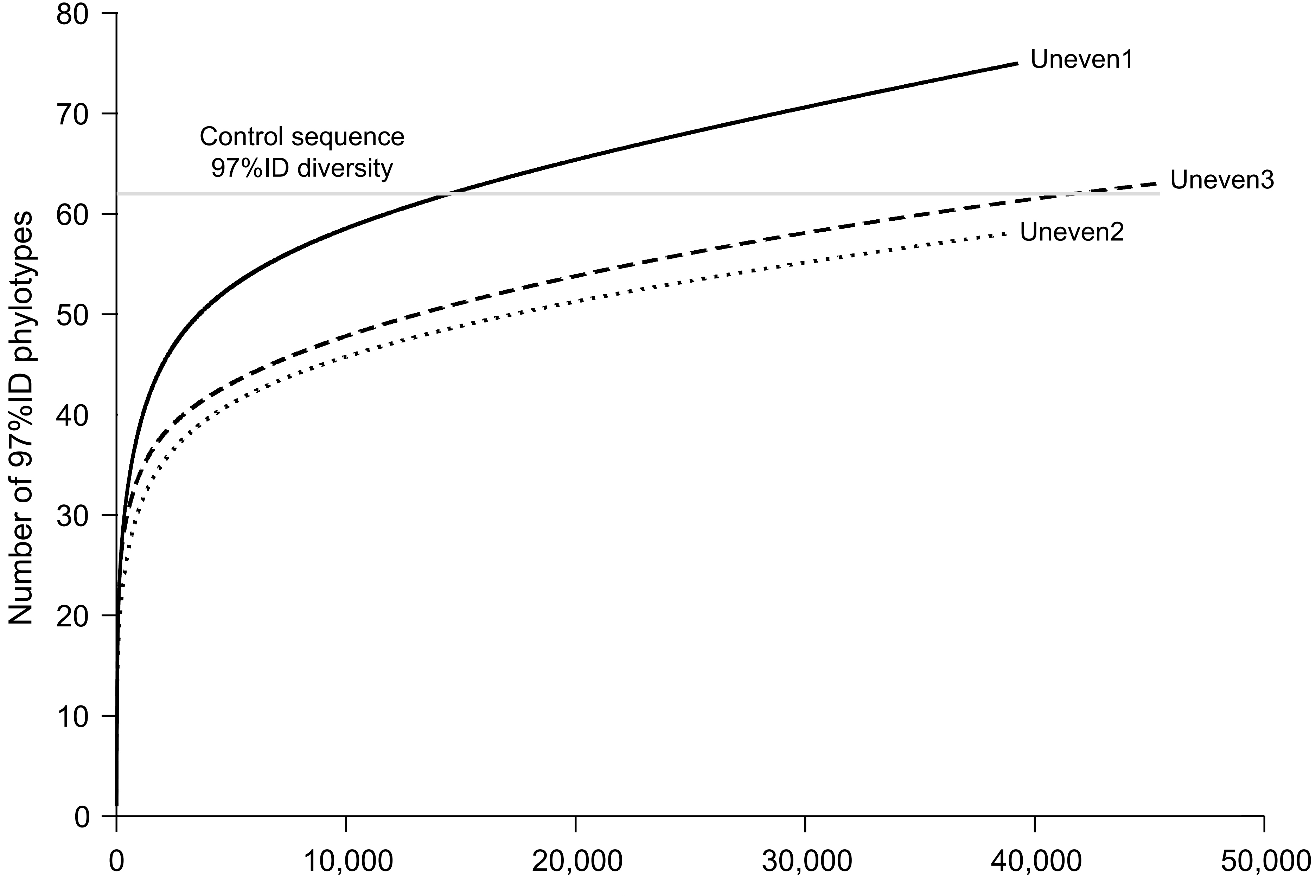

Number of 97%ID phylotypes
80
70
60
50
40
30
20
10
0
0
10,000
20,000
30,000
40,000
50,000
Number of 16S rRNA gene sequences
Control sequence
97%ID diversity
Uneven1
Uneven3
Uneven2

Fig. S16. Accuracy of phylotype construction for the ‘Artificial community’ dataset as a function of the percentage sequence difference. Regions represent phylotypes comprised of reference sequences and/or de-noised pyrosequencing reads.

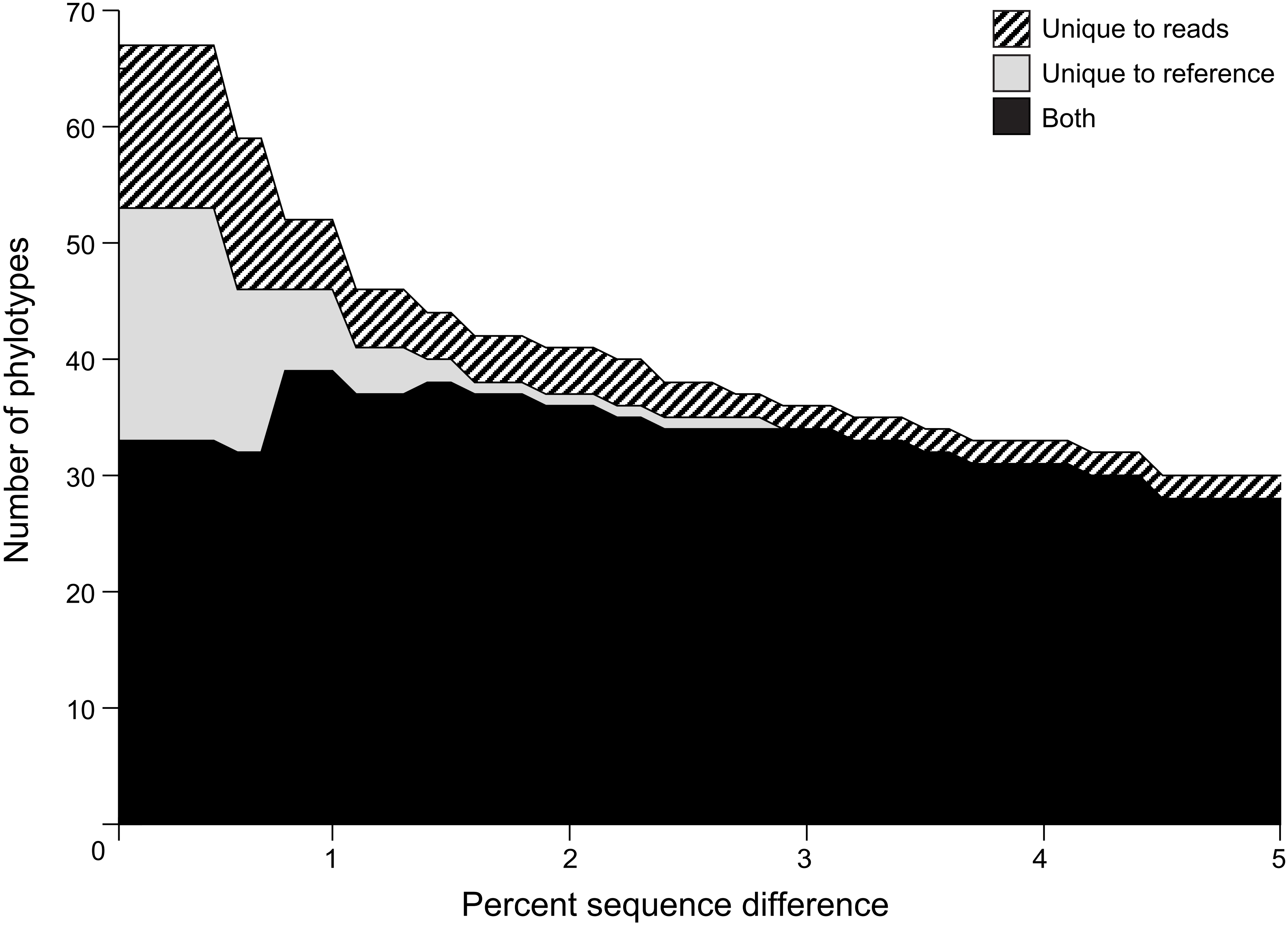

Unique to reads
Unique to reference
Both
Number of phylotypes
70
60
50
40
30
20
10
0
1
2
3
4
5
Percent sequence difference

Fig. S17. Correlation between the observed and the expected relative abundance of 97%ID phylotypes in the 'Artificial community'. The straight line gives the result of a linear regression forced through the origin which had R^2=0.96.

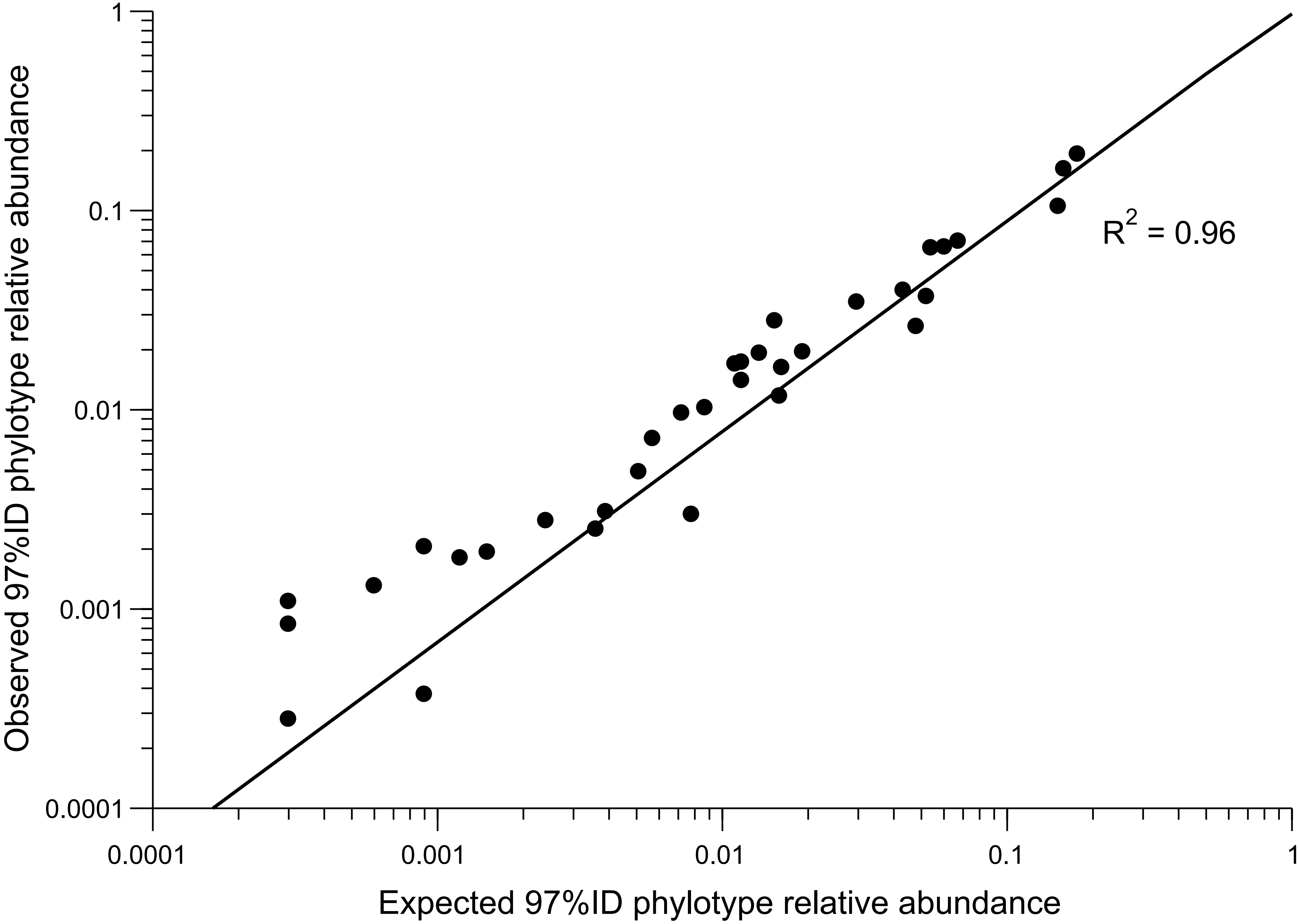

R^2 = 0.96
Observed 97%ID phylotype relative abundance
Expected 97%ID phylotype relative abundance
1
0.1
0.01
0.001
0.0001
0.0001
0.001
0.01
0.1
1

Fig. S18. Accuracy of phylotype construction for the ‘Uneven1’ dataset as a function of the percentage sequence difference. Regions represent phylotypes comprised of reference sequences and/or de-noised pyrosequencing reads.

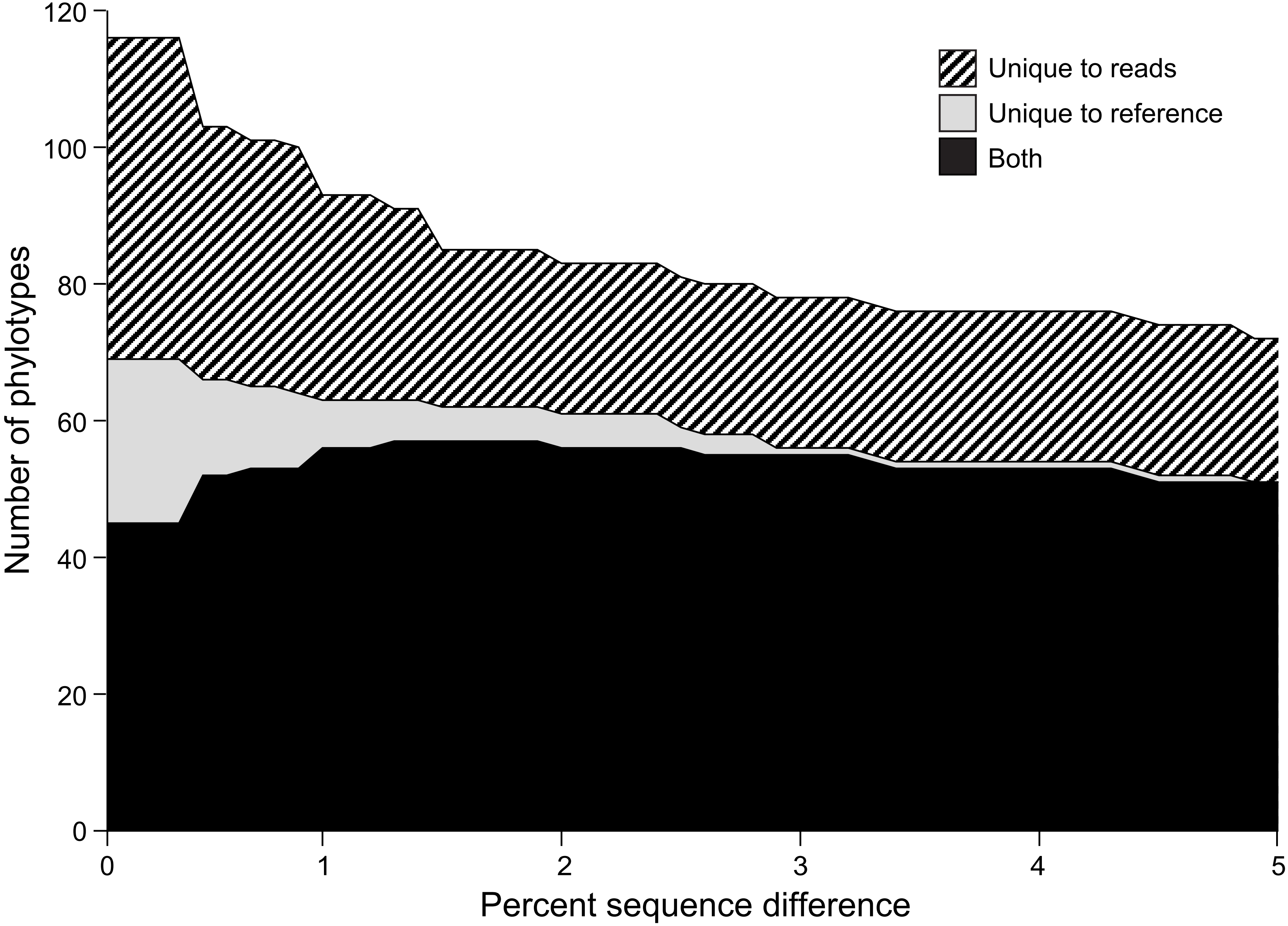

120
100
80
60
40
20
0
Number of phylotypes
0
1
2
3
4
5
Percent sequence difference
Unique to reads
Unique to reference
Both

Fig. S19. 97%ID phylotype rarefaction curves for the 'Deep Twins' datasets and two shallower datasets from the same fecal samples. The 50% probability cut-off was used to classify sequences as chimeric.

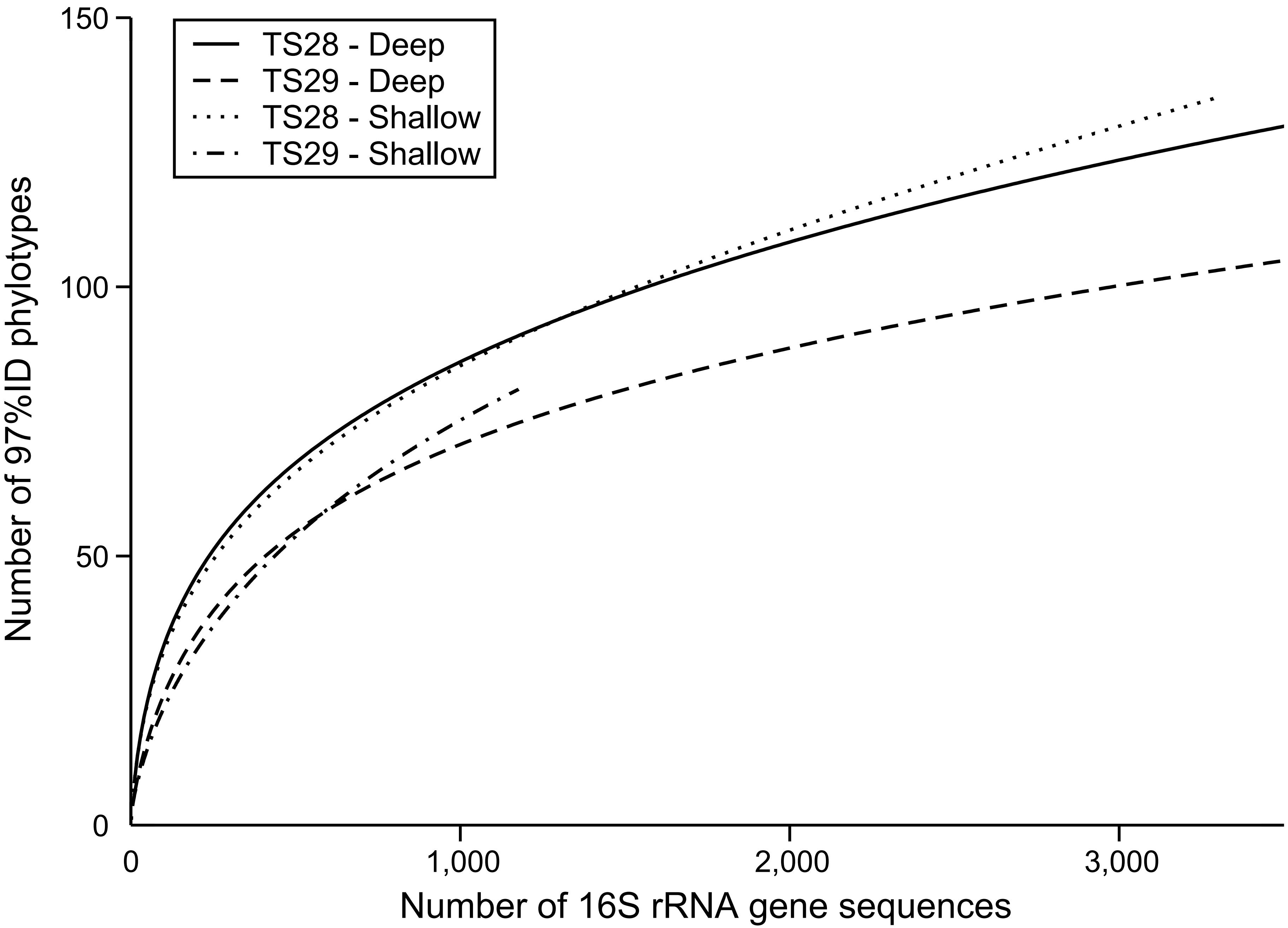

TS28 - Deep
TS29 - Deep
TS28 - Shallow
TS29 - Shallow
Number of 97%ID phylotypes
150
100
50
0
0
1,000
2,000
3,000
Number of 16S rRNA gene sequences

Fig. S20. The distribution of the relative abundance of shared 97%ID phylotypes in the 'Deep Twins' datasets. Relative abundance is calculated as the base 10 logarithm of the relative abundance in the fecal microbiota of TS29 divided by the relative abundance in the fecal microbiota of TS28.

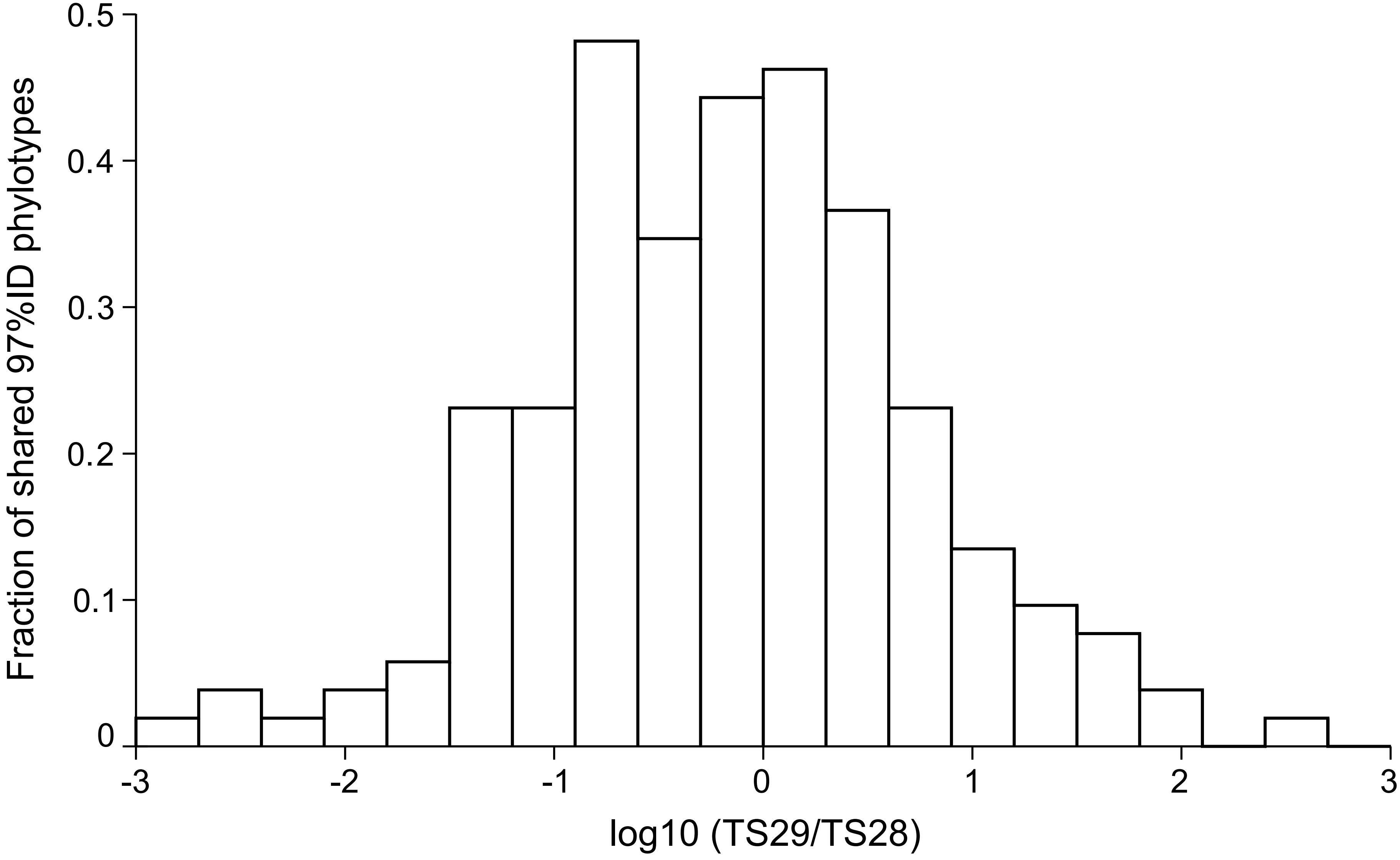
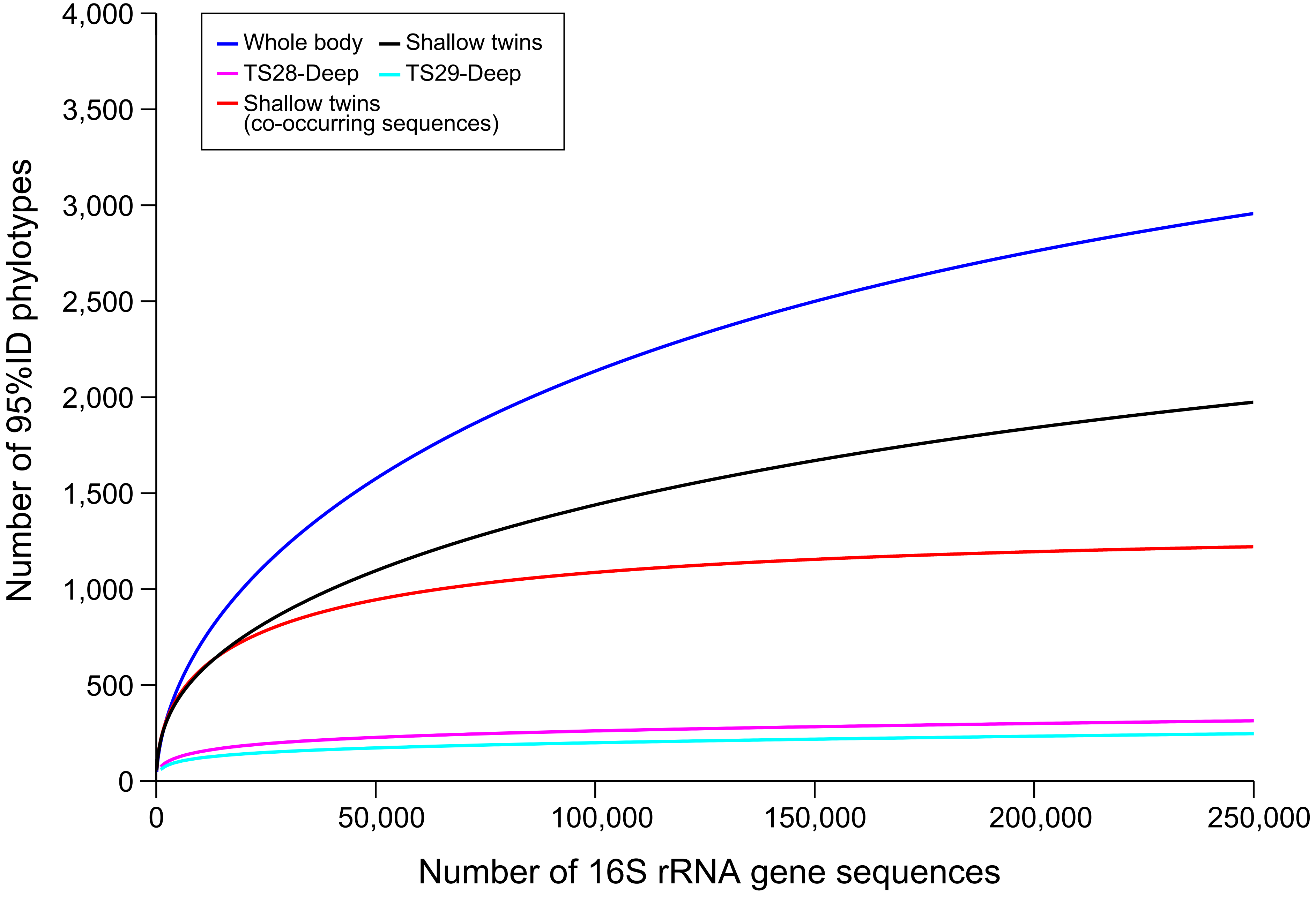

Fraction of shared 97%ID phylotypes
0.5
0.4
0.3
0.2
0.1
0
-3
-2
-1
0
1
2
3
log10 (TS29/TS28)

Fig. S21. Comparison of diversity within and between microbial communities. Curves at 95%ID phylotype cutoff are shown for 250 fecal (gut) samples taken from 146 individuals (‘Shallow twins’; 1,000 V2 16S rRNA gene sequences were randomly selected from each sample), 250 samples taken from multiple body habitats (‘Whole body’; 1,000 randomly selected sequences per sample), and the two deeply sequenced fecal samples (‘TS28-Deep’ and ‘TS29-Deep’). Phylotypes found in multiple fecal samples are labeled as ‘co-occuring.’


4,000
3,500
3,000
2,500
2,000
1,500
1,000
500
0
Number of 95%ID phylotypes
Whole body
Shallow twins
TS28-Deep
TS29-Deep
Shallow twins
(co-occurring sequences)
0
50,000
100,000
150,000
200,000
250,000
Number of 16S rRNA gene sequences

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